

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe
65 70 75 80
Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser
85 90 95
Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
100 105 110
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
115 120 125
Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His
130 135 140
Leu Val Phe Ala Ser Ala Trp Arg Tyr Ala Asp Leu Arg Lys Asp Phe
145 150 155 160
Asp Arg Lys Asp His His Ser
165

(2) INFORMATION FOR SEQ ID NO:1321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp
20 25 30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu
50 55 60
Ser Thr Leu His Leu Val Phe Ala Ser Ala Trp Arg Tyr Ala Asp Leu
65 70 75 80
Arg Lys Asp Phe Asp Arg Lys Asp His His Ser
85 90

(2) INFORMATION FOR SEQ ID NO:1322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1338
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:

ctctctcteggt gtctgcgcac tcttctctctt cttcttccaat ggcttttcgcg tttgagaaac 60
cataaaaagga aactttttcag agttttctctt tgtctctctgt gccgtgtatgt 120
tcactaaatt taggtttatc aatggagatg aaatgcacat ttcaatcaac tcgtgctcca 180
ttccaattgcg ctigtgtggtt occaaaattca atctattgga ctctcaaaga accaatcgtt 240
ttgaaaatac ctaattcact tgcctctttt aggtctatca gacacttgga gttgaaatct 300
gtagggttcat tgtacaatgt gtttgagatt cataggaag aagtcaattc aagctctttt 360
gaagtgaagc ctatgaacaa agatactgaa gctgatagt atagtgatag gaagattaaa 420
gaagagagaaa ggagaaggaa gattggatta gctaataagag gaaagggtgcc atggaacaaa 480
gggaggaacac acagtgaaga cactcgaaga cgaatcaagc agagaacaat cgaagctttg 540
acaaatcccca aggttcggaa gaagatgtcc gatcatcaac aaccacacag taatgaaac 600
aaggagaaga taagagcttc agtgaacaaa gtttgggcag aacggtccaag atcgaagcga 660

ttaaaggaga	agttcatgtc	tctgtgtgta	gaaaacattg	cagaagctgc	aaggaaaagga	720
ggaagtggcg	aggcagaact	tgactgggac	agctatgaaa	gaataaaaca	agatttttca	780
tctgagcagc	ttcagtttagc	tgaagagaaa	gcaagagcta	aggaacaaac	caagatgata	840
gcaaaagaag	ctgcaaaagc	caggaccgag	aagatgagga	gagccgcaga	aaaaaagaaa	900
gaacgtgagg	agaaagaccg	acgagaagga	aagattcgaa	agccaaaagca	ggaaggaggag	960
aatccaacca	ttgcttcacg	ttctaaacta	aagaagagac	taacaaagat	tcacaagaag	1020
aaaacaagtc	ttgtgtaaat	cgcaattgga	acggataggg	ttgtttcagt	tcgcagctaaa	1080
ctggagaaac	tggatttggg	tttgataaag	aaagagcgaa	caagaggaga	tatcttcact	1140
gctgatcaga	tccaagctgc	taagaaccaa	cgagggaagt	atgtttttatc	gagattttggt	1200
cttttttgcca	tgaaatcaat	ggattttgat	taactctttt	ctactcctag	tttatagagc	1260
tttctctttt	tttttcttgt	gccactaat	aaataaacia	gattgacttg	agatatataat	1320
aaataaataag	attgacgc					

(2) INFORMATION FOR SEQ ID NO:1323:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 410 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..410
(D) OTHER INFORMATION: / Ceres Seq. ID 1500058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:

Leu	Ser	Ser	Cys	Leu	Arg	Thr	Leu	Leu	Leu	Leu	Gln	Trp	Leu	Ser
1			5				10				15			
Arg	Leu	Arg	Asn	His	Lys	Arg	Lys	Leu	Phe	Arg	Val	Phe	Ser	Cys
			20				25				30			
Leu	Phe	Val	Ser	Val	Pro	Cys	Met	Ser	Leu	Asn	Leu	Gly	Leu	Met
			35				40				45			
Glu	Met	Lys	Cys	Thr	Phe	Gln	Ser	Thr	Arg	Ala	Pro	Phe	Gln	Cys
			50				55				60			
Trp	Trp	Phe	Pro	Asn	Ser	Ile	Tyr	Trp	Thr	Leu	Lys	Glu	Pro	Ile
							70				75			
Leu	Lys	Ile	Pro	Asn	Ser	Leu	Ala	Ser	Leu	Arg	Ser	Ile	Arg	His
							85				90			
Glu	Leu	Lys	Ser	Val	Gly	Ser	Leu	Tyr	Asn	Val	Phe	Glu	Ile	His
							100				105			
Lys	Glu	Val	Asn	Ser	Ser	Leu	Leu	Glu	Val	Lys	Ala	Met	Asn	Lys
							110				115			
Thr	Glu	Ala	Asp	Ser	Asp	Ser	Asp	Arg	Lys	Ile	Lys	Glu	Glu	Arg
							120				125			
Arg	Arg	Lys	Ile	Gly	Leu	Ala	Asn	Arg	Gly	Lys	Val	Pro	Trp	Asn
							130				135			
Gly	Arg	Lys	His	Ser	Glu	Asp	Thr	Arg	Arg	Arg	Ile	Lys	Gln	Arg
							140				145			
Ile	Glu	Ala	Leu	Thr	Asn	Pro	Lys	Val	Arg	Lys	Lys	Met	Ser	Asp
							150				155			
Gln	Gln	Pro	His	Ser	Asn	Glu	Thr	Lys	Glu	Lys	Ile	Arg	Ala	Ser
							160				165			
Lys	Gln	Val	Trp	Ala	Glu	Arg	Ser	Arg	Ser	Lys	Arg	Leu	Lys	Glu
							170				175			
Phe	Met	Ser	Ser	Trp	Ser	Glu	Asn	Ile	Ala	Glu	Ala	Ala	Arg	Lys
							180				185			
Gly	Ser	Gly	Glu	Ala	Glu	Leu	Asp	Trp	Asp	Ser	Tyr	Glu	Arg	Ile
							190				195			
Gln	Asp	Phe	Ser	Ser	Glu	Gln	Leu	Gln	Leu	Ala	Glu	Glu	Lys	Ala
							200				205			
Ala	Lys	Glu	Gln	Thr	Lys	Met	Ile	Ala	Lys	Glu	Ala	Ala	Lys	Ala
							210				215			
Thr	Glu	Lys	Met	Arg	Arg	Ala	Ala	Glu	Lys	Lys	Glu	Arg	Glu	Glu
							220				225			

290	295	300
Lys Asp Arg Arg Glu Gly Lys Ile Arg Lys Pro Lys Gln Glu Arg Glu		
305	310	315
Asn Pro Thr Ile Ala Ser Arg Ser Lys Leu Lys Lys Arg Leu Thr Lys		
	325	335
Ile His Lys Lys Lys Thr Ser Leu Gly Lys Ile Ala Ile Gly Thr Asp		
	340	350
Arg Val Val Ser Val Ala Ala Lys Leu Glu Lys Leu Asp Leu Asp Leu		
	355	365
Ile Arg Lys Glu Arg Thr Arg Gly Asp Ile Ser Leu Ala Asp Gln Ile		
	370	380
Gln Ala Ala Lys Asn Gln Arg Gly Ser Asp Val Leu Ser Arg Phe Gly		
385	390	400
Leu Phe Ala Met Lys Ser Met Asp Phe Asp		
	405	410

(2) INFORMATION FOR SEQ ID NO:1324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..371

(D) OTHER INFORMATION: / Ceres Seq. ID 1500059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:

Met Ser Leu Asn Leu Gly Leu Ser Met Glu Met Lys Cys Thr Phe Gln	
1	5
Ser Thr Arg Ala Pro Phe Gln Cys Ala Trp Trp Phe Pro Asn Ser Ile	10
	20
Tyr Trp Thr Leu Lys Glu Pro Ile Val Leu Lys Ile Pro Asn Ser Leu	25
	30
Ala Ser Leu Arg Ser Ile Arg His Leu Glu Leu Lys Ser Val Gly Ser	35
	40
Leu Tyr Asn Val Phe Glu Ile His Arg Lys Glu Val Asn Ser Ser Leu	45
	50
Leu Glu Val Lys Ala Met Asn Lys Asp Thr Glu Ala Asp Ser Asp Ser	55
	60
Asp Arg Lys Ile Lys Glu Glu Glu Arg Arg Arg Lys Ile Gly Leu Ala	65
	70
Asn Arg Gly Lys Val Pro Trp Asn Lys Gly Arg Lys His Ser Glu Asp	75
	80
Thr Arg Arg Arg Ile Lys Gln Arg Thr Ile Glu Ala Leu Thr Asn Pro	85
	90
Lys Val Arg Lys Lys Met Ser Asp His Gln Gln Pro His Ser Asn Glu	95
	100
Thr Lys Glu Lys Ile Arg Ala Ser Val Lys Gln Val Trp Ala Glu Arg	105
	110
Ser Arg Ser Lys Arg Leu Lys Glu Lys Phe Met Ser Ser Trp Ser Glu	115
	120
Asn Ile Ala Glu Ala Ala Arg Lys Gly Gly Ser Gly Glu Ala Glu Leu	125
	130
Asp Trp Asp Ser Tyr Glu Arg Ile Lys Gln Asp Phe Ser Ser Glu Gln	135
	140
Leu Gln Leu Ala Glu Glu Lys Ala Arg Ala Lys Glu Gln Thr Lys Met	145
	150
Ile Ala Lys Glu Ala Ala Lys Ala Arg Thr Glu Lys Met Arg Arg Ala	155
	160
Ala Glu Lys Lys Lys Glu Arg Glu Glu Lys Asp Arg Arg Glu Gly Lys	165
	170
	175
	180
	185
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	200
	205
	210
	215
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	245
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	255
	260
	265
	270

Ile	Arg	Lys	Pro	Lys	Gln	Glu	Arg	Glu	Asn	Pro	Thr	Ile	Ala	Ser	Arg
	275						280					285			
Ser	Lys	Leu	Lys	Lys	Arg	Leu	Thr	Lys	Ile	His	Lys	Lys	Lys	Thr	Ser
	290					295				300					
Leu	Gly	Lys	Ile	Ala	Ile	Gly	Thr	Asp	Arg	Val	Val	Ser	Val	Ala	Ala
	305				310				315					320	
Lys	Leu	Glu	Lys	Leu	Asp	Leu	Asp	Leu	Ile	Arg	Lys	Glu	Arg	Thr	Arg
			325					330						335	
Gly	Asp	Ile	Ser	Leu	Ala	Asp	Gln	Ile	Gln	Ala	Ala	Lys	Asn	Gln	Arg
			340					345					350		
Gly	Ser	Asp	Val	Leu	Ser	Arg	Phe	Gly	Leu	Phe	Ala	Met	Lys	Ser	Met
		355					360					365			
Asp	Phe	Asp													
	370														

(2) INFORMATION FOR SEQ ID NO:1325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..363
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:

Met	Glu	Met	Lys	Cys	Thr	Phe	Gln	Ser	Thr	Arg	Ala	Pro	Phe	Gln	Cys
1			5					10					15		
Ala	Trp	Trp	Phe	Pro	Asn	Ser	Ile	Tyr	Trp	Thr	Leu	Lys	Glu	Pro	Ile
			20				25					30			
Val	Leu	Lys	Ile	Pro	Asn	Ser	Leu	Ala	Ser	Leu	Arg	Ser	Ile	Arg	His
		35				40				45					
Leu	Glu	Leu	Lys	Ser	Val	Gly	Ser	Leu	Tyr	Asn	Val	Phe	Glu	Ile	His
	50				55					60					
Arg	Lys	Glu	Val	Asn	Ser	Ser	Leu	Leu	Glu	Val	Lys	Ala	Met	Asn	Lys
	65			70					75					80	
Asp	Thr	Glu	Ala	Asp	Ser	Asp	Ser	Asp	Arg	Lys	Ile	Lys	Glu	Glu	Glu
			85					90					95		
Arg	Arg	Arg	Lys	Ile	Gly	Leu	Ala	Asn	Arg	Gly	Lys	Val	Pro	Trp	Asn
			100					105					110		
Lys	Gly	Arg	Lys	His	Ser	Glu	Asp	Thr	Arg	Arg	Arg	Ile	Lys	Gln	Arg
		115				120						125			
Thr	Ile	Glu	Ala	Leu	Thr	Asn	Pro	Lys	Val	Arg	Lys	Lys	Met	Ser	Asp
	130				135					140					
His	Gln	Gln	Pro	His	Ser	Asn	Glu	Thr	Lys	Glu	Lys	Ile	Arg	Ala	Ser
	145				150					155				160	
Val	Lys	Gln	Val	Trp	Ala	Glu	Arg	Ser	Arg	Ser	Lys	Arg	Leu	Lys	Glu
			165					170					175		
Lys	Phe	Met	Ser	Ser	Trp	Ser	Glu	Asn	Ile	Ala	Glu	Ala	Ala	Arg	Lys
		180						185					190		
Gly	Gly	Ser	Gly	Glu	Ala	Glu	Leu	Asp	Trp	Asp	Ser	Tyr	Glu	Arg	Ile
		195					200					205			
Lys	Gln	Asp	Phe	Ser	Ser	Glu	Gln	Leu	Gln	Leu	Ala	Glu	Glu	Lys	Ala
	210					215				220					
Arg	Ala	Lys	Glu	Gln	Thr	Lys	Met	Ile	Ala	Lys	Glu	Ala	Ala	Lys	Ala
	225				230					235				240	
Arg	Thr	Glu	Lys	Met	Arg	Arg	Ala	Ala	Glu	Lys	Lys	Lys	Glu	Arg	Glu
			245					250					255		
Glu	Lys	Asp	Arg	Arg	Glu	Gly	Lys	Ile	Arg	Lys	Pro	Lys	Gln	Glu	Arg
		260						265					270		
Glu	Asn	Pro	Thr	Ile	Ala	Ser	Arg	Ser	Lys	Leu	Lys	Lys	Arg	Leu	Thr

275					280					285					
Lys	Ile	His	Lys	Lys	Lys	Thr	Ser	Leu	Gly	Lys	Ile	Ala	Ile	Gly	Thr
290					295					300					
Asp	Arg	Val	Val	Ser	Val	Ala	Ala	Lys	Leu	Glu	Lys	Leu	Asp	Leu	Asp
305					310					315					
Leu	Ile	Arg	Lys	Glu	Arg	Thr	Arg	Gly	Asp	Ile	Ser	Leu	Ala	Asp	Gln
320					325					330					
Ile	Gln	Ala	Ala	Lys	Asn	Gln	Arg	Gly	Ser	Asp	Val	Leu	Ser	Arg	Phe
335					340					345					
Gly	Leu	Phe	Ala	Met	Lys	Ser	Met	Asp	Phe	Asp					
350					355					360					

(2) INFORMATION FOR SEQ ID NO:1326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1367
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:

ccaattcttaa	accaaacac	agattctcat	aatcatctct	tcttttttcc	tctttacgaa	60
aagaagaaa	atcaaacctt	ccaagtaate	attttctttt	tctctctcac	acacacacat	120
tcactagttt	tagctttcac	aaatgtgac	taacttcatt	tacctatatg	cagggtttaca	180
caaaaagaaa	aaagaacgat	ggctcttgtc	accttcttgt	ttattgttac	ccttggagca	240
atgacgtcac	atgtcaatgg	tacgcgcgga	ggaggttgga	tcaacgcaca	cgccacattc	300
tacggtgtgt	gtgatgtctt	cggcacaaat	ggaggtgtct	gtggatcagg	aaacctatat	360
agccaaagct	atggaaccaa	cacggcgccg	ctaagcacgg	ctctattcaa	taatggctta	420
agtttgttgt	cttgcttoga	gataaagatg	caaaacgatg	gaaaatgtgt	tcttctctgg	480
tcaattgtcg	tacacgccac	aaacttttgc	cctcctaaca	acgccttacc	gaacaacgca	540
ggaggtttgg	tgtaaccctc	ctcagcagca	ttttgatctc	tctcagcccg	tatttcaacg	600
catcgctcaa	tacagagccg	gcattgtccc	cgctcgcttac	cgaagagtgc	cgtgcgtgag	660
aagaggagga	atacgtttac	gataaacgga	cactcttact	tcaacctagt	tctgattact	720
aacgtcggag	gagccggaga	tgttcaactca	gcgatggtta	aaggttcaag	aactggatgg	780
caagcgatgt	caagaaactg	gggacagaac	tggcagagta	actcttacct	taacggacaa	840
ttctctgtcat	tcaaaagtcac	aacaagcgat	ggccaaacca	ttgtctctaa	caacgtcgct	900
aacgcaggct	ggctcttttg	ccagaccttc	accggtgcgc	agctacgtta	ggaagagtga	960
ttcggtgaaa	attcatctca	ttgatcgtgt	ggatttgacg	tggttgtagta	gaagcagtta	1020
gagagagggg	catgatagta	atttggtoct	ttctttcaat	tgaggtttac	ctaaaagaag	1080
gtggtgtctc	gagtgcttga	ttttgcacga	ggccttgatg	atgtcatctt	ttgggaacct	1140
tttcttatct	ttcttcatct	ttattggtaa	ggttttatgt	tatactagtg	cagaggtggg	1200
attgagttga	agtaccaccc	gctagtagta	gtagtctctc	atgtcatctt	tatccctctt	1260
cgaagcgaga	gggagagttt	tagattttta	ttaatctcgt	taaaagtcatt	tgtagttgtg	1320
aaatttttca	atttttcaaa	gtaagaata	ttggagattt	gtttgttt		

(2) INFORMATION FOR SEQ ID NO:1327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:

Met	Ala	Leu	Val	Thr	Phe	Leu	Phe	Ile	Ala	Thr	Leu	Gly	Ala	Met	Thr
1			5					10				15			
Ser	His	Val	Asn	Gly	Tyr	Ala	Gly	Gly	Gly	Trp	Val	Asn	Ala	His	Ala

20 25 30
Thr Phe Tyr Gly Gly Gly Asp Ala Ser Gly Thr Met Gly Gly Ala Cys
35 40 45
Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn Thr Ala Ala
50 55 60
Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala Cys Phe
65 70 75 80
Glu Ile Arg Cys Gln Asn Asp Gly Lys Trp Cys Leu Pro Gly Ser Ile
85 90 95
Val Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro Asn
100 105 110
Asn Ala Gly Gly Leu Val
115

(2) INFORMATION FOR SEQ ID NO:1328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

Met Thr Ser His Val Asn Gly Tyr Ala Gly Gly Gly Trp Val Asn Ala
1 5 10 15
His Ala Thr Phe Tyr Gly Gly Gly Asp Ala Ser Gly Thr Met Gly Gly
20 25 30
Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn Thr
35 40 45
Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala
50 55 60
Cys Phe Glu Ile Arg Cys Gln Asn Asp Gly Lys Trp Cys Leu Pro Gly
65 70 75 80
Ser Ile Val Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Asn Ala Leu
85 90 95
Pro Asn Asn Ala Gly Gly Leu Val
100

(2) INFORMATION FOR SEQ ID NO:1329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:

Met Phe Thr Gln Arg Trp Leu Lys Val Gln Glu Leu Asp Gly Lys Arg
1 5 10 15
Cys Gln Glu Thr Gly Asp Arg Thr Gly Arg Val Thr Leu Thr Thr
20 25 30
Asp Asn Leu Cys His Ser Lys Ser Gln Gln Ala Met Ala Lys Pro Leu
35 40 45
Ser Leu Thr Thr Ser Leu Thr Gln Ala Gly Leu Leu Ala Arg Pro Ser
50 55 60
Pro Val Arg Ser Tyr Val Arg Lys Ser Asp Ser Val Lys Ile His Leu
65 70 75 80

Ile Asp Arg Val Val Leu Thr Cys Cys Ser Arg Ser Ser
85 90

(2) INFORMATION FOR SEQ ID NO:1330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1676

(D) OTHER INFORMATION: / Ceres Seq. ID 1500069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:

aagattttatt	ataaactcct	ttttttttta	aattcaagag	atatcaaaca	actacttcat	60
tttttttttt	ttgtagcagc	cgagtagctt	tttttgacgg	gttccgtggt	cgtgcttggt	120
ctgaaattga	cgaaaaatat	tccgacaaga	caacaacaac	aattagagag	attcagacaa	180
gggatttgaa	attcgagaga	tggtttggat	ccaaagcaga	cgtgatttaa	cgatggagct	240
acaatctcag	attccgattc	tccgtccaag	catccacgca	agacgagcca	acatcgctgt	300
taaattccag	gacttgtacg	gtttcacggt	ggaaggaaat	gtcgacgacg	ttaatgtgtt	360
gaacgagagt	agagagaaaag	tcaggaaatca	aggacgagtt	tggtggggctc	ttgaagctag	420
caaaaggagt	aattgggtatc	ttcagccgga	gattctcttg	atcggtgacg	gtatcgcttt	480
gaaaacttct	ctcaagctct	ccactttgac	taatgcgatt	acgttgaaga	gattgattcg	540
gaaagggatc	cctcctgtgc	ttagacctaa	gggttgggtt	tctctttctg	gtgctgctaa	600
gaagaaatcc	accgtccccag	agagtattata	tagtgatttg	acccaagccg	tcgaagggat	660
gggtcagccg	gtcacgagcg	agattgatca	tgatctgcca	cgtagctttcc	caggccattcc	720
atggtttgac	actccggaga	gtcatgctgc	tctacgacgt	gtgcttggtt	ggatttccct	780
tcgtgattca	gatgttggct	attgtcaggg	tctaaaacta	gttcgacggt	tactattact	840
gtgtcatga	acagaaagaag	acgcatctct	gatgctagcg	gtccttttgg	aaaaacgtatt	900
agtcctgtat	tggttaacaca	ccaacttata	tggatgtcat	gttgagcagc	gggttttcaa	960
agatttgcct	gcccaaaaat	gttctcgaat	agctactcat	cttgaagata	tgggctttga	1020
tgtttccctt	gtagccactg	aattggtttt	atgcctcttc	tctaaaagcc	ttcctctaga	1080
gacaactcta	aggggtgtgg	atgtactttt	ctatgaagga	gcgaaggttg	tattccatgc	1140
agcttttagca	atattacaaga	tgaaagagaa	cgagctgtct	atgacccacc	aggtcgggca	1200
tgttatcaac	dtattacaga	aaacttcaca	ccagcttttt	gaocccgatg	aattattaac	1260
gggtggcattt	gagaaaaatc	gatcaatgac	taccaaacac	atatcaaaag	agaggaagaa	1320
gcaggaacca	gcagtgtatg	cagaacttga	ccagagactt	cgagactta	actctcttaa	1380
agaaagtggg	aagagcacat	aaataaaaaa	gaactgttgg	gagaagatga	gcaaaaaagt	1440
gcaaacgagg	gagttccaaca	atggttttatt	tatccctctt	gatgtttttt	tttttttttc	1500
ctttttttct	aagtataatt	aaataggatt	ttttaagttt	atttttgagag	caaaacattca	1560
accaagatcc	atttctgaga	tgggaaatgt	caagtttctt	cacattccaa	gaggtgtcac	1620
ttgccttttg	cattttttac	ccctcttcat	atatcaattg	tgatcttcat	gttttt	

(2) INFORMATION FOR SEQ ID NO:1331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..400

(D) OTHER INFORMATION: / Ceres Seq. ID 1500070

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:

Met	Phe	Gly	Ile	Gln	Ser	Arg	Arg	Asp	Leu	Thr	Met	Glu	Leu	Gln	Ser
1			5						10					15	
Gln	Ile	Pro	Ile	Leu	Arg	Pro	Ser	Ile	His	Ala	Arg	Arg	Ala	Asn	Ile
			20					25					30		
Val	Val	Lys	Phe	Gln	Asp	Leu	Tyr	Gly	Phe	Thr	Val	Glu	Gly	Asn	Val
		35					40					45			
Asp	Asp	Val	Asn	Val	Leu	Asn	Glu	Val	Arg	Glu	Lys	Val	Arg	Asn	Gln

50	55	60
Gly Arg Val Trp Trp Ala Leu Glu Ala Ser Lys Gly Ala Asn Trp Tyr		
65	70	75
Leu Gln Pro Glu Ile Leu Leu Ile Gly Asp Gly Ile Ala Leu Lys Thr		80
	85	90
Ser Leu Lys Leu Ser Thr Leu Thr Asn Ala Ile Thr Leu Lys Arg Leu		95
	100	105
Ile Arg Lys Gly Ile Pro Pro Val Leu Arg Pro Lys Val Trp Phe Ser		110
	115	120
Leu Ser Gly Ala Ala Lys Lys Lys Ser Thr Val Pro Glu Ser Tyr Tyr		125
	130	135
Ser Asp Leu Thr Lys Ala Val Glu Gly Met Val Thr Pro Ala Thr Arg		140
	145	150
Gln Ile Asp His Asp Leu Pro Arg Thr Phe Pro Gly His Pro Trp Leu		155
	155	160
Asp Thr Pro Glu Gly His Ala Ala Leu Arg Arg Val Leu Val Gly Tyr		165
	165	170
Ser Phe Arg Asp Ser Asp Val Gly Tyr Cys Gln Gly Leu Asn Tyr Val		175
	180	185
Ala Ala Leu Leu Leu Leu Val Met Lys Thr Glu Glu Asp Ala Phe Trp		190
	195	200
Met Leu Ala Val Leu Leu Glu Asn Val Leu Val Arg Asp Cys Tyr Thr		205
	210	215
Thr Asn Leu Ser Gly Cys His Val Glu Gln Arg Val Phe Lys Asp Leu		220
	225	230
Leu Ala Gln Lys Cys Ser Arg Ile Ala Thr His Leu Glu Asp Met Gly		235
	245	250
Phe Asp Val Ser Leu Val Ala Thr Glu Trp Phe Leu Cys Leu Phe Ser		255
	260	265
Lys Ser Leu Pro Ser Glu Thr Thr Leu Arg Val Trp Asp Val Leu Phe		270
	275	280
Tyr Glu Gly Ala Lys Val Leu Phe His Ala Ala Leu Ala Ile Phe Lys		285
	290	295
Met Lys Glu Asn Glu Leu Leu Met Thr His Gln Val Gly Asp Val Ile		300
	305	310
Asn Xaa Leu Gln Lys Thr Ser His Gln Leu Phe Asp Pro Asp Glu Leu		315
	325	330
Leu Thr Val Ala Phe Glu Lys Ile Gly Ser Met Thr Thr Asn Thr Ile		335
	340	345
Ser Lys Gln Arg Lys Lys Gln Glu Pro Ala Val Met Ala Glu Leu Asp		350
	355	360
Gln Arg Leu Arg Arg Leu Asn Ser Leu Lys Glu Ser Gly Lys Ser Thr		365
	370	375
	385	390
		395
		400

(2) INFORMATION FOR SEQ ID NO:1332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..389
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:

Met Glu Leu Gln Ser Gln Ile Pro Ile Leu Arg Pro Ser Ile His Ala		
1	5	10
Arg Arg Ala Asn Ile Val Val Lys Phe Gln Asp Leu Tyr Gly Phe Thr		15
	20	25
		30

Val Glu Gly Asn Val Asp Asp Val Asn Val Leu Asn Glu Val Arg Glu
35 40 45
Lys Val Arg Asn Gln Gly Arg Val Trp Trp Ala Leu Glu Ala Ser Lys
50 55 60
Gly Ala Asn Trp Tyr Leu Gln Pro Glu Ile Leu Leu Ile Gly Asp Gly
65 70 75 80
Ile Ala Leu Lys Thr Ser Leu Lys Leu Ser Thr Leu Thr Asn Ala Ile
85 90 95
Thr Leu Lys Arg Leu Ile Arg Lys Gly Ile Pro Pro Val Leu Arg Pro
100 105 110
Lys Val Trp Phe Ser Leu Ser Gly Ala Ala Lys Lys Lys Ser Thr Val
115 120 125
Pro Glu Ser Tyr Tyr Ser Asp Leu Thr Lys Ala Val Glu Gly Met Val
130 135 140
Thr Pro Ala Thr Arg Gln Ile Asp His Asp Leu Pro Arg Thr Phe Pro
145 150 155 160
Gly His Pro Trp Leu Asp Thr Pro Glu Gly His Ala Ala Leu Arg Arg
165 170 175
Val Leu Val Gly Tyr Ser Phe Arg Asp Ser Asp Val Gly Tyr Cys Gln
180 185 190
Gly Leu Asn Tyr Val Ala Ala Leu Leu Leu Val Met Lys Thr Glu
195 200 205
Glu Asp Ala Phe Trp Met Leu Ala Val Leu Leu Glu Asn Val Leu Val
210 215 220
Arg Asp Cys Tyr Thr Thr Asn Leu Ser Gly Cys His Val Glu Gln Arg
225 230 235 240
Val Phe Lys Asp Leu Leu Ala Gln Lys Cys Ser Arg Ile Ala Thr His
245 250 255
Leu Glu Asp Met Gly Phe Asp Val Ser Leu Val Ala Thr Glu Trp Phe
260 265 270
Leu Cys Leu Phe Ser Lys Ser Leu Pro Ser Glu Thr Thr Leu Arg Val
275 280 285
Trp Asp Val Leu Phe Tyr Glu Gly Ala Lys Val Leu Phe His Ala Ala
290 295 300
Leu Ala Ile Phe Lys Met Lys Glu Asn Glu Leu Leu Met Thr His Gln
305 310 315 320
Val Gly Asp Val Ile Asn Xaa Leu Gln Lys Thr Ser His Gln Leu Phe
325 330 335
Asp Pro Asp Glu Leu Leu Thr Val Ala Phe Glu Lys Ile Gly Ser Met
340 345 350
Thr Thr Asn Thr Ile Ser Lys Gln Arg Lys Lys Gln Glu Pro Ala Val
355 360 365
Met Ala Glu Leu Asp Gln Arg Leu Arg Arg Leu Asn Ser Leu Lys Glu
370 375 380

Ser Gly Lys Ser Thr
385

(2) INFORMATION FOR SEQ ID NO:1333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..247
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:

Met Val Thr Pro Ala Thr Arg Gln Ile Asp His Asp Leu Pro Arg Thr
1 5 10 15
Phe Pro Gly His Pro Trp Leu Asp Thr Pro Glu Gly His Ala Ala Leu

Arg	Arg	Val	Leu	Val	Gly	Tyr	Ser	Phe	Arg	Asp	Ser	Asp	Val	Gly	Tyr
35							40					45			
Cys	Gln	Gly	Leu	Asn	Tyr	Val	Ala	Ala	Leu	Leu	Leu	Leu	Val	Met	Lys
50						55					60				
Thr	Glu	Glu	Asp	Ala	Phe	Trp	Met	Leu	Ala	Val	Leu	Leu	Glu	Asn	Val
65						70				75				80	
Leu	Val	Arg	Asp	Cys	Tyr	Thr	Thr	Asn	Leu	Ser	Gly	Cys	His	Val	Glu
			85					90					95		
Gln	Arg	Val	Phe	Lys	Asp	Leu	Leu	Ala	Gln	Lys	Cys	Ser	Arg	Ile	Ala
			100					105					110		
Thr	His	Leu	Glu	Asp	Met	Gly	Phe	Asp	Val	Ser	Leu	Val	Ala	Thr	Glu
			115					120					125		
Trp	Phe	Leu	Cys	Leu	Phe	Ser	Lys	Ser	Leu	Pro	Ser	Glu	Thr	Thr	Leu
			130				135				140				
Arg	Val	Trp	Asp	Val	Leu	Phe	Tyr	Glu	Gly	Ala	Lys	Val	Leu	Phe	His
145					150					155				160	
Ala	Ala	Leu	Ala	Ile	Phe	Lys	Met	Lys	Glu	Asn	Glu	Leu	Leu	Met	Thr
			165						170					175	
His	Gln	Val	Gly	Asp	Val	Ile	Asn	Xaa	Leu	Gln	Lys	Thr	Ser	His	Gln
			180					185					190		
Leu	Phe	Asp	Pro	Asp	Glu	Leu	Leu	Thr	Val	Ala	Phe	Glu	Lys	Ile	Gly
			195				200					205			
Ser	Met	Thr	Thr	Asn	Thr	Ile	Ser	Lys	Gln	Arg	Lys	Lys	Gln	Glu	Pro
			210				215				220				
Ala	Val	Met	Ala	Glu	Leu	Asp	Gln	Arg	Leu	Arg	Arg	Leu	Asn	Ser	Leu
225					230					235				240	
Lys	Glu	Ser	Gly	Lys	Ser	Thr									
					245										

(2) INFORMATION FOR SEQ ID NO:1334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1674
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:

agatgtaatt	tgtataattt	tagtaactct	tcaggttttt	tttgttttaa	aaatatattt	60
tctctctctc	tgtcttctcg	caatctatcg	ccggccgatt	caataatttc	gctttactct	120
gccaaaaaag	tttgttcttt	tgttttctcg	gattatccaa	agagaagaaa	cagaggagaa	180
cagtcctctt	tttagtttca	gacctaaat	octaggtttt	gaagtttttg	tctcttagta	240
attttgtcag	gttttgtgtc	tggtgttggt	atttttcgga	gcttggtttc	ttgaaccagc	300
tccatttttt	aaaaattcct	tctttaaatc	cccattgttg	taagtcctaa	agaaaaaaga	360
agatgacttg	tgttttctct	tggttgaatc	ctcgaaccaa	ggacataaga	gtcgacattg	420
ataacgctcg	atgcaactct	cgttaccaaa	ccgattcatc	agttcatgga	agtgatacaa	480
caggaaacaga	gtcgatttgc	ggatctctag	taaatggtaa	agtgaaatgt	ccgataacctg	540
gtggtggagc	tcggagcttc	acgttcaagg	agtttagctgc	agctacaaga	aaactccggg	600
aaagttaatt	gctcaggaga	ggaggttttg	gcagagttaa	taagggaactg	ttagattcag	660
gacaagtagt	ggctattaag	caattgaatc	cagatgggct	tcaagggaac	cgagagttta	720
tagtagaagt	tcttatgctt	agcttattgc	atcatcccaa	tctcgttaca	tgtatcggtt	780
actgtacttc	tggtgatcaa	agacttcttg	tctatgaata	catgccaatg	ggagcgtagt	840
aagataccct	ttttgatctt	gagtcctaac	aagaaccatt	aagctggaat	actcgaatga	900
aaatcgcggt	tggtgcagct	cgaggaatag	actatcttca	ctgcacagct	aaaccgccag	960
tgattttaccg	tgatttgaaa	tcgcgaacaa	tattgttaga	taaaagagttc	agtcacaaac	1020
tctcggattt	cggatttgccg	aaactcggtc	cagtttgtga	ctgaactcat	gtatcgactc	1080
gtgtcatcggg	aaactacggt	tactgtgctc	ctgaatacgc	aatgagcggg	aaattaaactg	1140
ttaaatccga	tatctactgc	ttcgggtgtag	tgttgcttga	gctgattact	gggagaaaag	1200

ctattgattt	agggtcaaaa	caaggcgagc	agaatcttgt	tacttgggtca	cgctccatacc	1260
tcaaggatca	gaagaagttt	ggacatttag	tggatccgct	tctacgagga	aaatacccaa	1320
gacgggtgtt	aaactatgcg	atgctgatta	ttgcaatgtg	tcttaaatga	gaagctcatt	1380
atcgaccggt	cataggtgac	atagttgttg	cactagagta	cttagccgca	cagagcagat	1440
ctcatgaagc	tcgaaaagtc	tcatacccg	caccagagat	ttcaagaacg	ccgcgacgag	1500
acttgtaaaa	actcaaaaac	agcttttaag	aatttcagtt	tggtgtgtgt	taaaaatggt	1560
ttttttgttt	ctttctcaga	aaacaatata	tgtttggtaa	atgtttcgtt	attagtctct	1620
tttacttgat	gtatatggca	attatggaaa	caattaaagt	tcttttatat	gtgt	

(2) INFORMATION FOR SEQ ID NO:1335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..381
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

Met	Thr	Cys	Cys	Phe	Ser	Cys	Leu	Asn	Pro	Arg	Thr	Lys	Asp	Ile	Arg
1			5						10					15	
Val	Asp	Ile	Asp	Asn	Ala	Arg	Cys	Asn	Ser	Arg	Tyr	Gln	Thr	Asp	Ser
			20					25					30		
Ser	Val	His	Gly	Ser	Asp	Thr	Thr	Gly	Thr	Glu	Ser	Ile	Ser	Gly	Ile
			35					40				45			
Leu	Val	Asn	Gly	Lys	Val	Asn	Ser	Pro	Ile	Pro	Gly	Gly	Gly	Ala	Arg
			50				55				60				
Ser	Phe	Thr	Phe	Lys	Glu	Leu	Ala	Ala	Ala	Thr	Arg	Asn	Phe	Arg	Glu
			65			70				75				80	
Val	Asn	Leu	Leu	Gly	Glu	Gly	Gly	Phe	Gly	Arg	Val	Tyr	Lys	Gly	Arg
			85					90					95		
Leu	Asp	Ser	Gly	Gln	Val	Val	Ala	Ile	Lys	Gln	Leu	Asn	Pro	Asp	Gly
			100					105				110			
Leu	Gln	Gly	Asn	Arg	Glu	Phe	Ile	Val	Glu	Val	Leu	Met	Leu	Ser	Leu
			115				120					125			
Leu	His	His	Pro	Asn	Leu	Val	Thr	Leu	Ile	Gly	Tyr	Cys	Thr	Ser	Gly
			130				135				140				
Asp	Gln	Arg	Leu	Leu	Val	Tyr	Glu	Tyr	Met	Pro	Met	Gly	Ser	Leu	Glu
			145				150			155				160	
Asp	His	Leu	Phe	Asp	Leu	Glu	Ser	Asn	Gln	Glu	Pro	Leu	Ser	Trp	Asn
			165					170					175		
Thr	Arg	Met	Lys	Ile	Ala	Val	Gly	Ala	Ala	Arg	Gly	Ile	Glu	Tyr	Leu
			180				185					190			
His	Cys	Thr	Ala	Asn	Pro	Pro	Val	Ile	Tyr	Arg	Asp	Leu	Lys	Ser	Ala
			195				200				205				
Asn	Ile	Leu	Leu	Asp	Lys	Glu	Phe	Ser	Pro	Lys	Leu	Ser	Asp	Phe	Gly
			210				215				220				
Leu	Ala	Lys	Leu	Gly	Pro	Val	Gly	Asp	Arg	Thr	His	Val	Ser	Thr	Arg
			225				230			235				240	
Val	Met	Gly	Thr	Tyr	Gly	Tyr	Cys	Ala	Pro	Glu	Tyr	Ala	Met	Ser	Gly
			245					250					255		
Lys	Leu	Thr	Val	Lys	Ser	Asp	Ile	Tyr	Cys	Phe	Gly	Val	Val	Leu	Leu
			260					265				270			
Glu	Leu	Ile	Thr	Gly	Arg	Lys	Ala	Ile	Asp	Leu	Gly	Gln	Lys	Gln	Gly
			275				280				285				
Glu	Gln	Asn	Leu	Val	Thr	Trp	Ser	Arg	Pro	Tyr	Leu	Lys	Asp	Gln	Lys
			290				295				300				
Lys	Phe	Gly	His	Leu	Val	Asp	Pro	Ser	Leu	Arg	Gly	Lys	Tyr	Pro	Arg
			305			310				315				320	
Arg	Cys	Leu	Asn	Tyr	Ala	Ile	Ala	Ile	Ile	Ala	Met	Cys	Leu	Asn	Glu

325 330 335
Glu Ala His Tyr Arg Pro Phe Ile Gly Asp Ile Val Val Ala Leu Glu
340 345 350
Tyr Leu Ala Ala Gln Ser Arg Ser His Glu Ala Arg Asn Val Ser Ser
355 360 365
Pro Ser Pro Glu Ile Ser Arg Thr Pro Arg Arg Asp Leu
370 375 380

(2) INFORMATION FOR SEQ ID NO:1336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..257

(D) OTHER INFORMATION: / Ceres Seq. ID 1500075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

Met Leu Ser Leu Leu His His Pro Asn Leu Val Thr Leu Ile Gly Tyr
1 5 10 15
Cys Thr Ser Gly Asp Gln Arg Leu Leu Val Tyr Glu Tyr Met Pro Met
20 25 30
Gly Ser Leu Glu Asp His Leu Phe Asp Leu Glu Ser Asn Gln Glu Pro
35 40 45
Leu Ser Trp Asn Thr Arg Met Lys Ile Ala Val Gly Ala Ala Arg Gly
50 55 60
Ile Glu Tyr Leu His Cys Thr Ala Asn Pro Pro Val Ile Tyr Arg Asp
65 70 75 80
Leu Lys Ser Ala Asn Ile Leu Leu Asp Lys Glu Phe Ser Pro Lys Leu
85 90 95
Ser Asp Phe Gly Leu Ala Lys Leu Gly Pro Val Gly Asp Arg Thr His
100 105 110
Val Ser Thr Arg Val Met Gly Thr Tyr Gly Tyr Cys Ala Pro Glu Tyr
115 120 125
Ala Met Ser Gly Lys Leu Thr Val Lys Ser Asp Ile Tyr Cys Phe Gly
130 135 140
Val Val Leu Leu Glu Leu Ile Thr Gly Arg Lys Ala Ile Asp Leu Gly
145 150 155 160
Gln Lys Gln Gly Glu Gln Asn Leu Val Thr Trp Ser Arg Pro Tyr Leu
165 170 175
Lys Asp Gln Lys Lys Phe Gly His Leu Val Asp Pro Ser Leu Arg Gly
180 185 190
Lys Tyr Pro Arg Arg Cys Leu Asn Tyr Ala Ile Ala Ile Ile Ala Met
195 200 205
Cys Leu Asn Glu Glu Ala His Tyr Arg Pro Phe Ile Gly Asp Ile Val
210 215 220
Val Ala Leu Glu Tyr Leu Ala Ala Gln Ser Arg Ser His Glu Ala Arg
225 230 235 240
Asn Val Ser Ser Pro Ser Pro Glu Ile Ser Arg Thr Pro Arg Arg Asp
245 250 255
Leu

(2) INFORMATION FOR SEQ ID NO:1337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..228
(D) OTHER INFORMATION: / Ceres Seq. ID 1500076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:

Met Pro Met Gly Ser Leu Glu Asp His Leu Phe Asp Leu Glu Ser Asn
1 5 10 15
Gln Glu Pro Leu Ser Trp Asn Thr Arg Met Lys Ile Ala Val Gly Ala
20 25 30
Ala Arg Gly Ile Glu Tyr Leu His Cys Thr Ala Asn Pro Pro Val Ile
35 40 45
Tyr Arg Asp Leu Lys Ser Ala Asn Ile Leu Leu Asp Lys Glu Phe Ser
50 55 60
Pro Lys Leu Ser Asp Phe Gly Leu Ala Lys Leu Gly Pro Val Gly Asp
65 70 75
Arg Thr His Val Ser Thr Arg Val Met Gly Thr Tyr Gly Tyr Cys Ala
85 90 95
Pro Glu Tyr Ala Met Ser Gly Lys Leu Thr Val Lys Ser Asp Ile Tyr
100 105 110
Cys Phe Gly Val Val Leu Leu Glu Leu Ile Thr Gly Arg Lys Ala Ile
115 120 125
Asp Leu Gly Gln Lys Gln Gly Glu Gln Asn Leu Val Thr Trp Ser Arg
130 135 140
Pro Tyr Leu Lys Asp Gln Lys Lys Phe Gly His Leu Val Asp Pro Ser
145 150 155
Leu Arg Gly Lys Tyr Pro Arg Arg Cys Leu Asn Tyr Ala Ile Ala Ile
160 165 170
Ile Ala Met Cys Leu Asn Glu Glu Ala His Tyr Arg Pro Phe Ile Gly
180 185 190
Asp Ile Val Val Ala Leu Glu Tyr Leu Ala Ala Gln Ser Arg Ser His
195 200 205
Glu Ala Arg Asn Val Ser Ser Pro Ser Pro Glu Ile Ser Arg Thr Pro
210 215 220
Arg Arg Asp Leu
225

(2) INFORMATION FOR SEQ ID NO:1338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1690 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1690
(D) OTHER INFORMATION: / Ceres Seq. ID 1500077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:

atcaataaac acaaaaaacaa aagaagaaga gaataaacaa aagaagaaaa aaaactaata 60
aaacaaatc aataaaaaa gaataaaaaa tgggtgggttc tcacaaagca agcgaggtgc 120
ttctgtgtct actagtgggtt atggccacca caatagcaaa cgggacaccg gttgtcgata 180
aagcaaaaaa tgcagctaca gcagttgaag atacagcaaa aatgacagct acagcagttg 240
gcggtgcagc tgcacagttt ggtgctaagg tatcaggtgc caaaccaggc gcagcagttg 300
atgttaaaag atcaggagacc aaaggagacg gcaaaaactga tgatagtgcg gcatttgcgg 360
ctgcattgaa agaaagctgt gcagcaggga gcacaattac agtcactttg gaattgaatg 420
tggtagagag cctagagttc aaaggtccat gcaaaagttc agtcgcogga tggattgatt 480
gcaatttcaa ggtcccggtc acggtcaaga ccactaagcc acatgcogga gggtcaaggt 540
tcgaaaatat agctgatttc actttgaatg gaaacaaagc tatttttgac gggtcaaggt 600
cctcgctgtg gaagcccaat gattgtgcca aaactggcaa atgcaactct ctccctatca 660
acatccgatt cactggtcta acaaaactcaa agattaatag tattacatca acaaacagca 720
aaacttttcca catgaacatc cttaactgca agaactttac tctttcgatt attggtattg 780
atgcacctcc ggagagtttc aacacccgat gtatccacat cggaaggtcc aatggagatca 840
acttaattgg ggcaagatc aaaaccggag atgactgcgt ttccattgga gatggtaccg 900

aaaatctcat	tgttgagacg	gtagaatgtg	gaccaggaca	cggaatttcc	attggaagtc	960
ttggaagata	ccctaataag	caaccagtaa	aaggagtcac	cgtaggagaa	tgccctcatca	1020
agaacactga	caatgggtgt	gcgatcaaga	catggccagg	atctccccc	ggcatcgccct	1080
ccaacattct	tttogaagat	atcacaaatg	acaatgttag	ccttcccgtt	ctcatcgacc	1140
aagagtagct	tccttatggc	cactgcaaa	ctgggggtacc	atcgcaagtg	aagttgtcag	1200
acgtgactat	caaggggcatt	aagggtacat	cagcaacaaa	ggtagctgtg	aagctaatgt	1260
gcagcaaaag	agtgcccttg	accaaatattg	ctctctctga	catcaacttg	gtccacaacg	1320
gcaaaagagg	accagctgtc	tcggcatgtt	ctaaccatcaa	gcctattctc	agcggaaggt	1380
tggttccagc	ggcttgcaat	gaagttgcta	aaccgggtcc	ataaattaaa	gtcgctgtgtc	1440
caccataaat	ccatccaatc	tggcgaagac	gctttgatta	gggtgcgatg	aaaaaatttt	1500
gcaatatttt	tttgacaat	aaattatatg	gatattttat	agataagacg	gagtcatttc	1560
aggattggag	tttataacct	gaagagtgaac	tcgtgaattg	ggtagtaatt	gttgtgtgga	1620
ttgcgattta	tgcgagaaag	ttttaataat	tattcgaaaa	gtaataatat	cattgaaatt	1680
ttgaagtttt						

(2) INFORMATION FOR SEQ ID NO:1339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..444
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:

Met	Val	Gly	Ser	His	Lys	Ala	Ser	Gly	Val	Leu	Leu	Val	Leu	Leu	Val
1			5					10					15		
Val	Met	Ala	Thr	Thr	Ile	Ala	Asn	Gly	Thr	Pro	Val	Val	Asp	Lys	Ala
			20					25					30		
Lys	Asn	Ala	Ala	Thr	Ala	Val	Glu	Asp	Thr	Ala	Lys	Asn	Ala	Ala	Thr
			35					40					45		
Ala	Val	Gly	Gly	Ala	Ala	Ala	Ser	Val	Gly	Ala	Lys	Val	Ser	Gly	Ala
			50					55					60		
Lys	Pro	Gly	Ala	Ala	Val	Asp	Val	Lys	Ala	Ser	Gly	Ala	Lys	Gly	Asp
			65					70					75		
Gly	Lys	Thr	Asp	Asp	Ser	Ala	Ala	Phe	Ala	Ala	Ala	Trp	Lys	Glu	Ala
			85					90					95		
Cys	Ala	Ala	Gly	Ser	Thr	Ile	Thr	Val	Pro	Lys	Gly	Glu	Tyr	Met	Val
			100					105					110		
Glu	Ser	Leu	Glu	Phe	Lys	Gly	Pro	Cys	Lys	Gly	Pro	Val	Thr	Leu	Glu
			115					120					125		
Leu	Asn	Gly	Asn	Phe	Lys	Ala	Pro	Ala	Thr	Val	Lys	Thr	Thr	Lys	Pro
			130					135					140		
His	Ala	Gly	Trp	Ile	Asp	Phe	Glu	Asn	Ile	Ala	Asp	Phe	Thr	Leu	Asn
			145					150					155		
Gly	Asn	Lys	Ala	Ile	Phe	Asp	Gly	Gln	Gly	Ser	Leu	Ala	Trp	Lys	Ala
			165					170					175		
Asn	Asp	Cys	Ala	Lys	Thr	Gly	Lys	Cys	Asn	Ser	Leu	Pro	Ile	Asn	Ile
			180					185					190		
Arg	Phe	Thr	Gly	Leu	Thr	Asn	Ser	Lys	Ile	Asn	Ser	Ile	Thr	Ser	Thr
			195					200					205		
Asn	Ser	Lys	Leu	Phe	His	Met	Asn	Ile	Leu	Asn	Cys	Lys	Asn	Ile	Thr
			210					215					220		
Leu	Ser	Asp	Ile	Gly	Ile	Asp	Ala	Pro	Pro	Glu	Ser	Leu	Asn	Thr	Asp
			225					230					235		
Gly	Ile	His	Ile	Gly	Arg	Ser	Asn	Gly	Val	Asn	Leu	Ile	Gly	Ala	Lys
			245					250					255		
Ile	Lys	Thr	Gly	Asp	Asp	Cys	Val	Ser	Ile	Gly	Asp	Gly	Thr	Glu	Asn
			260					265					270		
Leu	Ile	Val	Glu	Asn	Val	Glu	Cys	Gly	Pro	Gly	His	Gly	Ile	Ser	Ile

Met	Ala	Thr	Thr	Ile	Ala	Asn	Gly	Thr	Pro	Val	Val	Asp	Lys	Ala	Lys
1				5					10					15	
Asn	Ala	Ala	Thr	Ala	Val	Glu	Asp	Thr	Ala	Lys	Asn	Ala	Ala	Thr	Ala
			20					25					30		
Val	Gly	Gly	Ala	Ala	Ala	Ser	Val	Gly	Ala	Lys	Val	Ser	Gly	Ala	Lys
		35				40						45			
Pro	Gly	Ala	Ala	Val	Asp	Val	Lys	Ala	Ser	Gly	Ala	Lys	Gly	Asp	Gly
	50				55						60				
Lys	Thr	Asp	Asp	Ser	Ala	Ala	Phe	Ala	Ala	Ala	Trp	Lys	Glu	Ala	Cys
65					70				75						80
Ala	Ala	Gly	Ser	Thr	Ile	Thr	Val	Pro	Lys	Gly	Glu	Tyr	Met	Val	Glu
			85						90				95		
Ser	Leu	Glu	Phe	Lys	Gly	Pro	Cys	Lys	Gly	Pro	Val	Thr	Leu	Glu	Leu
		100						105					110		
Asn	Gly	Asn	Phe	Lys	Ala	Pro	Ala	Thr	Val	Lys	Thr	Thr	Lys	Pro	His
		115						120					125		
Ala	Gly	Trp	Ile	Asp	Phe	Glu	Asn	Ile	Ala	Asp	Phe	Thr	Leu	Asn	Gly
		130				135					140				
Asn	Lys	Ala	Ile	Phe	Asp	Gly	Gln	Gly	Ser	Leu	Ala	Trp	Lys	Ala	Asn
145					150					155					160
Asp	Cys	Ala	Lys	Thr	Gly	Lys	Cys	Asn	Ser	Leu	Pro	Ile	Asn	Ile	Arg
			165					170					175		
Phe	Thr	Gly	Leu	Thr	Asn	Ser	Lys	Ile	Asn	Ser	Ile	Thr	Ser	Thr	Asn
		180						185					190		
Ser	Lys	Leu	Phe	His	Met	Asn	Ile	Leu	Asn	Cys	Lys	Asn	Ile	Thr	Leu
		195					200					205			
Ser	Asp	Ile	Gly	Ile	Asp	Ala	Pro	Pro	Glu	Ser	Leu	Asn	Thr	Asp	Gly
	210					215					220				

Ile His Ile Gly Arg Ser Asn Gly Val Asn Leu Ile Gly Ala Lys Ile
225 230 235 240
Lys Thr Gly Asp Asp Cys Val Ser Ile Gly Asp Gly Thr Glu Asn Leu
245 250 255
Ile Val Glu Asn Val Glu Cys Gly Pro Gly His Gly Ile Ser Ile Gly
260 265 270
Ser Leu Gly Arg Tyr Pro Asn Glu Gln Pro Val Lys Gly Val Thr Val
275 280 285
Arg Lys Cys Leu Ile Lys Asn Thr Asp Asn Gly Val Arg Ile Lys Thr
290 295 300
Trp Pro Gly Ser Pro Pro Gly Ile Ala Ser Asn Ile Leu Phe Glu Asp
305 310 315 320
Ile Thr Met Asp Asn Val Ser Leu Pro Val Leu Ile Asp Gln Glu Tyr
325 330 335
Cys Pro Tyr Gly His Cys Lys Ala Gly Val Pro Ser Gln Val Lys Leu
340 345 350
Ser Asp Val Thr Ile Lys Gly Ile Lys Gly Thr Ser Ala Thr Lys Val
355 360 365
Ala Val Lys Leu Met Cys Ser Lys Gly Val Pro Cys Thr Asn Ile Ala
370 375 380
Leu Ser Asp Ile Asn Leu Val His Asn Gly Lys Glu Gly Pro Ala Val
385 390 395 400
Ser Ala Cys Ser Asn Ile Lys Pro Ile Leu Ser Gly Lys Leu Val Pro
405 410 415
Ala Ala Cys Thr Glu Val Ala Lys Pro Gly Pro
420 425

(2) INFORMATION FOR SEQ ID NO:1341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..334
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

Met Val Glu Ser Leu Glu Phe Lys Lys Gly Pro Cys Lys Gly Pro Val Thr
1 5 10 15
Leu Glu Leu Asn Gly Asn Phe Lys Ala Pro Ala Thr Val Lys Thr Thr
20 25 30
Lys Pro His Ala Gly Trp Ile Asp Phe Glu Asn Ile Ala Asp Phe Thr
35 40 45
Leu Asn Gly Asn Lys Ala Ile Phe Asp Gly Gln Gly Ser Leu Ala Trp
50 55 60
Lys Ala Asn Asp Cys Ala Lys Thr Gly Lys Cys Asn Ser Leu Pro Ile
65 70 75 80
Asn Ile Arg Phe Thr Gly Leu Thr Asn Ser Lys Ile Asn Ser Ile Thr
85 90 95
Ser Thr Asn Ser Lys Leu Phe His Met Asn Ile Leu Asn Cys Lys Asn
100 105 110
Ile Thr Leu Ser Asp Ile Gly Ile Asp Ala Pro Pro Glu Ser Leu Asn
115 120 125
Thr Asp Gly Ile His Ile Gly Arg Ser Asn Gly Val Asn Leu Ile Gly
130 135 140
Ala Lys Ile Lys Thr Gly Asp Asp Cys Val Ser Ile Gly Asp Gly Thr
145 150 155 160
Glu Asn Leu Ile Val Glu Asn Val Glu Cys Gly Pro Gly His Gly Ile
165 170 175
Ser Ile Gly Ser Leu Gly Arg Tyr Pro Asn Glu Gln Pro Val Lys Gly

180										185										190																																			
Val	Thr	Val	Arg	Lys	Cys	Leu	Ile	Lys	Asn	Thr	Asp	Asn	Gly	Val	Arg					Val	Thr	Val	Arg	Lys	Cys	Leu	Ile	Lys	Asn	Thr	Asp	Asn	Gly	Val	Arg			Val	Thr	Val	Arg	Lys	Cys	Leu	Ile	Lys	Asn	Thr	Asp	Asn	Gly	Val	Arg		
195										200										205																																			
Ile	Lys	Thr	Trp	Pro	Gly	Ser	Pro	Pro	Gly	Ile	Ala	Ser	Asn	Ile	Leu					Ile	Lys	Thr	Trp	Pro	Gly	Ser	Pro	Pro	Gly	Ile	Ala	Ser	Asn	Ile	Leu			Ile	Lys	Thr	Trp	Pro	Gly	Ser	Pro	Pro	Gly	Ile	Ala	Ser	Asn	Ile	Leu		
210										215										220																																			
Phe	Glu	Asp	Ile	Thr	Met	Asp	Asn	Val	Ser	Leu	Pro	Val	Leu	Ile	Asp					Phe	Glu	Asp	Ile	Thr	Met	Asp	Asn	Val	Ser	Leu	Pro	Val	Leu	Ile	Asp			Phe	Glu	Asp	Ile	Thr	Met	Asp	Asn	Val	Ser	Leu	Pro	Val	Leu	Ile	Asp		
225										230										235																																			
Gln	Glu	Tyr	Cys	Pro	Tyr	Gly	His	Cys	Lys	Ala	Gly	Val	Pro	Ser	Gln					Gln	Glu	Tyr	Cys	Pro	Tyr	Gly	His	Cys	Lys	Ala	Gly	Val	Pro	Ser	Gln			Gln	Glu	Tyr	Cys	Pro	Tyr	Gly	His	Cys	Lys	Ala	Gly	Val	Pro	Ser	Gln		
245										250										255																																			
Val	Lys	Leu	Ser	Asp	Val	Thr	Ile	Lys	Gly	Ile	Lys	Gly	Thr	Ser	Ala					Val	Lys	Leu	Ser	Asp	Val	Thr	Ile	Lys	Gly	Ile	Lys	Gly	Thr	Ser	Ala			Val	Lys	Leu	Ser	Asp	Val	Thr	Ile	Lys	Gly	Ile	Lys	Gly	Thr	Ser	Ala		
260										265										270																																			
Thr	Lys	Val	Ala	Val	Lys	Leu	Met	Cys	Ser	Lys	Gly	Val	Pro	Cys	Thr					Thr	Lys	Val	Ala	Val	Lys	Leu	Met	Cys	Ser	Lys	Gly	Val	Pro	Cys	Thr			Thr	Lys	Val	Ala	Val	Lys	Leu	Met	Cys	Ser	Lys	Gly	Val	Pro	Cys	Thr		
275										280										285																																			
Asn	Ile	Ala	Leu	Ser	Asp	Ile	Asn	Leu	Val	His	Asn	Gly	Lys	Glu	Gly					Asn	Ile	Ala	Leu	Ser	Asp	Ile	Asn	Leu	Val	His	Asn	Gly	Lys	Glu	Gly			Asn	Ile	Ala	Leu	Ser	Asp	Ile	Asn	Leu	Val	His	Asn	Gly	Lys	Glu	Gly		
290										295										300																																			
Pro	Ala	Val	Ser	Ala	Cys	Ser	Asn	Ile	Lys	Pro	Ile	Leu	Ser	Gly	Lys					Pro	Ala	Val	Ser	Ala	Cys	Ser	Asn	Ile	Lys	Pro	Ile	Leu	Ser	Gly	Lys			Pro	Ala	Val	Ser	Ala	Cys	Ser	Asn	Ile	Lys	Pro	Ile	Leu	Ser	Gly	Lys		
305										310										315																																			
Leu	Val	Pro	Ala	Ala	Cys	Thr	Glu	Val	Ala	Lys	Pro	Gly	Pro						Leu	Val	Pro	Ala	Ala	Cys	Thr	Glu	Val	Ala	Lys	Pro	Gly	Pro					Leu	Val	Pro	Ala	Ala	Cys	Thr	Glu	Val	Ala	Lys	Pro	Gly	Pro					
325										330																																													

(2) INFORMATION FOR SEQ ID NO:1342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1396
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:

aatgtattaa	gacttgacaa	cttgtcttct	tcacacacaa	ccctctctct	ctgttttcata	60
acatcttctc	tttttttttt	tcctaagccc	ctaagtacaa	accataatgc	cttaatatctt	120
gatgctaaga	gcagcatcgg	agttgcgggt	agagttccaa	accaatctct	gtttttctcc	180
ggaggtggcc	gatacatcag	cattccccgg	aagaaactcg	tgcagaagat	agaggccgac	240
ccgagtcaca	cccgatatca	cacttggatc	gaagccatga	gggctctctc	cccaaccctg	300
acccgaccgg	ggaacataatc	tccccctcac	gagtcctgat	aggaggatga	atactcttct	360
tgatgtggct	aacacccgtc	agctttaacc	atgtttgaag	agatagctga	agcttcaaaa	420
gggaacaaaa	tcgtgatggt	tctcgactat	gacggtaacat	tatcccccat	tgttgaaaaa	480
ctgatgcgag	cttacatgtc	tgaagagatg	agagaggcag	tgaaggcggt	ggctagatat	540
ttccgaccgc	cgattgtcac	tggaaagatg	cggtataaag	tctgatagtt	tgtgaacctt	600
cccgagactt	actatgcagg	tagccatgga	atggacatca	aaggaccttc	caaaagaaac	660
aaacataata	agaacaataa	aggagttctt	ttccaaagcg	cgaatgagtt	tttgctatg	720
attgacaagg	tctctaagtg	tctagtagag	aaaatgagag	acatagaagg	agcaaacgtc	780
gagaacaaca	agtttttgtt	ctccgtacat	taccgttgtg	ttgatcaaaa	ggactgggga	840
ttggtagcgg	aacacgtgac	atcgatatgt	agtgaagtac	cgaaaactgag	tttgacacaa	900
ggaagaaaaa	tcttagagat	tcgaccaacc	atcaaatggg	ataaaggcaa	agctctcgag	960
ttcttgctcg	aatcccttag	attcgctaac	tctaacacgt	ttttgcccac	ctatatagga	1020
gatgatcgta	cgagcagaga	tgccttcaag	gttttgagaa	acaaaggaca	agcctttggt	1080
atacttgtgt	ccaaaattcc	aaaggaaacg	agtgctacat	attctctaca	agaaaccttc	1140
gaggtaggag	agtttttgca	gcgactcgtg	gaatggaaac	aaatgtcaat	aagagggaag	1200
tagccaattt	cctgacataa	atttattttc	aattaataaa	tgaattagtt	ttcaactatg	1260
aacaaaaatt	gttgatatata	tgatcaatgt	ttttttaatt	attttactct	tcatgaacaa	1320
atgtaagtgt	atagggaactt	tcttaaccaa	gaaaaaaagt	aagtttgcta	tataatatatt	1380
tcacattctt	cttttt					

(2) INFORMATION FOR SEQ ID NO:1343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..400

(D) OTHER INFORMATION: / Ceres Seq. ID 1500082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:

Asn	Val	Leu	Arg	Leu	Asp	Asn	Leu	Ser	Phe	Ser	His	Gln	Thr	Pro	Leu	
1				5				10					15			
Leu	Cys	Phe	Ile	Thr	Ser	Ser	Leu	Phe	Phe	Phe	Pro	Lys	Pro	Leu	Met	
				20			25					30				
Thr	Asn	His	Asn	Ala	Leu	Ile	Ser	Asp	Ala	Lys	Gly	Ser	Ile	Gly	Val	
				35			40				45					
Ala	Val	Arg	Val	Pro	Asn	Gln	Ser	Leu	Phe	Ser	Pro	Gly	Gly	Gly	Arg	
				50		55					60					
Tyr	Ile	Ser	Ile	Pro	Arg	Lys	Lys	Leu	Val	Gln	Lys	Leu	Glu	Ala	Asp	
				65		70				75				80		
Pro	Ser	Gln	Thr	Arg	Ile	His	Thr	Trp	Ile	Glu	Ala	Met	Arg	Ala	Ser	
				85					90				95			
Ser	Pro	Thr	Arg	Thr	Arg	Pro	Gly	Asn	Ile	Ser	Pro	Leu	Thr	Glu	Ser	
				100			105						110			
Asp	Glu	Glu	Asp	Glu	Tyr	Ser	Ser	Trp	Met	Ala	Gln	His	Pro	Ser	Ala	
				115			120				125					
Leu	Thr	Met	Phe	Glu	Glu	Ile	Ala	Glu	Ala	Ser	Lys	Gly	Lys	Gln	Ile	
				130			135				140					
Val	Met	Phe	Leu	Asp	Tyr	Asp	Gly	Thr	Leu	Ser	Pro	Ile	Val	Glu	Asn	
				145		150				155				160		
Pro	Asp	Arg	Ala	Tyr	Met	Ser	Glu	Glu	Met	Arg	Glu	Ala	Val	Lys	Gly	
				165					170				175			
Val	Ala	Arg	Tyr	Phe	Pro	Thr	Ala	Ile	Val	Thr	Gly	Arg	Cys	Arg	Asp	
				180				185					190			
Lys	Val	Arg	Arg	Phe	Val	Lys	Leu	Pro	Gly	Leu	Tyr	Tyr	Ala	Gly	Ser	
				195			200					205				
His	Gly	Met	Asp	Ile	Lys	Gly	Pro	Ser	Lys	Arg	Asn	Lys	His	Asn	Lys	
				210		215					220					
Asn	Asn	Lys	Gly	Val	Leu	Phe	Gln	Ala	Ala	Asn	Glu	Phe	Leu	Pro	Met	
				225		230				235				240		
Ile	Asp	Lys	Val	Ser	Lys	Cys	Leu	Val	Glu	Lys	Met	Arg	Asp	Ile	Glu	
				245					250				255			
Gly	Ala	Asn	Val	Glu	Asn	Asn	Lys	Phe	Cys	Val	Ser	Val	His	Tyr	Arg	
				260			265						270			
Cys	Val	Asp	Gln	Lys	Asp	Trp	Gly	Leu	Val	Ala	Glu	His	Val	Thr	Ser	
				275			280					285				
Ile	Leu	Ser	Glu	Tyr	Pro	Lys	Leu	Ser	Leu	Thr	Gln	Gly	Arg	Lys	Val	
				290		295					300					
Leu	Glu	Ile	Arg	Pro	Thr	Ile	Lys	Trp	Asp	Lys	Gly	Lys	Ala	Leu	Glu	
				305		310				315				320		
Phe	Leu	Leu	Glu	Ser	Leu	Gly	Phe	Ala	Asn	Ser	Asn	Asp	Val	Leu	Pro	
				325					330				335			
Ile	Tyr	Ile	Gly	Asp	Asp	Arg	Thr	Asp	Glu	Asp	Ala	Phe	Lys	Val	Leu	
				340			345					350				
Arg	Asn	Lys	Gly	Gln	Gly	Phe	Gly	Ile	Leu	Val	Ser	Lys	Ile	Pro	Lys	
				355			360					365				
Glu	Thr	Ser	Ala	Thr	Tyr	Ser	Leu	Gln	Glu	Pro	Ser	Glu	Val	Gly	Glu	
				370		375					380					
Phe	Leu	Gln	Arg	Leu	Val	Glu	Trp	Lys	Gln	Met	Ser	Leu	Arg	Gly	Arg	
				385		390				395				400		

(2) INFORMATION FOR SEQ ID NO:1344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..369
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500083
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:
Met Thr Asn His Asn Ala Leu Ile Ser Asp Ala Lys Gly Ser Ile Gly
1 5 10 15
Val Ala Val Arg Val Pro Asn Gln Ser Leu Phe Ser Pro Gly Gly Gly
 20 25 30
Arg Tyr Ile Ser Ile Pro Arg Lys Leu Val Gln Lys Leu Glu Ala
 35 40 45
Asp Pro Ser Gln Thr Arg Ile His Thr Trp Ile Glu Ala Met Arg Ala
50 55 60
Ser Ser Pro Thr Arg Thr Arg Pro Gly Asn Ile Ser Pro Leu Thr Glu
65 70 75 80
Ser Asp Glu Glu Asp Glu Tyr Ser Ser Trp Met Ala Gln His Pro Ser
 85 90 95
Ala Leu Thr Met Phe Glu Glu Ile Ala Glu Ala Ser Lys Gly Lys Gln
 100 105 110
Ile Val Met Phe Leu Asp Tyr Asp Gly Thr Leu Ser Pro Ile Val Glu
 115 120 125
Asn Pro Asp Arg Ala Tyr Met Ser Ser Glu Glu Met Arg Glu Ala Val Lys
130 135 140
Gly Val Ala Arg Tyr Phe Pro Thr Ala Ile Val Thr Gly Arg Cys Arg
145 150 155 160
Asp Lys Val Arg Arg Phe Val Lys Leu Pro Gly Leu Tyr Tyr Ala Gly
 165 170 175
Ser His Gly Met Asp Ile Lys Gly Pro Ser Lys Arg Asn Lys His Asn
 180 185 190
Lys Asn Asn Lys Gly Val Leu Phe Gln Ala Ala Asn Glu Phe Leu Pro
195 200 205
Met Ile Asp Lys Val Ser Lys Cys Leu Val Glu Lys Met Arg Asp Ile
210 215 220
Glu Gly Ala Asn Val Glu Asn Asn Lys Phe Cys Val Ser Val His Tyr
225 230 235 240
Arg Cys Val Asp Gln Lys Asp Trp Gly Leu Val Ala Glu His Val Thr
 245 250 255
Ser Ile Leu Ser Glu Tyr Pro Lys Leu Ser Leu Thr Gln Gly Arg Lys
260 265 270
Val Leu Glu Ile Arg Pro Thr Ile Lys Trp Asp Lys Gly Lys Ala Leu
275 280 285
Glu Phe Leu Leu Glu Ser Leu Gly Phe Ala Asn Ser Asn Asp Val Leu
290 295 300
Pro Ile Tyr Ile Gly Asp Asp Arg Thr Asp Glu Asp Ala Phe Lys Val
305 310 315 320
Leu Arg Asn Lys Gly Gln Gly Phe Gly Ile Leu Val Ser Lys Ile Pro
 325 330 335
Lys Glu Thr Ser Ala Thr Tyr Ser Leu Gln Glu Pro Ser Glu Val Gly
340 345 350
Glu Phe Leu Gln Arg Leu Val Glu Trp Lys Gln Met Ser Leu Arg Gly
355 360 365

Arg

(2) INFORMATION FOR SEQ ID NO:1345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..308
(D) OTHER INFORMATION: / Ceres Seq. ID 1500084
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:
Met Arg Ala Ser Ser Pro Thr Arg Thr Arg Pro Gly Asn Ile Ser Pro
1 5 10 15
Leu Thr Glu Ser Asp Glu Glu Asp Glu Tyr Ser Ser Trp Met Ala Gln
20 25 30
His Pro Ser Ala Leu Thr Met Phe Glu Glu Ile Ala Glu Ala Ser Lys
35 40 45
Gly Lys Gln Ile Val Met Phe Leu Asp Tyr Asp Gly Thr Leu Ser Pro
50 55 60
Ile Val Glu Asn Pro Asp Arg Ala Tyr Met Ser Glu Glu Met Arg Glu
65 70 75 80
Ala Val Lys Gly Val Ala Arg Tyr Phe Pro Thr Ala Ile Val Thr Gly
85 90 95
Arg Cys Arg Asp Lys Val Arg Arg Phe Val Lys Leu Pro Gly Leu Tyr
100 105 110
Tyr Ala Gly Ser His Gly Met Asp Ile Lys Gly Pro Ser Lys Arg Asn
115 120 125
Lys His Asn Lys Asn Asn Lys Gly Val Leu Phe Gln Ala Ala Asn Glu
130 135 140
Phe Leu Pro Met Ile Asp Lys Val Ser Lys Cys Leu Val Glu Lys Met
145 150 155 160
Arg Asp Ile Glu Gly Ala Asn Val Glu Asn Asn Lys Phe Cys Val Ser
165 170 175
Val His Tyr Arg Cys Val Asp Gln Lys Asp Trp Gly Leu Val Ala Glu
180 185 190
His Val Thr Ser Ile Leu Ser Glu Tyr Pro Lys Leu Ser Leu Thr Gln
195 200 205
Gly Arg Lys Val Leu Glu Ile Arg Pro Thr Ile Lys Trp Asp Lys Gly
210 215 220
Lys Ala Leu Glu Phe Leu Leu Glu Ser Leu Gly Phe Ala Asn Ser Asn
225 230 235 240
Asp Val Leu Pro Ile Tyr Ile Gly Asp Asp Arg Thr Asp Glu Asp Ala
245 250 255
Phe Lys Val Leu Arg Asn Lys Gly Gln Gly Phe Gly Ile Leu Val Ser
260 265 270
Lys Ile Pro Lys Glu Thr Ser Ala Thr Tyr Ser Leu Gln Glu Pro Ser
275 280 285
Glu Val Gly Glu Phe Leu Gln Arg Leu Val Glu Trp Lys Gln Met Ser
290 295 300
Leu Arg Gly Arg
305
(2) INFORMATION FOR SEQ ID NO:1346:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1510 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1510
(D) OTHER INFORMATION: / Ceres Seq. ID 1500085
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:
ttttaatttt ttcattcttct tgggtttggt tgggtcactc ttcaggtcag gtgtgtaaaa

aagaaagaaa	gaaaaagagag	attgttgtgt	tgtaacccct	tgtactaaaa	tctaatagaac	120
ttttttaaaca	caacaaaact	ccttcagatc	tgaagggtgt	cttctctctc	cttagtctct	180
ctgtcccttt	attctccgtc	gtcgtttcat	gatctgactc	cttggtcttc	tcttctctt	240
cttctttctc	tattttttct	tactctgtca	ctgttgtgtc	tgaacatgcc	acgccccttc	300
ttccataagt	tgattttctc	atccactatc	caagaaaaac	gtctgaggg	ccagataag	360
tttgtgagta	aattcaagga	tgagctttcg	gttgctgttg	cactcacagt	acctgaggt	420
catgtttggc	gtgtaggact	aaggaaagct	gacaacaaaa	tttgttttca	agatgggttg	480
caagagtttg	ttgaccgtta	ctccattcgc	attgattatc	ttttgatttt	tagatatgaa	540
ggaaactctg	ccttcagcgt	ctacattttc	aatttatccc	actctgagat	caattacocat	600
tcaccoggct	tcattggattc	cgctcacaaac	cacttcaaac	gcgcccgttt	gtttgaagac	660
cttgaagatg	aagatgcgga	ggtcatcttt	ccttctcttg	tgtacccatc	accacttctc	720
gagctctacg	taccagccaa	caaagggtat	gctagtctcag	ccatccaaac	cttgttcaact	780
ggaccagtta	aagctgaaga	gccaaacgcca	accccaaaaa	tacctaaaaa	gagagggagg	840
aagaagaaaa	atgctgatcc	tgaggaaata	aaactcatcag	ctccgcgaga	tgatgatcca	900
gagaaccggt	caaaatttcta	cgagagtgct	ctctcgagaa	agagaaccgt	gactgcagaa	960
gaaagagaga	gagccatcaa	tgcagccaaa	acgttcgaac	caacaaaccc	tttcttcaga	1020
gtggtttctg	gaccatccta	tctatacaga	ggttgcatca	tgtatcttcc	ttttgggttt	1080
gctgagaagt	acctaagtg	gatctccggg	ttcatcaaa	tcagctctgc	ggagaacaaa	1140
tggcgtgttc	gatgtctcta	caaagccggg	agagccaaat	tcagtcaagg	atggtacgaa	1200
ttcactctag	agaacaactt	aggagaagga	gacgtctgtg	tgtttgagct	gctcagaacc	1260
agagatttgc	ttttgaaagt	gacagccttt	cgagtcaacg	agtacgtctg	aacaaagcat	1320
tatggtgtga	tcattcttga	tttgcaagta	caatgtctgt	taggagatc	taattttaaa	1380
aaacaactaaa	aaactctctt	ctggtctgtg	tcattattgc	gtcagtgctc	cgttttttct	1440
ctcggtgtta	ctttgtgtta	tcgatgtgga	taagttggt	ttacctcatt	atatataacc	1500
tcttgagtgg						

(2) INFORMATION FOR SEQ ID NO:1347:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1500086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:

Met	Pro	Arg	Pro	Phe	His	Lys	Leu	Ile	Phe	Ser	Ser	Thr	Ile	Gln
1			5				10						15	
Glu	Lys	Arg	Leu	Arg	Val	Pro	Asp	Lys	Phe	Val	Ser	Lys	Phe	Asp
			20				25					30		
Glu	Leu	Ser	Val	Ala	Val	Ala	Leu	Thr	Val	Pro	Asp	Gly	His	Val
			35				40					45		
Arg	Val	Gly	Leu	Arg	Lys	Ala	Asp	Asn	Lys	Ile	Trp	Phe	Gln	Asp
			50				55				60			
Trp	Gln	Glu	Phe	Val	Asp	Arg	Tyr	Ser	Ile	Arg	Ile	Asp	Tyr	Leu
			65				70			75			80	
Ile	Phe	Arg	Tyr	Glu	Gly	Asn	Ser	Ala	Phe	Ser	Val	Tyr	Ile	Phe
			85				90					95		Asn
Leu	Ser	His	Ser	Glu	Ile	Asn	Tyr	His	Ser	Thr	Gly	Leu	Met	Asp
			100				105					110		Ser
Ala	His	Asn	His	Phe	Lys	Arg	Ala	Arg	Leu	Phe	Glu	Asp	Leu	Glu
			115				120				125			Asp
Glu	Asp	Ala	Glu	Val	Ile	Phe	Pro	Ser	Ser	Val	Tyr	Pro	Ser	Pro
			130				135				140			Leu
Pro	Glu	Ser	Thr	Val	Pro	Ala	Asn	Lys	Gly	Tyr	Ala	Ser	Ser	Ala
			145				150			155				Ile
Gln	Thr	Leu	Phe	Thr	Gly	Pro	Val	Lys	Ala	Glu	Glu	Pro	Thr	Pro
			165				170					175		Thr
Pro	Lys	Ile	Pro	Lys	Lys	Arg	Gly	Arg	Lys	Lys	Lys	Asn	Ala	Asp
			180				185					190		Pro

Glu Glu Ile Asn Ser Ser Ala Pro Arg Asp Asp Asp Pro Glu Asn Arg
195 200 205
Ser Lys Phe Tyr Glu Ser Ala Ser Ala Arg Lys Arg Thr Val Thr Ala
210 215 220
Glu Glu Arg Glu Arg Ala Ile Asn Ala Ala Lys Thr Phe Glu Pro Thr
225 230 235 240
Asn Pro Phe Phe Arg Val Val Leu Arg Pro Ser Tyr Leu Tyr Arg Gly
245 250 255
Cys Ile Met Tyr Leu Pro Ser Gly Phe Ala Glu Lys Tyr Leu Ser Gly
260 265 270
Ile Ser Gly Phe Ile Lys Val Gln Leu Ala Glu Lys Gln Trp Pro Val
275 280 285
Arg Cys Leu Tyr Lys Ala Gly Arg Ala Lys Phe Ser Gln Gly Trp Tyr
290 295 300
Glu Phe Thr Leu Glu Asn Asn Leu Gly Glu Gly Asp Val Cys Val Phe
305 310 315 320
Glu Leu Leu Arg Thr Arg Asp Phe Val Leu Lys Val Thr Ala Phe Arg
325 330 335
Val Asn Glu Tyr Val
340

(2) INFORMATION FOR SEQ ID NO:1348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..232
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

Met Asp Ser Ala His Asn His Phe Lys Arg Ala Arg Leu Phe Glu Asp
1 5 10 15
Leu Glu Asp Glu Asp Ala Glu Val Ile Phe Pro Ser Ser Val Tyr Pro
20 25 30
Ser Pro Leu Pro Glu Ser Thr Val Pro Ala Asn Lys Gly Tyr Ala Ser
35 40 45
Ser Ala Ile Gln Thr Leu Phe Thr Gly Pro Val Lys Ala Glu Glu Pro
50 55 60
Thr Pro Thr Pro Lys Ile Pro Lys Lys Arg Gly Arg Lys Lys Lys Asn
65 70 75 80
Ala Asp Pro Glu Glu Ile Asn Ser Ser Ala Pro Arg Asp Asp Pro
85 90 95
Glu Asn Arg Ser Lys Phe Tyr Glu Ser Ala Ser Ala Arg Lys Arg Thr
100 105 110
Val Thr Ala Glu Glu Arg Glu Arg Ala Ile Asn Ala Ala Lys Thr Phe
115 120 125
Glu Pro Thr Asn Pro Phe Phe Arg Val Val Leu Arg Pro Ser Tyr Leu
130 135 140
Tyr Arg Gly Cys Ile Met Tyr Leu Pro Ser Gly Phe Ala Glu Lys Tyr
145 150 155 160
Leu Ser Gly Ile Ser Gly Phe Ile Lys Val Gln Leu Ala Glu Lys Gln
165 170 175
Trp Pro Val Arg Cys Leu Tyr Lys Ala Gly Arg Ala Lys Phe Ser Gln
180 185 190
Gly Trp Tyr Glu Phe Thr Leu Glu Asn Asn Leu Gly Glu Gly Asp Val
195 200 205
Cys Val Phe Glu Leu Leu Arg Thr Arg Asp Phe Val Leu Lys Val Thr
210 215 220
Ala Phe Arg Val Asn Glu Tyr Val

225

230

(2) INFORMATION FOR SEQ ID NO:1349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1597
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

```
aaaataaaga accctgacaa cttctctaca acactcaatt tttctctcta atgggtggaag      60
caagaagctt gaagaaacca atccaattgg gtaataaaga agatcaaaac cctagaaaaat      120
tctactctcg attcatcttt aaagctctta tctcaccgtt gcctcgccgc gtcgtacctg      180
tcttctcttc tcagacacca gagcttgcta accaaacaag actcctcgag ctctccacc      240
ttgttttcgt cggtatcgca gtctcttcag gtctcttcag ccgcagggaac tacgcaggag      300
gaggaggtgg aggaacaagc aatagtgata acacaagaag tgatcatagt aataataatt      360
cgcattcata tgtgcctaag attcttgaag tatcctctgt ttttaacgtg ggctcacgaga      420
gtgaatcga accgtccgat gattcctccg gtgatcaacg taagtttcag acatggaaga      480
acaagtacca catgaaaaat cccgaggttg agactcgttt cgttgatcga gttagttcag      540
aaaaacagaga gaagcctctg cttttgccgg ttcggagett gaattattct cgtgtttctg      600
attcttccgg cgataatttc ggtcgatggg agaaagtggag atctaagaga gaactttcta      660
agactcttgg cgatgataat agtgatgtgc ttcttctctc gattccatgg aggtcaagat      720
catcttcaat atcatcatca tcatcaaaag aggttgaatt tctaccgtcc gttaaagaatc      780
tgactacagt tgaatcacag ccggtgatca agaactcgac accatcttct tctttctctt      840
ctccaagaaa gtcgaaatcct atacctaatc tgcgactctga gttccatctta ctcccgccac      900
cgccctctcc gccgcgccca ccaactaccg cgttttataa ctctctctgc agaaaagatc      960
atcccggaat ttacagggtt gagaggagag aatcatcagt tcacaagacg aaaaattgcag      1020
gaggtgagtt tcatctctcc cgccctctct ctccaccacc tccggtggag tattataagt      1080
caccctccga aaaaattcaga ctaagtaacg aacggagaaa gtctctcggg caaagatgtw      1140
aaagaaacgc tcctaaaaag gtttggtggt ccgatccaat cgtggaatcg aaggaaacaag      1200
acacagagaa gaatgatcaa agaagtaact tgggaagcaa ggcagtggaa gaatccgaga      1260
atggagacaa gagaagagga gaaaatgaaa tccacgacga ggttgagaag aaatatagtag      1320
aggaagaagg agttagttag atcaacaatg gaagtgaact ggacaagaag gcagatagagt      1380
tcattgcmaa gtccagagaa cagattaggt tacaaagaat cgagtcctatc aagagatcta      1440
ctaataagat ctctgcaaat tcttcgaggt agaactcatt atttattaat aataggata      1500
cattttaagt atgttttggt aatcatcata aggttgtaat attaagggga acaaatattt      1560
ttgttacatt tattcagcca caaaaacagg attggag
```

(2) INFORMATION FOR SEQ ID NO:1350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..473
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:

```
Met Val Glu Ala Arg Ser Leu Lys Lys Pro Ile Gln Leu Gly Asn Lys
1           5           10           15
Glu Asp Gln Asn Pro Arg Lys Phe Tyr Ser Arg Phe Ile Phe Lys Ala
20           25           30
Leu Ile Leu Thr Val Leu Cys Ala Val Val Pro Val Phe Leu Ser Gln
35           40           45
Thr Pro Glu Leu Ala Asn Gln Thr Arg Leu Leu Glu Leu Leu His Leu
50           55           60
Val Phe Val Gly Ile Ala Val Ser Tyr Gly Leu Phe Ser Arg Arg Asn
```

65					70					75					80
Tyr	Asp	Gly	Gly	Gly	Gly	Gly	Gly	Thr	Ser	Asn	Ser	Asp	His	Asn	Lys
				85					90					95	
Ala	Asp	His	Ser	Asn	Asn	Asn	Ser	His	Ser	Tyr	Val	Pro	Lys	Ile	Leu
				100					105				110		
Glu	Val	Ser	Ser	Val	Phe	Asn	Val	Gly	His	Glu	Ser	Glu	Ser	Glu	Pro
				115				120				125			
Ser	Asp	Asp	Ser	Ser	Gly	Asp	Gln	Arg	Lys	Phe	Gln	Thr	Trp	Lys	Asn
				130		135					140				
Lys	Tyr	His	Met	Lys	Ile	Pro	Glu	Val	Glu	Thr	Arg	Phe	Val	Asp	Arg
				145		150				155				160	
Val	Ser	Ser	Glu	Asn	Arg	Glu	Lys	Pro	Leu	Leu	Pro	Val	Arg	Ser	
				165				170					175		
Leu	Asn	Tyr	Ser	Arg	Val	Ser	Asp	Ser	Ser	Gly	Asp	Asn	Ser	Gly	Arg
				180				185					190		
Trp	Glu	Lys	Val	Arg	Ser	Lys	Arg	Glu	Leu	Leu	Lys	Thr	Leu	Gly	Asp
				195			200					205			
Asp	Asn	Ser	Asp	Val	Leu	Pro	Ser	Pro	Ile	Pro	Trp	Arg	Ser	Arg	Ser
				210		215					220				
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Lys	Glu	Val	Glu	Ser	Leu	Pro	Ser
				225		230				235				240	
Val	Lys	Asn	Leu	Thr	Thr	Val	Glu	Ser	Gln	Pro	Leu	Ile	Lys	Asn	Leu
				245				250					255		
Thr	Pro	Ser	Ser	Ser	Phe	Ser	Ser	Pro	Arg	Lys	Ser	Asn	Pro	Ile	Pro
				260				265					270		
Asn	Leu	Ala	Ser	Glu	Phe	His	Pro	Ser	Pro	Pro	Pro	Pro	Pro	Pro	Pro
				275			280					285			
Pro	Pro	Pro	Leu	Pro	Ala	Phe	Tyr	Asn	Ser	Ser	Ser	Arg	Lys	Asp	His
				290		295					300				
Pro	Gly	Ile	Tyr	Arg	Val	Glu	Arg	Arg	Glu	Ser	Ser	Val	His	Lys	Thr
				305		310				315				320	
Lys	Phe	Ala	Gly	Gly	Glu	Phe	His	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
				325				330					335		
Pro	Pro	Val	Glu	Tyr	Tyr	Lys	Ser	Pro	Thr	Lys	Phe	Arg	Leu	Ser	
				340				345				350			
Asn	Glu	Arg	Arg	Lys	Ser	Ser	Glu	Gln	Lys	Met	Xaa	Arg	Asn	Ala	Pro
				355			360				365				
Lys	Lys	Val	Trp	Trp	Ser	Asp	Pro	Ile	Val	Glu	Ser	Lys	Glu	Gln	Asp
				370		375					380				
Thr	Glu	Lys	Asn	Asp	Gln	Arg	Ser	Asn	Leu	Gly	Ser	Lys	Ala	Val	Glu
				385		390				395				400	
Glu	Ser	Glu	Asn	Gly	Glu	Gln	Arg	Arg	Gly	Glu	Asn	Glu	Ile	His	Asp
				405					410				415		
Glu	Val	Glu	Lys	Lys	Ile	Val	Glu	Glu	Glu	Gly	Val	Ser	Glu	Ile	Asn
				420				425					430		
Asn	Gly	Ser	Asp	Val	Asp	Lys	Lys	Ala	Asp	Glu	Phe	Ile	Ala	Lys	Phe
				435			440				445				
Arg	Glu	Gln	Ile	Arg	Leu	Gln	Arg	Ile	Glu	Ser	Ile	Lys	Arg	Ser	Thr
				450		455					460				
Asn	Lys	Ile	Ser	Ala	Asn	Ser	Ser	Arg							
				465		470									

(2) INFORMATION FOR SEQ ID NO:1351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..326

(X1) SEQUENCE	DESCRIPTION	LENGTH
ttgtcctaaaag	ctgattctctc	60
acgggaagaat	tcaactaatgc	120
aaatacaccac	caccaccata	180
atacactatc	ctctcgagtc	240
qgcqacgttc	gttgagtgaa	300
	gccttatggc	60
	atcgattttg	120
	caaccttgaa	180
	cggcccaacc	240
	ctctaggagca	300
	tcctaatgga	60
	ttctgaacac	120
	tgatctatgc	180
	ttatctggta	240
	tcctgaatct	300
	ttggacgaca	60
	ctgactttct	120
	gattatgtaa	180
	ctctaatgga	240
	ctctgaatgc	300
	ctctgaatgc	60
	ctctgaatgc	120
	ctctgaatgc	180
	ctctgaatgc	240
	ctctgaatgc	300

gcgtgatttg	tgaaaatggt	acaaaagaga	tgttgaagaa	tgcaatgttc	acaatcacaa	360
ttggatcaaa	tgatatattt	aattatatcc	aaccatcaat	acctttcttc	tctcaagaca	420
agctccccac	tgaatgtcct	acaagattcc	atggctcctc	attttaacca	cacatcttaa	480
gcgattgcat	cagctaggag	gtagggaagt	cgtggtggtt	ggagtagggc	cactcggttg	540
catacccttt	gctcgagcgt	tgaattttat	accagccgga	aaatgctccg	aacaagtcaa	600
ccaagtagtc	cgaggttata	acatgaagct	tataactctc	cttaagacat	tgaacaatga	660
gttaagatcc	gaagattaca	acatacattt	tgtctacgcc	aactcttacg	acctattctt	720
gaaactagtt	ttgaaactac	aactatttgg	cttgaagaac	gcagacaagc	cgtgttggtg	780
cggtactttt	ccaccggt					

(2) INFORMATION FOR SEQ ID NO:1353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1500092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:

Leu	Ser	Lys	Ala	Asp	Ser	Ser	Pro	Tyr	Gly	Ile	Asp	Phe	Ala	Pro	Ser	
1				5					10					15		
Asn	Gly	Gln	Pro	Thr	Gly	Arg	Phe	Thr	Asn	Gly	Arg	Thr	Ile	Ser	Asp	
				20				25					30			
Ile	Val	Gly	Glu	Ala	Leu	Gly	Ala	Lys	Ser	Pro	Pro	Pro	Pro	Tyr	Leu	
				35				40					45			
Glu	Pro	Asn	Thr	Glu	Ala	Asn	Thr	Ile	Leu	Asn	Gly	Ile	Asn	Tyr	Ala	
				50				55					60			
Ser	Gly	Ala	Ala	Gly	Ile	Leu	Asp	Asp	Thr	Gly	Leu	Val	His	Arg		
				65				70					75		80	
Gly	Glu	Phe	Arg													

(2) INFORMATION FOR SEQ ID NO:1354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1500093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

Met	Ser	Tyr	Lys	Ile	Pro	Trp	Ser	Ser	Ile	Leu	Thr	Thr	His	Leu	Lys	
1				5					10					15		
Arg	Leu	His	Gln	Leu	Gly	Gly	Arg	Lys	Phe	Val	Val	Val	Gly	Val	Gly	
				20				25					30			
Pro	Leu	Gly	Cys	Ile	Pro	Phe	Ala	Arg	Ala	Leu	Asn	Xaa	Ile	Pro	Ala	
				35				40					45			
Gly	Lys	Cys	Ser	Glu	Gln	Val	Asn	Gln	Val	Val	Arg	Gly	Tyr	Asn	Met	
				50				55					60			
Lys	Leu	Ile	His	Ser	Leu	Lys	Thr	Leu	Asn	Asn	Glu	Leu	Arg	Ser	Glu	
				65				70					75		80	
Asp	Tyr	Asn	Thr	Thr	Phe	Val	Tyr	Ala	Asn	Ser	Tyr	Asp	Leu	Phe	Leu	
				85				90					95			
Lys	Leu	Val	Leu	Asn	Tyr	Gln	Leu	Phe	Gly	Leu	Lys	Asn	Ala	Asp	Lys	
				100				105					110			
Pro	Cys	Cys	Gly	Gly	Tyr	Phe	Pro	Pro								
				115				120								

(2) INFORMATION FOR SEQ ID NO:1355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1474
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

agttggagct	cgaaaccctt	cttcattctt	ttcttctctt	ccacctaacc	aatggggagca	60
attgatctct	ctttctcaca	gagtcctctc	ttctcttcgt	cgcgttccaa	tctttctctc	120
tccacacacc	gttccgctct	ttttttccg	ccgggaagca	agtcacgggt	tctgcccgcg	180
ttgcggtcaa	tgagtcata	cgacgacacg	gcctcaaaag	aggtgaagct	atgggggtgga	240
aggttcgaag	agagtgctac	tgagaaaagt	gagaagttca	ctgagtcatt	ttcatttgat	300
aaggtttctt	acaagcagga	cattatgggt	agcaaaagctc	atgcttcaat	gcttgctcac	360
caggggctaa	taactgatag	cgataaagat	agcattttga	gaggtcttga	tgatatggag	420
agacaaattg	aagcaataaa	gtttgaatgg	aggactgac	gagaagatgt	gcatatgaac	480
attgaagcag	ctcttactga	tcttattggt	gaacctgcaa	agaaacttca	tactgcaagg	540
agcagaaatg	accaagtgtc	tactgacttc	aggctttggt	gtcgtgatgc	tatcgataca	600
attatttgca	aaatcagaaa	tcttcagaga	gcactgtgtg	aactggcttt	gaagaatgag	660
gctttgattg	ttcctgggta	tactcatctt	caaagagctc	agcctgtttt	actcccacac	720
gttctcttaa	cttttgtata	gcagctcgaa	cgatgatgct	gtcgttatgt	ggaactgtcg	780
gcaaggctaa	attttctccc	cctgggagct	tgctgctttg	ctggaactgt	tctgcctatt	840
gataggttta	tgactgcaaa	tgctcttgga	tttaccgaa	caatgagaaa	cagatctgat	900
gcagctcag	accgagactt	cgctgtggag	ttcttatata	caaatgccaa	caccggttat	960
catttatac	ggcttggaga	agagtgggta	ctgtgggctt	ccgaggagtt	tggtgtcatg	1020
actccaagtg	attctgtgtc	aaccggaagt	agtataatg	cacagaagaa	aaatccagac	1080
ccaatggaac	ttgtcagagg	aaaatccgca	agagtcata	gcgatctggt	caactgtctta	1140
acactgtgca	aggagacttc	ccttgcttac	aacagagatt	ttcaagaagg	cacagagccg	1200
atgttcgata	gtaccaagac	aataatggga	atgatcgatg	tatctcgaga	atttgcctag	1260
aatgtttacat	tcaacgaaga	cagaatcaag	aaaagctctc	ccgcaggaca	tcttgatgcg	1320
actactctcg	ctgattattc	tgtgaagaag	gggattgcct	ttaggtcatc	tcatgacata	1380
gttggaanaac	tagttggagt	tgtgcgtctca	aaaggctgtg	aacttcagaa	cttaagtctt	1440
gaagagatga	aaaagctgag	ccctgtgttt	gaag			

(2) INFORMATION FOR SEQ ID NO:1356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..474
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

Met	Gly	Ala	Ile	Asp	Leu	Ser	Phe	Ser	Gln	Ser	Leu	Phe	Ser	Ser
1				5					10				15	
Ser	Arg	Ser	Asn	Leu	Ser	Ser	Ser	Thr	His	Arg	Ser	Val	Ser	Phe
Pro	Pro	Gly	Ser	Lys	Ser	Arg	Cys	Leu	Pro	Pro	Leu	Arg	Ser	Met
				20				25				30		
His	Asp	Asp	Asp	Thr	Ala	Ser	Lys	Glu	Val	Lys	Leu	Trp	Gly	Arg
Phe	Glu	Glu	Ser	Val	Thr	Glu	Lys	Val	Glu	Lys	Phe	Thr	Glu	Ser
65				70				75					80	
Ser	Phe	Asp	Lys	Val	Leu	Tyr	Lys	Gln	Asp	Ile	Met	Gly	Ser	Lys
				85				90					95	

His Ala Ser Met Leu Ala His Gln Gly Leu Ile Thr Asp Ser Asp Lys
100 105 110
Asp Ser Ile Leu Arg Gly Leu Asp Asp Ile Glu Arg Gln Ile Glu Ala
115 120 125
Asn Lys Phe Glu Trp Arg Thr Asp Arg Glu Asp Val His Met Asn Ile
130 135 140
Glu Ala Ala Leu Thr Asp Leu Ile Gly Glu Pro Ala Lys Lys Leu His
145 150 155 160
Thr Ala Arg Ser Arg Asn Asp Gln Val Ala Thr Asp Phe Arg Leu Trp
165 170 175
Cys Arg Asp Ala Ile Asp Thr Ile Ile Val Lys Ile Arg Asn Leu Gln
180 185 190
Arg Ala Leu Val Glu Leu Ala Leu Lys Asn Glu Ala Leu Ile Val Pro
195 200 205
Gly Tyr Thr His Leu Gln Arg Ala Gln Pro Val Leu Leu Pro His Val
210 215 220
Leu Leu Thr Phe Val Glu Gln Leu Glu Arg Asp Ala Gly Arg Tyr Val
225 230 235 240
Asp Cys Arg Ala Arg Leu Asn Phe Ser Pro Leu Gly Ala Cys Ala Leu
245 250 255
Ala Gly Thr Gly Leu Pro Ile Asp Arg Phe Met Thr Ala Asn Ala Leu
260 265 270
Gly Phe Thr Glu Pro Met Arg Asn Ser Ile Asp Ala Val Ser Asp Arg
275 280 285
Asp Phe Val Leu Glu Phe Leu Tyr Thr Asn Ala Asn Thr Gly Ile His
290 295 300
Leu Ser Arg Leu Gly Glu Glu Trp Val Leu Trp Ala Ser Glu Glu Phe
305 310 315 320
Gly Phe Met Thr Pro Ser Asp Ser Val Ser Thr Gly Ser Ser Ile Met
325 330 335
Pro Gln Lys Lys Asn Pro Asp Pro Met Glu Leu Val Arg Gly Lys Ser
340 345 350
Ala Arg Val Ile Gly Asp Leu Val Thr Val Leu Thr Leu Cys Lys Gly
355 360 365
Leu Pro Leu Ala Tyr Asn Arg Asp Phe Gln Glu Asp Lys Glu Pro Met
370 375 380
Phe Asp Ser Thr Lys Thr Ile Met Gly Met Ile Asp Val Ser Ala Glu
385 390 395 400
Phe Ala Gln Asn Val Thr Phe Asn Glu Asp Arg Ile Lys Lys Ser Leu
405 410 415
Pro Ala Gly His Leu Asp Ala Thr Thr Leu Ala Asp Tyr Leu Val Lys
420 425 430
Lys Gly Met Pro Phe Arg Ser Ser His Asp Ile Val Gly Lys Leu Val
435 440 445
Gly Val Cys Val Ser Lys Gly Cys Glu Leu Gln Asn Leu Ser Leu Glu
450 455 460
Glu Met Lys Lys Leu Ser Pro Val Phe Glu
465 470

(2) INFORMATION FOR SEQ ID NO:1357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 428 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..428

(D) OTHER INFORMATION: / Ceres Seq. ID 1500099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

Met Ser His Asp Asp Asp Thr Ala Ser Lys Glu Val Lys Leu Trp Gly

1	5	10	15
Gly Arg Phe Glu Glu Ser Val Thr Glu Lys Val Glu Lys Phe Thr Glu			
20		25	30
Ser Ile Ser Phe Asp Lys Val Leu Tyr Lys Gln Asp Ile Met Gly Ser			
35		40	45
Lys Ala His Ala Ser Met Leu Ala His Gln Gly Leu Ile Thr Asp Ser			
50	55	60	
Asp Lys Asp Ser Ile Leu Arg Gly Leu Asp Asp Ile Glu Arg Gln Ile			
65	70	75	80
Glu Ala Asn Lys Phe Glu Trp Arg Thr Asp Arg Glu Asp Val His Met			
	85	90	95
Asn Ile Glu Ala Ala Leu Thr Asp Leu Ile Gly Glu Pro Ala Lys Lys			
100	105	110	
Leu His Thr Ala Arg Ser Arg Asn Asp Gln Val Ala Thr Asp Phe Arg			
115	120	125	
Leu Trp Cys Arg Asp Ala Ile Asp Thr Ile Ile Val Lys Ile Arg Asn			
130	135	140	
Leu Gln Arg Ala Leu Val Glu Leu Ala Leu Lys Asn Glu Ala Leu Ile			
145	150	155	160
Val Pro Gly Tyr Thr His Leu Gln Arg Ala Gln Pro Val Leu Leu Pro			
	165	170	175
His Val Leu Leu Thr Phe Val Glu Gln Leu Glu Arg Asp Ala Gly Arg			
180	185	190	
Tyr Val Asp Cys Arg Ala Arg Leu Asn Phe Ser Pro Leu Gly Ala Cys			
195	200	205	
Ala Leu Ala Gly Thr Gly Leu Pro Ile Asp Arg Phe Met Thr Ala Asn			
210	215	220	
Ala Leu Gly Phe Thr Glu Pro Met Arg Asn Ser Ile Asp Ala Val Ser			
225	230	235	240
Asp Arg Asp Phe Val Leu Glu Phe Leu Tyr Thr Asn Ala Asn Thr Gly			
	245	250	255
Ile His Leu Ser Arg Leu Gly Glu Glu Trp Val Leu Trp Ala Ser Glu			
260	265	270	
Glu Phe Gly Phe Met Thr Pro Ser Asp Ser Val Ser Thr Gly Ser Ser			
275	280	285	
Ile Met Pro Gln Lys Lys Asn Pro Asp Pro Met Glu Leu Val Arg Gly			
290	295	300	
Lys Ser Ala Arg Val Ile Gly Asp Leu Val Thr Val Leu Thr Leu Cys			
305	310	315	320
Lys Gly Leu Pro Leu Ala Tyr Asn Arg Asp Phe Gln Glu Asp Lys Glu			
	325	330	335
Pro Met Phe Asp Ser Thr Lys Thr Ile Met Gly Met Ile Asp Val Ser			
340	345	350	
Ala Glu Phe Ala Gln Asn Val Thr Phe Asn Glu Asp Arg Ile Lys Lys			
355	360	365	
Ser Leu Pro Ala Gly His Leu Asp Ala Thr Thr Leu Ala Asp Tyr Leu			
370	375	380	
Val Lys Lys Gly Met Pro Phe Arg Ser Ser His Asp Ile Val Gly Lys			
385	390	395	400
Leu Val Gly Val Cys Val Ser Lys Gly Cys Glu Leu Gln Asn Leu Ser			
	405	410	415
Leu Glu Glu Met Lys Lys Leu Ser Pro Val Phe Glu			
420	425		

(2) INFORMATION FOR SEQ ID NO:1358:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..383
(D) OTHER INFORMATION: / Ceres Seq. ID 1500100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

Met Gly Ser Lys Ala His Ala Ser Met Leu Ala His Gln Gly Leu Ile
1 5 10 15
Thr Asp Ser Asp Lys Asp Ser Ile Leu Arg Gly Leu Asp Asp Ile Glu
20 25 30
Arg Gln Ile Glu Ala Asn Lys Phe Glu Trp Arg Thr Asp Arg Glu Asp
35 40 45
Val His Met Asn Ile Glu Ala Ala Leu Thr Asp Leu Ile Gly Glu Pro
50 55 60
Ala Lys Lys Leu His Thr Ala Arg Ser Arg Asn Asp Gln Val Ala Thr
65 70 75 80
Asp Phe Arg Leu Trp Cys Arg Asp Ala Ile Asp Thr Ile Ile Val Lys
85 90 95
Ile Arg Asn Leu Gln Arg Ala Leu Val Glu Leu Ala Leu Lys Asn Glu
100 105 110
Ala Leu Ile Val Pro Gly Tyr Thr His Leu Gln Arg Ala Gln Pro Val
115 120 125
Leu Leu Pro His Val Leu Leu Thr Phe Val Glu Gln Leu Glu Arg Asp
130 135 140
Ala Gly Arg Tyr Val Asp Cys Arg Ala Arg Leu Asn Phe Ser Pro Leu
145 150 155 160
Gly Ala Cys Ala Leu Ala Gly Thr Gly Leu Pro Ile Asp Arg Phe Met
165 170 175
Thr Ala Asn Ala Leu Gly Phe Thr Glu Pro Met Arg Asn Ser Ile Asp
180 185 190
Ala Val Ser Asp Arg Asp Phe Val Leu Glu Phe Leu Tyr Thr Asn Ala
195 200 205
Asn Thr Gly Ile His Leu Ser Arg Leu Gly Glu Glu Trp Val Leu Trp
210 215 220
Ala Ser Glu Glu Phe Gly Phe Met Thr Pro Ser Asp Ser Val Ser Thr
225 230 235 240
Gly Ser Ser Ile Met Pro Gln Lys Lys Asn Pro Asp Pro Met Glu Leu
245 250 255
Val Arg Gly Lys Ser Ala Arg Val Ile Gly Asp Leu Val Thr Val Leu
260 265 270
Thr Leu Cys Lys Gly Leu Pro Leu Ala Tyr Asn Arg Asp Phe Gln Glu
275 280 285
Asp Lys Glu Pro Met Phe Asp Ser Thr Lys Thr Ile Met Gly Met Ile
290 295 300
Asp Val Ser Ala Glu Phe Ala Gln Asn Val Thr Phe Asn Glu Asp Arg
305 310 315 320
Ile Lys Lys Ser Leu Pro Ala Gly His Leu Asp Ala Thr Thr Leu Ala
325 330 335
Asp Tyr Leu Val Lys Lys Gly Met Pro Phe Arg Ser Ser His Asp Ile
340 345 350
Val Gly Lys Leu Val Gly Val Cys Val Ser Lys Gly Cys Glu Leu Gln
355 360 365
Asn Leu Ser Leu Glu Glu Met Lys Lys Leu Ser Pro Val Phe Glu
370 375 380

(2) INFORMATION FOR SEQ ID NO:1359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..904

(D) OTHER INFORMATION: / Ceres Seq. ID 1500101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:

actcttactc	tggtctcgct	acagaatctc	ctgggaaaaa	aaaaagaaac	ttgatccacc	60
cgaattcccc	aaatcttcac	aatttctgga	aactctctcg	atcggtgaagc	agaaaaagtga	120
gggtccaaat	gggttctggt	tcgggtccaaa	cccggaattac	aacgatgaac	ctctcgctct	180
caacagacaga	gaagaaccct	aatttctgct	cggcgcttct	caattctaa	aacgcaattt	240
cagatacttt	aggggtctct	tccaaatgca	gtacattctc	caggggtcaa	tttcaaagaa	300
tacatttttt	ttggctacaa	cacactcgac	ctttgagaaa	acgaacagta	tttggtcacg	360
tgagctcgct	catgccgtta	acggaagaga	atgtggagag	agtgttagac	gaagtacacg	420
catctctaata	ggcgcagcga	ggaaacgtgg	cggtgcacga	aatcgacgga	cttgggtgtg	480
ttttaagagt	acaaaggagct	tggtgttctg	gtcctagctc	atcaatgacg	ttgaagattg	540
gaatcgagac	tcgtcttcga	gacaagattc	cagagatcat	gtccgttgag	cagtttcttg	600
aatccgagac	aggaggttta	gagctgaacg	atgagaacat	tgagaaggtt	ctctctgagt	660
taaggccgta	cctatccggt	actggaggtg	gggggcttga	gttagttgag	attgatgtgt	720
acgtggtcaa	gggttcgact	actggaccag	ctgctggagt	catgactgtt	cgtgtcgcgt	780
tgactcaaaa	actgagggaa	acaattcctt	ctataggtgc	agttccagctt	ctagagtgc	840
attaaccttt	ttattttgta	acttatatac	aaggcctatt	tttgattcaa	tatatattat	900

ttcc

(2) INFORMATION FOR SEQ ID NO:1360:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1500102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

Met	Gly	Ser	Val	Ser	Gly	Gln	Thr	Arg	Ile	Thr	Met	Asn	Leu	Ser
1					5				10				15	
Leu	Ser	Thr	Ala	Glu	Lys	Asn	Pro	Asn	Phe	Cys	Ser	Ala	Leu	Asn
			20					25					30	
Ser	Lys	Asn	Ala	Ile	Ser	Asp	Thr	Leu	Gly	Val	Ser	Ser	Lys	Cys
		35					40				45			
Thr	Phe	Leu	Arg	Gly	Gln	Phe	Gln	Arg	Ile	His	Phe	Ser	Trp	Leu
	50					55					60			
His	Thr	Arg	Pro	Leu	Arg	Lys	Arg	Thr	Val	Phe	Gly	His	Val	Ser
65					70					75				80
Val	Met	Pro	Leu	Thr	Glu	Glu	Asn	Val	Glu	Arg	Val	Leu	Asp	Glu
					85				90				95	
Arg	Pro	Ser	Leu	Met	Ala	Asp	Gly	Gly	Asn	Val	Ala	Leu	His	Glu
					100			105					110	
Asp	Gly	Leu	Val	Val	Val	Leu	Lys	Leu	Gln	Gly	Ala	Cys	Gly	Ser
		115				120					125			
Pro	Ser	Ser	Ser	Met	Thr	Leu	Lys	Met	Gly	Ile	Glu	Ser	Arg	Leu
		130				135				140				
Asp	Lys	Ile	Pro	Glu	Ile	Met	Ser	Val	Glu	Gln	Phe	Leu	Glu	Ser
145					150				155					160
Thr	Gly	Gly	Leu	Glu	Leu	Asn	Asp	Glu	Asn	Ile	Glu	Lys	Val	Leu
			165					170					175	
Glu	Leu	Arg	Pro	Tyr	Leu	Ser	Gly	Thr	Gly	Gly	Gly	Leu	Glu	Leu
			180					185					190	
Val	Glu	Ile	Asp	Gly	Tyr	Val	Val	Lys	Val	Arg	Leu	Thr	Gly	Pro
		195				200					205			
Ala	Gly	Val	Met	Thr	Val	Arg	Val	Ala	Leu	Thr	Gln	Lys	Leu	Arg
	210					215				220				
Thr	Ile	Pro	Ser	Ile	Gly	Ala	Val	Gln	Leu	Leu	Glu			
225					230					235				

(2) INFORMATION FOR SEQ ID NO:1361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..224
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

Met Asn Leu Ser Leu Ser Thr Ala Glu Lys Asn Pro Asn Phe Cys Ser
1 5 10 15
Ala Leu Leu Asn Ser Lys Asn Ala Ile Ser Asp Thr Leu Gly Val Ser
20 25 30
Ser Lys Cys Ser Thr Phe Leu Arg Gly Gln Phe Gln Arg Ile His Phe
35 40 45
Ser Trp Leu Gln His Thr Arg Pro Leu Arg Lys Arg Thr Val Phe Gly
50 55 60
His Val Ser Cys Val Met Pro Leu Thr Glu Glu Asn Val Glu Arg Val
65 70 75 80
Leu Asp Glu Val Arg Pro Ser Leu Met Ala Asp Gly Gly Asn Val Ala
85 90 95
Leu His Glu Ile Asp Gly Leu Val Val Leu Lys Leu Gln Gly Ala
100 105 110
Cys Gly Ser Cys Pro Ser Ser Ser Met Thr Leu Lys Met Gly Ile Glu
115 120 125
Ser Arg Leu Arg Asp Lys Ile Pro Glu Ile Met Ser Val Glu Gln Phe
130 135 140
Leu Glu Ser Glu Thr Gly Gly Leu Glu Leu Asn Asp Glu Asn Ile Glu
145 150 155 160
Lys Val Leu Ser Glu Leu Arg Pro Tyr Leu Ser Gly Thr Gly Gly Gly
165 170 175
Gly Leu Glu Leu Val Glu Ile Asp Gly Tyr Val Val Lys Val Arg Leu
180 185 190
Thr Gly Pro Ala Ala Gly Val Met Thr Val Arg Val Ala Leu Thr Gln
195 200 205
Lys Leu Arg Glu Thr Ile Pro Ser Ile Gly Ala Val Gln Leu Leu Glu
210 215 220

(2) INFORMATION FOR SEQ ID NO:1362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

Met Pro Thr Glu Glu Asn Val Glu Arg Val Leu Asp Glu Val Arg
1 5 10 15
Pro Ser Leu Met Ala Asp Gly Gly Asn Val Ala Leu His Glu Ile Asp
20 25 30
Gly Leu Val Val Val Leu Lys Leu Gln Gly Ala Cys Gly Ser Cys Pro
35 40 45
Ser Ser Ser Met Thr Leu Lys Met Gly Ile Glu Ser Arg Leu Arg Asp

50						55						60							
Lys	Ile	Pro	Glu	Ile	Met	Ser	Val	Glu	Gln	Phe	Leu	Glu	Ser	Glu	Thr				
65					70					75					80				
Gly	Gly	Leu	Glu	Leu	Asn	Asp	Glu	Asn	Ile	Glu	Lys	Val	Leu	Ser	Glu				
				85					90					95					
Leu	Arg	Pro	Tyr	Leu	Ser	Gly	Thr	Gly	Gly	Gly	Gly	Leu	Glu	Leu	Val				
			100					105						110					
Glu	Ile	Asp	Gly	Tyr	Val	Val	Lys	Val	Arg	Leu	Thr	Gly	Pro	Ala	Ala				
			115					120					125						
Gly	Val	Met	Thr	Val	Arg	Val	Ala	Leu	Thr	Gln	Lys	Leu	Arg	Glu	Thr				
			130				135					140							
Ile	Pro	Ser	Ile	Gly	Ala	Val	Gln	Leu	Leu	Glu									
145				150						155									

(2) INFORMATION FOR SEQ ID NO:1363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1640
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

acatgggtctt	gttctttctc	tctccttctt	tctccttctt	gcgggtctccc	tttctctctc	60
tatcgccaca	atgatcatta	ccaaccaaac	tgattgaaac	tcatttggtc	tctctctctc	120
aaatccactc	tctctcttct	tttctctctc	tctctctctg	gtctctatcg	ccatgggtga	180
tgataaggag	atgcctgctg	ctgtagtgtg	tgacatgat	caagtcaactg	gtcatattat	240
ttccaccaca	atcggtggca	aaaatggtga	accaaaccag	acaattagtt	acatggcgga	300
sgagttgttg	gtacaggctc	gttcgggcat	gttttccaa	caaaatgttt	ggagactgga	360
gaaacccgtg	cgataaagaa	ggttttgcaa	gatagaagat	acaagaaccg	agaacttcag	420
ttgatgcgtg	tgatggatca	tccgaatgtg	gtttgtttga	agcattgtct	ctttcgcact	480
acaagtaaa	acgagctttt	cttggaacttg	gttatggagt	atgtccctga	gagcttgtat	540
cgagttctga	aacattatag	tagtgcaaac	caaagaatgc	ctctgtgtct	tgttaaactt	600
tacatgtatc	agatcttccg	gggacttgct	tacattcaca	atgttgctgg	agtttgtcac	660
agagatctaa	agcctcaaaa	tcttctggtt	gatcctctta	ctcatcaagt	caaaatctgt	720
gactttggca	gtgcgaaaca	gctcgtttaa	ggtgaagcca	acatttctta	catctgtctc	780
cgattctacc	gtgcaccctg	gtcatattt	ggtgccactg	agtacacaac	ttctattgat	840
atctggctct	ctggttggtg	tcttgctgag	cttcttcttg	gtcagccatt	atttcccgga	900
gaaaatgcgt	tggtatcagc	cgttgaaatt	ataaaagttc	ttggtacacc	aatcgagaaa	960
gaaaatccgt	gtatgaatcc	acattacaca	gatttcaggt	ttccacagat	aaaggcacat	1020
ccctggcaca	agatcttcca	caaaaggatg	ccccagaaag	cgattgattt	tgcatcaagg	1080
ctgcttcaat	actctccaag	tctaagatgc	acagcgctcg	aaagctgtgc	acatccgttc	1140
tttgatgaac	tcagagaagc	whmccaaacg	ctcgtttmcg	aaatggacgg	cttttccgcg	1200
ctctcttcaa	cttcaaacaa	gaagttagctg	gatcatcacc	tgaactggct	aacaagttag	1260
ttccagacca	tatcaagaga	caattgggct	taagcttctt	gaatcaatct	ggaacttaaa	1320
agggatctct	caaaaagaca	ctactttttt	atatataatg	taccattaca	cgagccacaa	1380
ggtcgtagtt	gaaggcaaac	gtggaggaca	caattcaaa	tttttctctc	tcaaaactctg	1440
tcagacaaag	ccagctgccta	gcaaaaccac	ctaccacaa	ctcgcaaaac	aaaaactctc	1500
cagtggttga	tctgttattt	tctctctctc	tttcaagttt	ggtgaaaaac	acagctctct	1560
ctttgcttca	tttcttctt	ctttccccct	tatgtaaaat	agtttagtca	gaagtttttt	1620
tatatagtaa	agtttggggc					

(2) INFORMATION FOR SEQ ID NO:1364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..267
(D) OTHER INFORMATION: / Ceres Seq. ID 1500106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:

Met	Arg	Val	Met	Asp	His	Pro	Asn	Val	Val	Cys	Leu	Lys	His	Cys	Phe
1			5					10					15		
Phe	Ser	Thr	Thr	Ser	Lys	Asp	Glu	Leu	Phe	Leu	Asn	Leu	Val	Met	Glu
			20				25					30			
Tyr	Val	Pro	Glu	Ser	Leu	Tyr	Arg	Val	Leu	Lys	His	Tyr	Ser	Ser	Ala
		35					40				45				
Asn	Gln	Arg	Met	Pro	Leu	Val	Tyr	Val	Lys	Leu	Tyr	Met	Tyr	Gln	Ile
		50				55					60				
Phe	Arg	Gly	Leu	Ala	Tyr	Ile	His	Asn	Val	Ala	Gly	Val	Cys	His	Arg
65					70				75					80	
Asp	Leu	Lys	Pro	Gln	Asn	Leu	Leu	Val	Asp	Pro	Leu	Thr	His	Gln	Val
				85					90				95		
Lys	Ile	Cys	Asp	Phe	Gly	Ser	Ala	Lys	Gln	Leu	Val	Lys	Gly	Glu	Ala
			100					105					110		
Asn	Ile	Ser	Tyr	Ile	Cys	Ser	Arg	Phe	Tyr	Arg	Ala	Pro	Glu	Leu	Ile
		115					120					125			
Phe	Gly	Ala	Thr	Glu	Tyr	Thr	Thr	Ser	Ile	Asp	Ile	Trp	Ser	Ala	Gly
		130				135					140				
Cys	Val	Leu	Ala	Glu	Leu	Leu	Gly	Gln	Pro	Leu	Phe	Pro	Gly	Glu	
145				150					155					160	
Asn	Ala	Val	Asp	Gln	Leu	Val	Glu	Ile	Lys	Val	Leu	Gly	Thr	Pro	
			165					170					175		
Thr	Arg	Glu	Glu	Ile	Arg	Cys	Met	Asn	Pro	His	Tyr	Thr	Asp	Phe	Arg
		180						185					190		
Phe	Pro	Gln	Ile	Lys	Ala	His	Pro	Trp	His	Lys	Ile	Phe	His	Lys	Arg
		195					200					205			
Met	Pro	Pro	Glu	Ala	Ile	Asp	Phe	Ala	Ser	Arg	Leu	Leu	Gln	Tyr	Ser
		210				215					220				
Pro	Ser	Leu	Arg	Cys	Thr	Ala	Leu	Glu	Ala	Cys	Ala	His	Pro	Phe	Phe
225				230					235					240	
Asp	Glu	Leu	Arg	Glu	Xaa	Xaa	Gln	Thr	Leu	Val	Xaa	Gln	Met	Asp	Gly
			245					250					255		
Leu	Ser	Arg	Leu	Ser	Ser	Thr	Ser	Asn	Lys	Lys					
			260					265							

(2) INFORMATION FOR SEQ ID NO:1365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..264
(D) OTHER INFORMATION: / Ceres Seq. ID 1500107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:

Met	Asp	His	Pro	Asn	Val	Val	Cys	Leu	Lys	His	Cys	Phe	Phe	Ser	Thr
1			5					10					15		
Thr	Ser	Lys	Asp	Glu	Leu	Phe	Leu	Asn	Leu	Val	Met	Glu	Tyr	Val	Pro
			20					25				30			
Glu	Ser	Leu	Tyr	Arg	Val	Leu	Lys	His	Tyr	Ser	Ser	Ala	Asn	Gln	Arg
		35					40				45				
Met	Pro	Leu	Val	Tyr	Val	Lys	Leu	Tyr	Met	Tyr	Gln	Ile	Phe	Arg	Gly
		50				55					60				
Leu	Ala	Tyr	Ile	His	Asn	Val	Ala	Gly	Val	Cys	His	Arg	Asp	Leu	Lys
65				70					75				80		
Pro	Gln	Asn	Leu	Leu	Val	Asp	Pro	Leu	Thr	His	Gln	Val	Lys	Ile	Cys

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      85          90          95
Asp Phe Gly Ser Ala Lys Gln Leu Val Lys Gly Glu Ala Asn Ile Ser
      100          105          110
Tyr Ile Cys Ser Arg Phe Tyr Arg Ala Pro Glu Leu Ile Phe Gly Ala
      115          120          125
Thr Glu Tyr Thr Thr Ser Ile Asp Ile Trp Ser Ala Gly Cys Val Leu
      130          135          140
Ala Glu Leu Leu Leu Gly Gln Pro Leu Phe Pro Gly Glu Asn Ala Val
      145          150          155          160
Asp Gln Leu Val Glu Ile Ile Lys Val Leu Gly Thr Pro Thr Arg Glu
      165          170          175          180
Glu Ile Arg Cys Met Asn Pro His Tyr Thr Asp Phe Arg Phe Pro Gln
      180          185          190          195
Ile Lys Ala His Pro Trp His Lys Ile Phe His Lys Arg Met Pro Pro
      195          200          205          210
Glu Ala Ile Asp Phe Ala Ser Arg Leu Leu Gln Tyr Ser Pro Ser Leu
      210          215          220          225
Arg Cys Thr Ala Leu Glu Ala Cys Ala His Pro Phe Phe Asp Glu Leu
      225          230          235          240
Arg Glu Xaa Xaa Gln Thr Leu Val Xaa Gln Met Asp Gly Leu Ser Arg
      245          250          255
Leu Ser Ser Thr Ser Asn Lys Lys
      260

```

(2) INFORMATION FOR SEQ ID NO:1366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..237
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:

```

Met Glu Tyr Val Pro Glu Ser Leu Tyr Arg Val Leu Lys His Tyr Ser
1      5      10      15
Ser Ala Asn Gln Arg Met Pro Leu Val Tyr Val Lys Leu Tyr Met Tyr
      20      25      30
Gln Ile Phe Arg Gly Leu Ala Tyr Ile His Asn Val Ala Gly Val Cys
      35      40      45
His Arg Asp Leu Lys Pro Gln Asn Leu Leu Val Asp Pro Leu Thr His
      50      55      60      65
Gln Val Lys Ile Cys Asp Phe Gly Ser Ala Lys Gln Leu Val Lys Gly
      70      75      80
Glu Ala Asn Ile Ser Tyr Ile Cys Ser Arg Phe Tyr Arg Ala Pro Glu
      85      90      95
Leu Ile Phe Gly Ala Thr Glu Tyr Thr Thr Ser Ile Asp Ile Trp Ser
      100          105          110
Ala Gly Cys Val Leu Ala Glu Leu Leu Leu Gly Gln Pro Leu Phe Pro
      115          120          125
Gly Glu Asn Ala Val Asp Gln Leu Val Glu Ile Ile Lys Val Leu Gly
      130          135          140
Thr Pro Thr Arg Glu Glu Ile Arg Cys Met Asn Pro His Tyr Thr Asp
      145          150          155          160
Phe Arg Phe Pro Gln Ile Lys Ala His Pro Trp His Lys Ile Phe His
      165          170          175
Lys Arg Met Pro Pro Glu Ala Ile Asp Phe Ala Ser Arg Leu Leu Gln
      180          185          190
Tyr Ser Pro Ser Leu Arg Cys Thr Ala Leu Glu Ala Cys Ala His Pro
      195          200          205

```

Phe Phe Asp Glu Leu Arg Glu Xaa Xaa Gln Thr Leu Val Xaa Gln Met
210 215 220
Asp Gly Leu Ser Arg Leu Ser Ser Thr Ser Asn Lys Lys
225 230 235

(2) INFORMATION FOR SEQ ID NO:1367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1841 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1841

(D) OTHER INFORMATION: / Ceres Seq. ID 1500109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:

```
cattaggatt ttgaatttcc aaatacattt tcagaaaaaa aagaattaaa agatcccat 60
gttgattatcc tcacagtaaa tgcttttgct tgagagagag tctgttagag gttttttgtt 120
tgttctgtgtt tcctctgttc acccagaaaa ctaaaaagca acaaaattca agaagagaga 180
gagagagata gcctcaaaac caagtctcaa ccattgttga tagaagagaa agcttttctt 240
ttcttggtgc ttatggtgaa agaatgaaag agagagagga ggagaagtga gaagcagaga 300
aagtgtttag agcttttcat gttcctttct ctccaagttt atatcttcat cggtttca 360
agtccaatta aaaagtggaa aagagtcctt cttcttcaac tattgtataa gcgaatagg 420
tcgaagagat gaaatgggat tatccgggtc aggttcttac tatatccata gaggattacc 480
cggtgtcggtt cctccaacgt ttcattggat accacagcaa cagcaaggtc ttctgtca 540
acctaatcaa aactctccat tcgggtcagg ctccactggt ttcggtatct cttctttaca 600
cggtgatcct ttcttggtcaa cagcagccgg aggagccgga gctcttcctc atcatatcgg 660
cgttaatag attgtctctc ctccacctcc cagtgaaact ccgatgaaac gaagagaggg 720
acggcctaga aaatcaggtc aagacggctc tgtttctttg gctctgtcgt ctctctctgt 780
ttcgaccatt actcccaaca actctaacaa acggcgccgt ggtcgacctc cgggtccggg 840
caagaaacag aqaatgctt cggttgttga actgatgcct tcatcttctg gaatagcttt 900
cacgcacat gttatcggtt ttccaatagg agaagatttt gcatcaacgg ttatagcttt 960
ctctcaacaa ggctccgagag ccatttgcgt tttatctgca agtgggtcag tctctactgc 1020
aacacttatt caaccatcag catctcccggt agccattaaa tacgagggcc ggttttgaat 1080
cctagcggtta tcaacattct atatagtggc aactgatgga agcttcogta accgaactgg 1140
aaaattatcg gtttgcgttg cttagccccga tgggctgtgt attggcggtg ccattggttg 1200
gcctttaata gctgcaagtc ctgttcaggt tattgtaggg agctttatat gggcagctcc 1260
aaagatcaag agcaagaaac gagaagaaga agcttctgaa gttgttcaag aaactgatga 1320
tcaccacggt ctggacaata ataacaacac gatttcgcct gtccttcagc agcagccaaa 1380
ccaaaacctg atttgcgtcaa caggttcaag gcaaatggat atgcgtcatg ctcatgctga 1440
tattgattta atgctgggtt gatgatagcg agaaagaact ctgtgtcat atagcattga 1500
atctaggaag aagaagaagg aatataagct aacctctgaa caaaagtatg tggaaatggt 1560
agggaaaaaa attaactcta ttagtgtacc tctcatatct ctaagcttgt ttggttttac 1620
tgtttctgtg actctgaaga ttgacagagt tcttttctt ctctgtttta gattgttacc 1680
tcgtttatga atttgcgtgc aattctgatt ctacagctta gattcagcta attgtgtaga 1740
gtttacatg ggaacctgaa aattggcgtt ttcatatgat ttcattatg ccaatttatt 1800
ttcatcaaat ttgtattagt acataattaa tttgttttt t
```

(2) INFORMATION FOR SEQ ID NO:1368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..348
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:

Met Asp Arg Arg Asp Ala Met Gly Leu Ser Gly Ser Gly Ser Tyr Tyr
1 5 10 15

Ile His Arg Gly Leu Pro Gly Ser Gly Pro Pro Thr Phe His Gly Ser
20 25 30
Pro Gln Gln Gln Gln Gly Leu Arg His Leu Pro Asn Gln Asn Ser Pro
35 40 45
Phe Gly Ser Gly Ser Thr Gly Phe Gly Ser Pro Ser Leu His Gly Asp
50 55 60
Pro Ser Leu Ala Thr Ala Ala Gly Gly Ala Gly Ala Leu Pro His His
65 70 75 80
Ile Gly Val Asn Met Ile Ala Pro Pro Pro Pro Ser Glu Thr Pro
85 90 95
Met Lys Arg Lys Arg Gly Arg Pro Arg Lys Tyr Gly Gln Asp Gly Ser
100 105 110
Val Ser Leu Ala Leu Ser Ser Ser Ser Val Ser Thr Ile Thr Pro Asn
115 120 125
Asn Ser Asn Lys Arg Gly Arg Gly Arg Pro Pro Gly Ser Gly Lys Lys
130 135 140
Gln Arg Met Ala Ser Val Gly Glu Leu Met Pro Ser Ser Ser Gly Met
145 150 155 160
Ser Phe Thr Pro His Val Ile Ala Val Ser Ile Gly Glu Asp Ile Ala
165 170 175
Ser Lys Val Ile Ala Phe Ser Gln Gln Gly Pro Arg Ala Ile Cys Val
180 185 190
Leu Ser Ala Ser Gly Ala Val Ser Thr Ala Thr Leu Ile Gln Pro Ser
195 200 205
Ala Ser Pro Gly Ala Ile Lys Tyr Glu Gly Arg Phe Glu Ile Leu Ala
210 215 220
Leu Ser Thr Ser Tyr Ile Val Ala Thr Asp Gly Ser Phe Arg Asn Arg
225 230 235 240
Thr Gly Asn Leu Ser Val Ser Leu Ala Ser Pro Asp Gly Arg Val Ile
245 250 255
Gly Gly Ala Ile Gly Gly Pro Leu Ile Ala Ala Ser Pro Val Gln Val
260 265 270
Ile Val Gly Ser Phe Ile Trp Ala Ala Pro Lys Ile Lys Ser Lys Lys
275 280 285
Arg Glu Glu Glu Ala Ser Glu Val Val Gln Glu Thr Asp Asp His His
290 295 300
Val Leu Asp Asn Asn Asn Asn Thr Ile Ser Pro Val Pro Gln Gln Gln
305 310 315 320
Pro Asn Gln Asn Leu Ile Trp Ser Thr Gly Ser Arg Gln Met Asp Met
325 330 335
Arg His Ala His Ala Asp Ile Asp Leu Met Arg Gly
340 345

(2) INFORMATION FOR SEQ ID NO:1369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:

Met Gly Leu Ser Gly Ser Gly Ser Tyr Tyr Ile His Arg Gly Leu Pro
1 5 10 15
Gly Ser Gly Pro Pro Thr Phe His Gly Ser Pro Gln Gln Gln Gln Gly
20 25 30
Leu Arg His Leu Pro Asn Gln Asn Ser Pro Phe Gly Ser Gly Ser Thr
35 40 45
Gly Phe Gly Ser Pro Ser Leu His Gly Asp Pro Ser Leu Ala Thr Ala

50	55	60
Ala Gly Gly Ala Gly	Ala Leu Pro His His Ile	Gly Val Asn Met Ile
65	70	75
Ala Pro Pro Pro Pro	Ser Glu Thr Pro Met	Lys Arg Lys Arg Gly
85	90	95
Arg Pro Arg Lys Tyr	Gly Gln Asp Gly Ser	Val Ser Leu Ala Leu Ser
100	105	110
Ser Ser Ser Val Ser	Thr Ile Thr Pro Asn	Asn Ser Asn Lys Arg Gly
115	120	125
Arg Gly Arg Pro Pro	Gly Ser Gly Lys Lys	Gln Arg Met Ala Ser Val
130	135	140
Gly Glu Leu Met Pro	Ser Ser Ser Gly Met	Ser Phe Thr Pro His Val
145	150	155
Ile Ala Val Ser Ile	Gly Glu Asp Ile Ala	Ser Lys Val Ile Ala Phe
165	170	175
Ser Gln Gln Gly Pro	Arg Ala Ile Cys Val	Leu Ser Ala Ser Gly Ala
180	185	190
Val Ser Thr Ala Thr	Leu Ile Gln Pro Ser	Ala Ser Pro Gly Ala Ile
195	200	205
Lys Tyr Glu Gly Arg	Phe Glu Ile Leu Ala	Leu Ser Thr Ser Tyr Ile
210	215	220
Val Ala Thr Asp Gly	Ser Phe Arg Asn Arg	Thr Gly Asn Leu Ser Val
225	230	235
Ser Leu Ala Ser Pro	Asp Gly Arg Val Ile	Gly Gly Ala Ile Gly Gly
245	250	255
Pro Leu Ile Ala Ala	Ser Pro Val Gln Val	Ile Val Gly Ser Phe Ile
260	265	270
Trp Ala Ala Pro Lys	Ile Lys Ser Lys Lys	Arg Glu Glu Glu Ala Ser
275	280	285
Glu Val Val Gln Glu	Thr Asp Asp His His	Val Leu Asp Asn Asn Asn
290	295	300
Asn Thr Ile Ser Pro	Val Pro Gln Gln Gln	Pro Asn Gln Asn Leu Ile
305	310	315
Trp Ser Thr Gly Ser	Arg Gln Met Asp Met	Arg His Ala His Ala Asp
325	330	335
Ile Asp Leu Met Arg	Gly	
340		

(2) INFORMATION FOR SEQ ID NO:1370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..264
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:

Met Ile Ala Pro Pro Pro Pro Ser	Glu Thr Pro Met Lys Arg Lys
1	5
Arg Gly Arg Pro Arg Lys Tyr Gly	Gln Asp Gly Ser Val Ser Leu Ala
20	25
Leu Ser Ser Ser Val Ser Thr Ile	Thr Pro Asn Asn Ser Asn Lys
35	40
Arg Gly Arg Gly Arg Pro Pro Gly	Ser Gly Lys Lys Gln Arg Met Ala
50	55
Ser Val Gly Glu Leu Met Pro Ser	Ser Ser Gly Met Ser Phe Thr Pro
65	70
His Val Ile Ala Val Ser Ile Gly	Glu Asp Ile Ala Ser Lys Val Ile
85	90
	95

Ala Phe Ser Gln Gln Gly Pro Arg Ala Ile Cys Val Leu Ser Ala Ser
100 105 110
Gly Ala Val Ser Thr Ala Thr Leu Ile Gln Pro Ser Ala Ser Pro Gly
115 120 125
Ala Ile Lys Tyr Glu Gly Arg Phe Glu Ile Leu Ala Leu Ser Thr Ser
130 135 140
Tyr Ile Val Ala Thr Asp Gly Ser Phe Arg Asn Arg Thr Gly Asn Leu
145 150 155 160
Ser Val Ser Leu Ala Ser Pro Asp Gly Arg Val Ile Gly Gly Ala Ile
165 170 175
Gly Gly Pro Leu Ile Ala Ala Ser Pro Val Gln Val Ile Val Gly Ser
180 185 190
Phe Ile Trp Ala Ala Pro Lys Ile Lys Ser Lys Lys Arg Glu Glu Glu
195 200 205
Ala Ser Glu Val Val Gln Glu Thr Asp Asp His His Val Leu Asp Asn
210 215 220
Asn Asn Asn Thr Ile Ser Pro Val Pro Gln Gln Gln Pro Asn Gln Asn
225 230 235 240
Leu Ile Trp Ser Thr Gly Ser Arg Gln Met Asp Met Arg His Ala His
245 250 255
Ala Asp Ile Asp Leu Met Arg Gly
260

(2) INFORMATION FOR SEQ ID NO:1371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:

atctacaact	ttcattcttc	cactacattt	ctctccttga	gtatcttctt	atcctatttt	60
ccaaattcca	aaacaattca	caaaatggct	acatgctggc	ctgagccgat	tgtttccgtg	120
caatccttgt	cccaaacccg	tgtaccaact	gtaccaaacc	gctatgtgaa	gccggctcat	180
cagagaccgg	tccttaaacac	cacccaatcc	gatgctggga	tagaaatccc	tggtctagac	240
atgaacgacg	tttgggggaa	accagagggg	ctaaggctcg	tgaggagcgc	gtgtgaggag	300
tggtgtttct	tcctaatggt	gaaccatggt	gtgaccacct	cgttgatgga	gagagtgaga	360
ggagcgtggc	gagagttctt	cgagctaccg	ctagaggaga	aacggaagta	tgcaaatcca	420
ccggacacgt	acgagggata	tggaaagccg	cttgggggtg	tgagagatgc	taaattagat	480
tggagtgtat	atttcttctc	caattacttg	ccttcttcca	taagaaaccc	ttccaagtgg	540
ccatactcag	cctcctaaga	tcagagaatt	gatcgaaaag	tacggagaag	aagtgaagaa	600
actgtgcgaa	aggctaacag	agacgttgtc	agagagttta	ggtttaaaac	caacaagcgt	660
catgcaggct	ttaggaggag	gcgacaaagt	cggagcttct	ctgaggacaa	acttctaccc	720
aaaatgccct	cagccgcgac	tcacttttag	tctctcttct	cattctgacc	ctggagggcat	780
caccattctt	ctcccggagc	agaaggtcgc	tggtccttcag	gtccgtcggt	gtgatggctg	840
gggtcaccatt	aaatcagtc	ctaattgctt	gatcgttaac	attggagatc	aacttcagat	900
acttagcaat	ggaatttaca	aaagcgtgga	acatcaaagt	atcgtttaatt	ccggtatgga	960
acgagttctt	ttggcattct	tttataaacc	gagaagtgat	atcccgggtg	gaccaatcga	1020
agaactagtta	actgcaaaac	gacctgctct	ttataaacca	atcaggttgc	acgagtaccg	1080
ttctctgata	aggcaaaagg	gtcctgttgg	aaaaaaccaa	gtcgactcac	tggtattaac	1140
tagataataa	ttgataaaca	ttccaaagtat	tatctgttat	tcctatgttc	ttctataatg	1200
cgttactaaa	taatatgtaa	accgtatctt	cactttttct	tatttatattg	ctgctctctc	1260
ttgaggtttg						

(2) INFORMATION FOR SEQ ID NO:1372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..185
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500116
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:
Ile Tyr Asn Phe His Ser Ser Thr Thr Phe Leu Ser Leu Ser Ile Phe
1 5 10 15
Leu Ser Tyr Phe Pro Asn Ser Lys Thr Ile His Lys Met Ala Thr Cys
 20 25 30
Trp Pro Glu Pro Ile Val Ser Val Gln Ser Leu Ser Gln Thr Gly Val
 35 40 45
Pro Thr Val Pro Asn Arg Tyr Val Lys Pro Ala His Gln Arg Pro Val
 50 55 60
Phe Asn Thr Thr Gln Ser Asp Ala Gly Ile Glu Ile Pro Val Leu Asp
65 70 75 80
Met Asn Asp Val Trp Gly Lys Pro Glu Gly Leu Arg Leu Val Arg Ser
 85 90 95
Ala Cys Glu Glu Trp Gly Phe Phe Gln Met Val Asn His Gly Val Thr
 100 105 110
His Ser Leu Met Glu Arg Val Arg Gly Ala Trp Arg Glu Phe Phe Glu
 115 120 125
Leu Pro Leu Glu Glu Lys Arg Lys Tyr Ala Asn Ser Pro Asp Thr Tyr
 130 135 140
Glu Gly Tyr Gly Ser Arg Leu Gly Val Val Arg Asp Ala Lys Leu Asp
145 150 155 160
Trp Ser Asp Tyr Phe Phe Leu Asn Tyr Leu Pro Ser Ser Ile Arg Asn
 165 170 175
Pro Ser Lys Trp Pro Tyr Ser Ala Ser
 180 185
(2) INFORMATION FOR SEQ ID NO:1373:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..157
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500117
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:
Met Ala Thr Cys Trp Pro Glu Pro Ile Val Ser Val Gln Ser Leu Ser
1 5 10 15
Gln Thr Gly Val Pro Thr Val Pro Asn Arg Tyr Val Lys Pro Ala His
 20 25 30
Gln Arg Pro Val Phe Asn Thr Thr Gln Ser Asp Ala Gly Ile Glu Ile
 35 40 45
Pro Val Leu Asp Met Asn Asp Val Trp Gly Lys Pro Glu Gly Leu Arg
 50 55 60
Leu Val Arg Ser Ala Cys Glu Glu Trp Gly Phe Phe Gln Met Val Asn
65 70 75 80
His Gly Val Thr His Ser Leu Met Glu Arg Val Arg Gly Ala Trp Arg
 85 90 95
Glu Phe Phe Glu Leu Pro Leu Glu Glu Lys Arg Lys Tyr Ala Asn Ser
 100 105 110
Pro Asp Thr Tyr Glu Gly Tyr Gly Ser Arg Leu Gly Val Val Arg Asp
 115 120 125
Ala Lys Leu Asp Trp Ser Asp Tyr Phe Phe Leu Asn Tyr Leu Pro Ser
130 135 140

Ser Ile Arg Asn Pro Ser Lys Trp Pro Tyr Ser Ala Ser
145 150 155

(2) INFORMATION FOR SEQ ID NO:1374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1500118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

Met	Gln	Ala	Leu	Gly	Gly	Gly	Asp	Lys	Val	Gly	Ala	Ser	Leu	Arg	Thr
1			5						10					15	
Asn	Phe	Tyr	Pro	Lys	Cys	Pro	Gln	Pro	Gln	Leu	Thr	Leu	Gly	Leu	Ser
			20					25					30		
Ser	His	Ser	Asp	Pro	Gly	Gly	Ile	Thr	Ile	Leu	Leu	Pro	Asp	Gly	Lys
			35				40				45				
Val	Ala	Gly	Leu	Gln	Val	Arg	Gly	Asp	Gly	Trp	Val	Thr	Ile	Lys	
			50			55				60					
Ser	Val	Pro	Asn	Ala	Leu	Ile	Val	Asn	Ile	Gly	Asp	Gln	Leu	Gln	Ile
			65			70				75				80	
Leu	Ser	Asn	Gly	Ile	Tyr	Lys	Ser	Val	Glu	His	Gln	Val	Ile	Val	Asn
				85					90					95	
Ser	Gly	Met	Glu	Arg	Val	Ser	Leu	Ala	Phe	Phe	Tyr	Asn	Pro	Arg	Ser
			100					105					110		
Asp	Ile	Pro	Val	Gly	Pro	Ile	Glu	Glu	Leu	Val	Thr	Ala	Asn	Arg	Pro
			115				120					125			
Ala	Leu	Tyr	Lys	Pro	Ile	Arg	Phe	Asp	Glu	Tyr	Arg	Ser	Leu	Ile	Arg
			130			135					140				
Gln	Lys	Gly	Pro	Cys	Gly	Lys	Asn	Gln	Val	Asp	Ser	Leu	Leu	Leu	Thr
				150						155					160
145															
Arg															

(2) INFORMATION FOR SEQ ID NO:1375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1756

(D) OTHER INFORMATION: / Ceres Seq. ID 1500131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

gctctgattc	attcacaaat	aacaatcctc	tcttcgtttt	tgtttttctt	ttggatccaa	60
agctctctta	aattctgtaa	tcaacaatgg	ccgccaccac	tgagaatctc	cctcaactca	120
aatccgccgt	cgatggcctt	actgagatga	gtgagagtga	gaagagcgga	ttcatcagcc	180
tggtttcacc	ttacctgagc	ggtagggcac	aacacattga	gtggagtaag	atccagactc	240
ctaccgatga	aatcgttgtt	ccctacgaga	aaatgacccc	tgctctccaa	gatgttgccc	300
agaccagaag	tctgtttggc	aaacttgttg	tggtgaagct	taattggaggt	cttggaaaca	360
caatgggatg	cactggcccg	aagtccgtta	tcgaagtctg	tgatggtttg	acattttctg	420
atctgattgt	tatccagatt	gagaatctca	acaacaagta	tggtctgcaa	gttccgttag	480
ttctcatgaa	ctcgtttta	acacatgatg	acagacataa	gattgtggaa	aagtacacca	540
actcaaatgt	tgacattcac	acttttaacc	agagcaataa	tcccctgtgt	gtggcagatg	600
agtttgtgcc	atggcccacg	aagggaagga	ccgacaagga	gggctgtgat	cctcccggtc	660
atggtgatgt	attcccagcc	ctcatgaaca	gtggaaagct	cgatactttc	ttatcacagg	720
gtaaggaata	tggtgttgtt	gccaatccag	acaacttggg	tgccatcgtt	gacttaacaa	780

tctgaagca	tttgcacag	aacaagaacg	aatactgcat	ggaggttaca	cccaaacct	840
tagctgatgt	aaagggggga	actctcatt	cttatgaagg	caaagtcacg	cttctggaga	900
ttgctcagtt	tcctgatgaa	catgtcaatg	agttcaaatc	aattgagaag	ttcaagatat	960
tcaacacaaa	caacctatgg	gttaacttga	aggccatcaa	aaagctgttg	gaagctgatg	1020
cacttaaaat	ggagatcatt	ccaaacccaa	aggaagtgtg	tggagtcгаа	gttcttcaac	1080
tggaacctgc	agccggtgct	gcgataaggt	tctttgacaa	cgtatcggt	gttaatgtac	1140
ctcgctcacg	gttcttgcca	gtgaaggcaa	gttcagactt	gctgctcgtc	cagctcgatc	1200
tctacacctt	agttgatggc	tttgtcacct	gaaacaaagc	tagaactaac	ccctcgaaac	1260
cgtaaatgga	attgggaccc	gagttcaaga	agggtggctac	tttcttgagc	cggtttaagt	1320
ccattctcat	tatagtcgag	ctcgacagcc	ttaaggtgtc	tggtgatgtc	tggtttggct	1380
cttccattgt	tctcaagggc	aaggtgactg	tggcggcaaa	atccggtgtg	aagcttgaaa	1440
ttccggcacg	ggcgtgtgtg	gagaaacaaga	acatcaatgg	tccagaagac	ctctgaataa	1500
aacaaaattca	agtcttcttc	ctctctctcat	ggaagacaca	tcttgatact	cctttaattg	1560
gtgtgaaaaa	atcacaaagt	gcacagcaaa	gcaagtttat	gaagaagaaa	taaataatgt	1620
ttctttttct	ttttgcagct	tagcaaaagtc	ttttctctct	tggaacttat	tttaattttg	1680
ctctttgaat	tttcccaaaa	catcacattt	atatgttcga	ttatatattg	gttctatcca	1740
caatcatttt	tctttt					

(2) INFORMATION FOR SEQ ID NO:1376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..469
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:

Met	Ala	Ala	Thr	Thr	Glu	Asn	Leu	Pro	Gln	Leu	Lys	Ser	Ala	Val	Asp
1				5					10					15	
Gly	Leu	Thr	Glu	Met	Ser	Glu	Ser	Glu	Lys	Ser	Gly	Phe	Ile	Ser	Leu
			20					25					30		
Val	Ser	Arg	Tyr	Leu	Ser	Gly	Glu	Ala	Gln	His	Ile	Glu	Trp	Ser	Lys
		35					40				45				
Ile	Gln	Thr	Pro	Thr	Asp	Glu	Ile	Val	Val	Pro	Tyr	Glu	Lys	Met	Thr
	50				55					60					
Pro	Val	Ser	Gln	Asp	Val	Ala	Glu	Thr	Lys	Asn	Leu	Leu	Asp	Lys	Leu
65				70					75					80	
Val	Val	Leu	Lys	Leu	Asn	Gly	Gly	Leu	Gly	Thr	Thr	Met	Gly	Cys	Thr
		85						90					95		
Gly	Pro	Lys	Ser	Val	Ile	Glu	Val	Arg	Asp	Gly	Leu	Thr	Phe	Leu	Asp
	100						105				110				
Leu	Ile	Val	Ile	Gln	Ile	Glu	Asn	Leu	Asn	Asn	Lys	Tyr	Gly	Cys	Lys
	115				120						125				
Val	Pro	Leu	Val	Leu	Met	Asn	Ser	Phe	Asn	Thr	His	Asp	Asp	Arg	His
	130				135					140					
Lys	Ile	Val	Glu	Lys	Tyr	Thr	Asn	Ser	Asn	Val	Asp	Ile	His	Thr	Phe
145				150					155					160	
Asn	Gln	Ser	Lys	Tyr	Pro	Arg	Val	Val	Ala	Asp	Glu	Phe	Val	Pro	Trp
		165					170						175		
Pro	Ser	Lys	Gly	Lys	Thr	Asp	Lys	Glu	Gly	Trp	Tyr	Pro	Pro	Gly	His
	180						185					190			
Gly	Asp	Val	Phe	Pro	Ala	Leu	Met	Asn	Ser	Gly	Lys	Leu	Asp	Thr	Phe
	195					200					205				
Leu	Ser	Gln	Gly	Lys	Glu	Tyr	Val	Phe	Val	Ala	Asn	Ser	Asp	Asn	Leu
	210				215						220				
Gly	Ala	Ile	Val	Asp	Leu	Thr	Ile	Leu	Lys	His	Leu	Ile	Gln	Asn	Lys
225				230					235					240	
Asn	Glu	Tyr	Cys	Met	Glu	Val	Thr	Pro	Lys	Thr	Leu	Ala	Asp	Val	Lys
		245					250						255		

Gly Gly Thr Leu Ile Ser Tyr Glu Gly Lys Val Gln Leu Leu Glu Ile
260 265 270
Ala Gln Phe Pro Asp Glu His Val Asn Glu Phe Lys Ser Ile Glu Lys
275 280 285
Phe Lys Ile Phe Asn Thr Asn Asn Leu Trp Val Asn Leu Lys Ala Ile
290 295 300
Lys Lys Leu Val Glu Ala Asp Ala Leu Lys Met Glu Ile Ile Pro Asn
305 310 315 320
Pro Lys Glu Val Asp Gly Val Lys Val Leu Gln Leu Glu Thr Ala Ala
325 330 335
Gly Ala Ala Ile Arg Phe Phe Asp Asn Ala Ile Gly Val Asn Val Pro
340 345 350
Arg Ser Arg Phe Leu Pro Val Lys Ala Ser Ser Asp Leu Leu Val
355 360 365
Gln Ser Asp Leu Tyr Thr Leu Val Asp Gly Phe Val Thr Arg Asn Lys
370 375 380
Ala Arg Thr Asn Pro Ser Asn Pro Ser Ile Glu Leu Gly Pro Glu Phe
385 390 395 400
Lys Lys Val Ala Thr Phe Leu Ser Arg Phe Lys Ser Ile Pro Ser Ile
405 410 415
Val Glu Leu Asp Ser Leu Lys Val Ser Gly Asp Val Trp Phe Gly Ser
420 425 430
Ser Ile Val Leu Lys Gly Lys Val Thr Val Ala Ala Lys Ser Gly Val
435 440 445
Lys Leu Glu Ile Pro Asp Arg Ala Val Val Glu Asn Lys Asn Ile Asn
450 455 460
Gly Pro Glu Asp Leu
465

(2) INFORMATION FOR SEQ ID NO:1377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..449
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:

Met Ser Glu Ser Glu Lys Ser Gly Phe Ile Ser Leu Val Ser Arg Tyr
1 5 10 15
Leu Ser Gly Glu Ala Gln His Ile Glu Trp Ser Lys Ile Gln Thr Pro
20 25 30
Thr Asp Glu Ile Val Val Pro Tyr Glu Lys Met Thr Pro Val Ser Gln
35 40 45
Asp Val Ala Glu Thr Lys Asn Leu Leu Asp Lys Leu Val Val Leu Lys
50 55 60
Leu Asn Gly Gly Leu Gly Thr Thr Met Gly Cys Thr Gly Pro Lys Ser
65 70 75 80
Val Ile Glu Val Arg Asp Gly Leu Thr Phe Leu Asp Leu Ile Val Ile
85 90 95
Gln Ile Glu Asn Leu Asn Asn Lys Tyr Gly Cys Lys Val Pro Leu Val
100 105 110
Leu Met Asn Ser Phe Asn Thr His Asp Asp Arg His Lys Ile Val Glu
115 120 125
Lys Tyr Thr Asn Ser Asn Val Asp Ile His Thr Phe Asn Gln Ser Lys
130 135 140
Tyr Pro Arg Val Val Ala Asp Glu Phe Val Pro Trp Pro Ser Lys Gly
145 150 155 160
Lys Thr Asp Lys Glu Gly Trp Tyr Pro Pro Gly His Gly Asp Val Phe

	165		170		175
Pro Ala Leu Met Asn Ser Gly Lys Leu Asp Thr Phe Leu Ser Gln Gly					
	180		185		190
Lys Glu Tyr Val Phe Val Ala Asn Ser Asp Asn Leu Gly Ala Ile Val					
	195		200		205
Asp Leu Thr Ile Leu Lys His Leu Ile Gln Asn Lys Asn Glu Tyr Cys					
	210		215		220
Met Glu Val Thr Pro Lys Thr Leu Ala Asp Val Lys Gly Gly Thr Leu					
	225		230		235
Ile Ser Tyr Glu Gly Lys Val Gln Leu Leu Glu Ile Ala Gln Phe Pro					
	245		250		255
Asp Glu His Val Asn Glu Phe Lys Ser Ile Glu Lys Phe Lys Ile Phe					
	260		265		270
Asn Thr Asn Asn Leu Trp Val Asn Leu Lys Ala Ile Lys Lys Leu Val					
	275		280		285
Glu Ala Asp Ala Leu Lys Met Glu Ile Ile Pro Asn Pro Lys Glu Val					
	290		295		300
Asp Gly Val Lys Val Leu Gln Leu Glu Thr Ala Ala Gly Ala Ala Ile					
	305		310		315
Arg Phe Phe Asp Asn Ala Ile Gly Val Asn Val Pro Arg Ser Arg Phe					
	325		330		335
Leu Pro val Lys Ala Ser Ser Asp Leu Leu Leu Val Gln Ser Asp Leu					
	340		345		350
Tyr Thr Leu Val Asp Gly Phe Val Thr Arg Asn Lys Ala Arg Thr Asn					
	355		360		365
Pro Ser Asn Pro Ser Ile Glu Leu Gly Pro Glu Phe Lys Lys Val Ala					
	370		375		380
Thr Phe Leu Ser Arg Phe Lys Ser Ile Pro Ser Ile Val Glu Leu Asp					
	385		390		395
Ser Leu Lys Val Ser Gly Asp Val Trp Phe Gly Ser Ser Ile Val Leu					
	405		410		415
Lys Gly Lys Val Thr Val Ala Ala Lys Ser Gly Val Lys Leu Glu Ile					
	420		425		430
Pro Asp Arg Ala Val Val Glu Asn Lys Asn Ile Asn Gly Pro Glu Asp					
	435		440		445
Leu					

(2) INFORMATION FOR SEQ ID NO:1378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..407

(D) OTHER INFORMATION: / Ceres Seq. ID 1500134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:

Met Thr Pro Val Ser Gln Asp Val Ala Glu Thr Lys Asn Leu Leu Asp					
1	5		10		15
Lys Leu Val Val Leu Lys Leu Asn Gly Gly Leu Gly Thr Thr Met Gly					
	20		25		30
Cys Thr Gly Pro Lys Ser Val Ile Glu Val Arg Asp Gly Leu Thr Phe					
	35		40		45
Leu Asp Leu Ile Val Ile Gln Ile Glu Asn Leu Asn Asn Lys Tyr Gly					
	50		55		60
Cys Lys Val Pro Leu Val Leu Met Asn Ser Phe Asn Thr His Asp Asp					
65	70		75		80
Arg His Lys Ile Val Glu Lys Tyr Thr Asn Ser Asn Val Asp Ile His					
	85		90		95

Thr Phe Asn Gln Ser Lys Tyr Pro Arg Val Val Ala Asp Glu Phe Val
100 105 110
Pro Trp Pro Ser Lys Gly Lys Thr Asp Lys Glu Gly Trp Tyr Pro Pro
115 120 125
Gly His Gly Asp Val Phe Pro Ala Leu Met Asn Ser Gly Lys Leu Asp
130 135 140
Thr Phe Leu Ser Gln Gly Lys Glu Tyr Val Phe Val Ala Asn Ser Asp
145 150 155 160
Asn Leu Gly Ala Ile Val Asp Leu Thr Ile Leu Lys His Leu Ile Gln
165 170 175
Asn Lys Asn Glu Tyr Cys Met Glu Val Thr Pro Lys Thr Leu Ala Asp
180 185 190
Val Lys Gly Gly Thr Leu Ile Ser Tyr Glu Gly Lys Val Gln Leu Leu
195 200 205
Glu Ile Ala Gln Phe Pro Asp Glu His Val Asn Glu Phe Lys Ser Ile
210 215 220
Glu Lys Phe Lys Ile Phe Asn Thr Asn Asn Leu Trp Val Asn Leu Lys
225 230 235 240
Ala Ile Lys Lys Leu Val Glu Ala Asp Ala Leu Lys Met Glu Ile Ile
245 250 255
Pro Asn Pro Lys Glu Val Asp Gly Val Lys Val Leu Gln Leu Glu Thr
260 265 270
Ala Ala Gly Ala Ala Ile Arg Phe Phe Asp Asn Ala Ile Gly Val Asn
275 280 285
Val Pro Arg Ser Arg Phe Leu Pro Val Lys Ala Ser Ser Asp Leu Leu
290 295 300
Leu Val Gln Ser Asp Leu Tyr Thr Leu Val Asp Gly Phe Val Thr Arg
305 310 315 320
Asn Lys Ala Arg Thr Asn Pro Ser Asn Pro Ser Ile Glu Leu Gly Pro
325 330 335
Glu Phe Lys Lys Val Ala Thr Phe Leu Ser Arg Phe Lys Ser Ile Pro
340 345 350
Ser Ile Val Glu Leu Asp Ser Leu Lys Val Ser Gly Asp Val Trp Phe
355 360 365
Gly Ser Ser Ile Val Leu Lys Gly Lys Val Thr Val Ala Ala Lys Ser
370 375 380
Gly Val Lys Leu Glu Ile Pro Asp Arg Ala Val Val Glu Asn Lys Asn
385 390 395 400
Ile Asn Gly Pro Glu Asp Leu
405

(2) INFORMATION FOR SEQ ID NO:1379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1210
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:

atataaatgg	cagttcaacg	tcaacaccat	tcctccaatc	tcctcttcc	caataaaaaga	60
aacgggaaag	agaagaagaa	tagtaatttt	acattacaat	cacaagcagc	tggagattttt	120
cttgatcaaa	ccaatatggt	attcaacaat	ggaagttcta	atcagagaaa	aagaagaaga	180
gaaacgaaca	atcatcagtt	attacctatg	cagtcctcatc	agtttccctca	agtttatagac	240
ttatctctat	tacacaacta	caatcatcca	cogtcgaata	tggttcatac	aggactccga	300
ttattttccg	gcgaagatca	ggcacaaaag	attagtcacc	tgctgtaaga	tgtttttgct	360
gcacatatca	ataggcaaa	cgaagaactt	gatgagtttc	ttcatgcccc	ggcgaggagg	420
ctacggcgta	cattagcgga	gaagagggaag	atgcactata	aagcgctctt	tggtgccgtg	480
gaagagtcgt	tggttcgtaa	gctgaggagg	aaagagggtg	agatagagag	agccacgcgcg	540

cgtcacaaatg	agctggtggc	acgtgactcg	cagctgagag	cggaggtgca	agtatggcaa	600
gagagagcta	aagcgcaaga	agacgcccgc	gcgtcgctgc	agtctcagct	ccagcaagcc	660
gttaaccaat	gcgcgggttg	atgtgtatcg	gcgcaggata	gtagagcgcc	ggaggaagg	720
ctattatgca	ccacaatcag	cggagtggat	gacgcccagt	cggtgtacgt	ggatccggag	780
agagtaaaag	ggccgaattg	caaagcttgc	cgggaaagag	aggcaacggt	ggttgtgttg	840
ccgtgtcggc	atctgagcat	ctgccccgga	tgtgaccgga	cagcttttagc	tgcccgttg	900
tgtctcacgt	tgcggaattc	aagtgttgaa	gctatctttt	gctaaatggg	cctaattcaa	960
gccattatgg	ttgttatcgt	aaatagaact	tagtaggtaa	cacaaatata	aatttcattg	1020
gtatattgata	taccgtatat	cgaatccact	agctattaag	gaagccctct	aaattttaca	1080
acaaaagaag	tttttttttt	tttttttact	tttccattact	tgggattctt	tacacagata	1140
tgggatattg	aaatgttgct	attcgtacaa	aatagttaac	taagctaaga	aacccatttt	1200
tggtggggccc						

(2) INFORMATION FOR SEQ ID NO:1380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..314
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:

Ile	Lys	Met	Ala	Val	Gln	Ala	Gln	His	His	Ser	Ser	Asn	Leu	Leu	Phe	
1			5					10					15			
Leu	Asn	Lys	Arg	Asn	Gly	Lys	Glu	Lys	Glu	His	Ser	Asn	Phe	Thr	Leu	
			20				25						30			
Gln	Ser	Gln	Ala	Ala	Gly	Asp	Phe	Leu	Asp	Gln	Thr	Asn	Met	Leu	Phe	
		35				40					45					
Asn	Asn	Gly	Ser	Ser	Asn	Gln	Arg	Lys	Arg	Arg	Arg	Glu	Thr	Asn	Asn	
		50				55					60					
His	Gln	Leu	Leu	Pro	Met	Gln	Ser	His	Gln	Phe	Pro	Gln	Val	Ile	Asp	
		65			70					75					80	
Leu	Ser	Leu	Leu	His	Asn	Tyr	Asn	His	Pro	Pro	Ser	Asn	Met	Val	His	
			85						90					95		
Thr	Gly	Leu	Arg	Leu	Phe	Ser	Gly	Glu	Asp	Gln	Ala	Gln	Lys	Ile	Ser	
		100						105					110			
His	Leu	Ser	Glu	Asp	Val	Phe	Ala	Ala	His	Ile	Asn	Arg	Gln	Ser	Glu	
		115				120						125				
Glu	Leu	Asp	Glu	Phe	Leu	His	Ala	Gln	Ala	Glu	Glu	Leu	Arg	Arg	Thr	
		130				135						140				
Leu	Ala	Glu	Lys	Arg	Lys	Met	His	Tyr	Lys	Ala	Leu	Leu	Gly	Ala	Val	
		145			150					155					160	
Glu	Glu	Ser	Leu	Val	Arg	Lys	Leu	Arg	Glu	Lys	Glu	Val	Glu	Ile	Glu	
			165						170					175		
Arg	Ala	Thr	Arg	Arg	His	Asn	Glu	Leu	Val	Ala	Arg	Asp	Ser	Gln	Leu	
		180						185					190			
Arg	Ala	Glu	Val	Gln	Val	Trp	Gln	Glu	Arg	Ala	Lys	Ala	His	Glu	Asp	
		195				200						205				
Ala	Ala	Ala	Ser	Leu	Gln	Ser	Gln	Leu	Gln	Gln	Ala	Val	Asn	Gln	Cys	
		210				215						220				
Ala	Gly	Gly	Cys	Val	Ser	Ala	Gln	Asp	Ser	Arg	Ala	Ala	Glu	Glu	Gly	
		225			230					235					240	
Leu	Leu	Cys	Thr	Thr	Ile	Ser	Gly	Val	Asp	Asp	Ala	Glu	Ser	Val	Tyr	
			245						250					255		
Val	Asp	Pro	Glu	Arg	Val	Lys	Arg	Pro	Asn	Cys	Lys	Ala	Cys	Arg	Glu	
			260					265					270			
Arg	Glu	Ala	Thr	Val	Val	Val	Leu	Pro	Cys	Arg	His	Leu	Ser	Ile	Cys	
		275					280					285				
Pro	Gly	Cys	Asp	Arg	Thr	Ala	Leu	Ala	Cys	Pro	Leu	Cys	Leu	Thr	Leu	

290 295 300
Arg Asn Ser Ser Val Glu Ala Ile Phe Cys
305 310
(2) INFORMATION FOR SEQ ID NO:1381:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..312
(D) OTHER INFORMATION: / Ceres Seq. ID 1500137
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:
Met Ala Val Gln Ala Gln His His Ser Ser Asn Leu Leu Phe Leu Asn
1 5 10 15
Lys Arg Asn Gly Lys Glu Lys Glu His Ser Asn Phe Thr Leu Gln Ser
20 25 30
Gln Ala Ala Gly Asp Phe Leu Asp Gln Thr Asn Met Leu Phe Asn Asn
35 40 45
Gly Ser Ser Asn Gln Arg Lys Arg Arg Arg Glu Thr Asn Asn His Gln
50 55 60
Leu Leu Pro Met Gln Ser His Gln Phe Pro Gln Val Ile Asp Leu Ser
65 70 75 80
Leu Leu His Asn Tyr Asn His Pro Pro Ser Asn Met Val His Thr Gly
85 90 95
Leu Arg Leu Phe Ser Gly Glu Asp Gln Ala Gln Lys Ile Ser His Leu
100 105 110
Ser Glu Asp Val Phe Ala Ala His Ile Asn Arg Gln Ser Glu Glu Leu
115 120 125
Asp Glu Phe Leu His Ala Gln Ala Glu Glu Leu Arg Thr Leu Ala
130 135 140
Glu Lys Arg Lys Met His Tyr Lys Ala Leu Leu Gly Ala Val Glu Glu
145 150 155 160
Ser Leu Val Arg Lys Leu Arg Glu Lys Glu Val Glu Ile Glu Arg Ala
165 170 175
Thr Arg Arg His Asn Glu Leu Val Ala Arg Asp Ser Gln Leu Arg Ala
180 185 190
Glu Val Gln Val Trp Gln Glu Arg Ala Lys Ala His Glu Asp Ala Ala
195 200 205
Ala Ser Leu Gln Ser Gln Leu Gln Gln Ala Val Asn Gln Cys Ala Gly
210 215 220
Gly Cys Val Ser Ala Gln Asp Ser Arg Ala Ala Glu Glu Gly Leu Leu
225 230 235 240
Cys Thr Thr Ile Ser Gly Val Asp Asp Ala Glu Ser Val Tyr Val Asp
245 250 255
Pro Glu Arg Val Lys Arg Pro Asn Cys Lys Ala Cys Arg Glu Arg Glu
260 265 270
Ala Thr Val Val Val Leu Pro Cys Arg His Leu Ser Ile Cys Pro Gly
275 280 285
Cys Asp Arg Thr Ala Leu Ala Cys Pro Leu Cys Leu Thr Leu Arg Asn
290 295 300
Ser Ser Val Glu Ala Ile Phe Cys
305 310
(2) INFORMATION FOR SEQ ID NO:1382:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..269

(D) OTHER INFORMATION: / Ceres Seq. ID 1500138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:

```
Met Leu Phe Asn Asn Gly Ser Ser Asn Gln Arg Lys Arg Arg Arg Gly
1      5      10      15
Thr Asn Asn His Gln Leu Leu Pro Met Gln Ser His Gln Phe Pro Gln
20      25      30
Val Ile Asp Leu Ser Leu Leu His Asn Tyr Asn His Pro Pro Ser Asn
35      40      45
Met Val His Thr Gly Leu Arg Leu Phe Ser Gly Glu Asp Gln Ala Gln
50      55      60
Lys Ile Ser His Leu Ser Glu Asp Val Phe Ala Ala His Ile Asn Arg
65      70      75      80
Gln Ser Glu Glu Leu Asp Glu Phe Leu His Ala Gln Ala Glu Glu Leu
85      90      95
Arg Arg Thr Leu Ala Glu Lys Arg Lys Met His Tyr Lys Ala Leu Leu
100     105     110
Gly Ala Val Glu Glu Ser Leu Val Arg Lys Leu Arg Glu Lys Glu Val
115     120     125
Glu Ile Glu Arg Ala Thr Arg Arg His Asn Glu Leu Val Ala Arg Asp
130     135     140
Ser Gln Leu Arg Ala Glu Val Gln Val Trp Gln Glu Arg Ala Lys Ala
145     150     155     160
His Glu Asp Ala Ala Ala Ser Leu Gln Ser Gln Leu Gln Gln Ala Val
165     170     175
Asn Gln Cys Ala Gly Gly Cys Val Ser Ala Gln Asp Ser Arg Ala Ala
180     185     190
Glu Glu Gly Leu Leu Cys Thr Thr Ile Ser Gly Val Asp Asp Ala Glu
195     200     205
Ser Val Tyr Val Asp Pro Glu Arg Val Lys Arg Pro Asn Cys Lys Ala
210     215     220
Cys Arg Glu Arg Glu Ala Thr Val Val Val Leu Pro Cys Arg His Leu
225     230     235     240
Ser Ile Cys Pro Gly Cys Asp Arg Thr Ala Leu Ala Cys Pro Leu Cys
245     250     255
Leu Thr Leu Arg Asn Ser Ser Val Glu Ala Ile Phe Cys
260     265
```

(2) INFORMATION FOR SEQ ID NO:1383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 719 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..719

(D) OTHER INFORMATION: / Ceres Seq. ID 1500149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383:

```
gttgatatg cggatctcca ttcaaccaat gccttcctgt cgccctcccg ctccggtcgg 60
cgaacgcgat ctgttcccca acctccgcag ccgctccacc gtccctccact ccggtgcgcg 120
aatcgaccgc ccccgatcca gatcaggagc tgagggatgg acgcgaacag cgcgccagagt 180
gggatccagc agttgctggc tgcggascag gaggctcagc aaattgtgaa tgcccgtcag 240
agctgccaa gtcagcgaggc tcaggcaacg aaaaaggagg gctgagcggg aatatgcgga 300
ataccgtgcc cagatggagg ctgagtttca gaggaaggtt gcagagagca gcggcgactc 360
cggtgcaaac gtcaagcgctc tcgaggaaga aacggcgcgcg aagatcgagc aactcaccac 420
gcaggccgca agcatctccc cggatgtcat tcagatgctt ctgcgcatg tcaccaccgt 480
caagaactga ggagtgcgtg tcccgaaacta tgctcgacga cttgtacgct cgatctattt 540
```

atttttgtca agagtggagag tgggtaggaa taatatgcc gcttgatcc ataattcctg 600
ttcgtacta cggataaagc cgccgcagct ttacgggcaa acgtgactag tactgtcaga 660
acctaccatt gttatttggt acaattggta aataatattg ttttaaaactg gatttttcg

(2) INFORMATION FOR SEQ ID NO:1384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:

Leu	Tyr	Met	Arg	Ile	Ser	Ile	His	Gln	Ser	Pro	Ser	Cys	Arg	Pro	Pro
1			5					10					15		
Ala	Arg	Leu	Gly	Glu	Arg	Asp	Leu	Phe	Pro	Asn	Leu	Arg	Ser	Arg	Ser
			20				25					30			
Thr	Val	Leu	His	Ser	Gly	Cys	Arg	Ile	Asp	Pro	Pro	Arg	Ser	Arg	Ser
			35				40					45			
Gly	Ala	Glu	Gly	Trp	Thr	Arg	Thr	Gly	Ala	Arg	Val	Gly	Ser	Ser	Ser
			50				55				60				
Cys	Trp	Leu	Arg	Xaa	Arg	Arg	Leu	Ser	Lys	Leu					
			65				70			75					

(2) INFORMATION FOR SEQ ID NO:1385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:

Cys	Ile	Cys	Gly	Ser	Pro	Phe	Thr	Asn	Arg	Leu	Pro	Val	Ala	Leu	Pro
1			5					10					15		
Leu	Gly	Ser	Ala	Asn	Ala	Ile	Cys	Ser	Pro	Thr	Ser	Ala	Ala	Ala	Pro
			20				25					30			
Pro	Ser	Ser	Thr	Pro	Ala	Ala	Glu	Ser	Thr	Arg	Pro	Asp	Pro	Asp	Gln
			35				40					45			
Glu	Leu	Arg	Asp	Gly	Arg	Glu	Gln	Ala	Pro	Glu	Trp	Asp	Pro	Ala	Val
			50				55				60				
Ala	Gly	Cys	Gly	Xaa	Gly	Gly	Ser	Ala	Asn	Cys	Glu	Cys	Pro	Leu	Glu
			65				70				75			80	
Leu	Pro	Ser	Gln	Arg	Gly	Ser	Gly	Lys	Gln	Lys	Arg	Arg	Leu	Ser	Gly
			85				90						95		

Lys

(2) INFORMATION FOR SEQ ID NO:1386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1500152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:

Met Pro Ala Arg Ala Ala Lys Ser Ala Arg Leu Arg Gln Ala Lys Glu
1 5 10 15
Glu Ala Glu Arg Glu Ile Ala Glu Tyr Arg Ala Gln Met Glu Ala Glu
20 25 30
Phe Gln Arg Lys Val Ala Glu Ser Ser Gly Asp Ser Gly Ala Asn Val
35 40 45
Lys Arg Leu Glu Glu Glu Thr Ala Ala Lys Ile Glu Gln Leu Thr Gln
50 55 60
Gln Ala Ala Ser Ile Ser Pro Asp Val Ile Gln Met Leu Leu Arg His
65 70 75 80
Val Thr Thr Val Lys Asn
85

(2) INFORMATION FOR SEQ ID NO:1387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..460

(D) OTHER INFORMATION: / Ceres Seq. ID 1500153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:

cttcgggtcc tgcattttgt tgtccctctc cgtagcggga gacgttcggt cactttctct 60
ctctcgctcc ccgtttgccc cgcgtgcgct ctgtgtcgct ccctctcttg tgaggagtga 120
ggacgactgg ggcgaccgcc gccgcgccgc cgcctctacg ccagatgccc aggtaggggc 180
cattcgctag ctcttcttcg tgcccttcgc cggcgacgag cattcaccag ttgctgatgc 240
aaggctttca aaagttaaac agtctcactt gatgcaaaag caacacaaatc actctaaaag 300
tttgatcag tcatttcaga gcatgggttc cgggtttcca tcccatcagc taagcaatgg 360
cttgatgtc tctggccgac ctgagcaacc taaagagaag gccccagtca ttgctcctc 420
ggctatgcgt acactggcgg ggcataaag aaatctggag

(2) INFORMATION FOR SEQ ID NO:1388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1500154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:

Phe Arg Ser Cys Ile Leu Leu Ser Pro Leu Arg Ser Gly Asp Val Arg
1 5 10 15
Ser Leu Ser Leu Ser Arg Leu Pro Phe Ala Pro Arg Ala Leu Cys Val
20 25 30
Ala Pro Ser Leu Val Arg Ser Glu Asp Asp Trp Gly Asp Arg Arg Arg
35 40 45
Arg Arg Arg Pro Thr Pro Asp Ala Gln Val Gly Ala Ile Arg
50 55 60

(2) INFORMATION FOR SEQ ID NO:1389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1500155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:

Met	Gln	Lys	Gln	His	Asn	His	Ser	Lys	Gly	Leu	Asp	Gln	Ser	Phe	Gln
1										10				15	
Ser	Met	Gly	Ser	Arg	Phe	Pro	Ser	His	Gln	Leu	Ser	Asn	Gly	Leu	Tyr
			20					25					30		
Val	Ser	Gly	Arg	Pro	Glu	Gln	Pro	Lys	Glu	Lys	Ala	Pro	Val	Ile	Cys
			35				40					45			
Ser	Ser	Ala	Met	Arg	Thr	Leu	Ala	Gly	Thr						
			50			55									

(2) INFORMATION FOR SEQ ID NO:1390:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..41

(D) OTHER INFORMATION: / Ceres Seq. ID 1500156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:

Met	Gly	Ser	Arg	Phe	Pro	Ser	His	Gln	Leu	Ser	Asn	Gly	Leu	Tyr	Val
1														15	
Ser	Gly	Arg	Pro	Glu	Gln	Pro	Lys	Glu	Lys	Ala	Pro	Val	Ile	Cys	Ser
			20				25					30			
Ser	Ala	Met	Arg	Thr	Leu	Ala	Gly	Thr							
			35			40									

(2) INFORMATION FOR SEQ ID NO:1391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 522 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..522

(D) OTHER INFORMATION: / Ceres Seq. ID 1500157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

aaaacaactg	tgtaaagtgc	tgaagattgc	attttggaga	gtcagagtttc	aaatagaatc	60
gtgagataga	gagtgaaaca	gggacaatct	gagtgacgta	cattatatgt	acagcrtgcc	120
tggctgttrca	ggaggcctac	ctgggtgacgt	cgaggaaagta	cagcccggtg	cccagggaacc	180
agctgtgtgag	cccgctgac	gtgcacgacg	gccgcctcgt	gcagcgcgcc	acgcgcgtcg	240
tccgcgtcgt	caccttcctc	tggatgcgct	tccgcttcgc	gctggcgctc	atgcgcgtgt	300
acatcaacct	gcgcgtgccc	gagcgcacgt	tctactaac	ctacaagctc	atgggcatca	360
rgctcgtcgt	caagddcacc	ccgccgcgcg	cgcccaagaa	gggccaccgc	ggcgctcctt	420
tcgtctgcaa	ccaccgcacc	gtgctcgacc	ccgtcgaggt	ggccgtrgcs	ctgcgcgcga	480
aggtcagctg	cgctcacctac	agsatctcca	agttctccga	gc		

(2) INFORMATION FOR SEQ ID NO:1392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1500158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:

Met Pro Phe Gly Phe Ala Leu Ala Leu Met Arg Val Tyr Ile Asn Leu
1 5 10 15
Pro Leu Pro Glu Arg Ile Val Tyr Tyr Thr Tyr Lys Leu Met Gly Ile
20 25 30
Xaa Leu Val Val Lys Xaa Thr Pro Pro Pro Pro Lys Lys Gly His
35 40 45
Pro Gly Val Leu Phe Val Cys Asn His Arg Thr Val Leu Asp Pro Val
50 55 60
Glu Val Ala Xaa Ala Leu Arg Arg Lys Val Ser Cys Val Thr Tyr Xaa
65 70 75 80
Ile Ser Lys Phe Ser Glu
85

(2) INFORMATION FOR SEQ ID NO:1393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1500159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:

Met Arg Val Tyr Ile Asn Leu Pro Leu Pro Glu Arg Ile Val Tyr Tyr
1 5 10 15
Thr Tyr Lys Leu Met Gly Ile Xaa Leu Val Val Lys Xaa Thr Pro Pro
20 25 30
Pro Pro Pro Lys Lys Gly His Pro Gly Val Leu Phe Val Cys Asn His
35 40 45
Arg Thr Val Leu Asp Pro Val Glu Val Ala Xaa Ala Leu Arg Arg Lys
50 55 60
Val Ser Cys Val Thr Tyr Xaa Ile Ser Lys Phe Ser Glu
65 70 75

(2) INFORMATION FOR SEQ ID NO:1394:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1500160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:

Met Gly Ile Xaa Leu Val Val Lys Xaa Thr Pro Pro Pro Pro Lys
1 5 10 15
Lys Gly His Pro Gly Val Leu Phe Val Cys Asn His Arg Thr Val Leu
20 25 30
Asp Pro Val Glu Val Ala Xaa Ala Leu Arg Arg Lys Val Ser Cys Val
35 40 45
Thr Tyr Xaa Ile Ser Lys Phe Ser Glu
50 55

(2) INFORMATION FOR SEQ ID NO:1395:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 508 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..508
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500165
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:
atatatgtga atcctaactg tacactgtct gaagtggacg aacggctctg gcttcggcgt 60
gttacgtgta tagtagggcc cttttgaacg aacggcgcg ggcggggcca ccaccagcat 120
ctgcggcgagg gagaatcgcg ttggttcgac gcaaacgcta ccggcgcccc ccttgccctt 180
ggggccggagt attttaccgc acccgttctc cctctctac cgcagatcag atcacactcg 240
tagagagagag gaaaaaatat cccaaacccat agctcccgat ctgatggcgc aaccctcgcg 300
tcttcttcga catgaccgcg ggcggcgccc cggcggggac gatcgtgat gagctgtacg 360
ccaacgaggt gcccaagacc gcggagaact tccgcgcgct gtgcacgggc gagaagggcg 420
tgggcaagtc cggaagccg ctccactaca agggctccac cttccaccgc gtcatecccc 480
arttcattgt ccaggggcgc gaattcac
(2) INFORMATION FOR SEQ ID NO:1396:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..74
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500166
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:
Met Ala Asn Pro Arg Val Phe Phe Asp Met Thr Val Gly Gly Ala Pro
1 5 10 15
Ala Gly Arg Ile Val Met Glu Leu Tyr Ala Asn Glu Val Pro Lys Thr
20 25 30
Ala Glu Asn Phe Arg Ala Leu Cys Thr Gly Glu Lys Gly Val Gly Lys
35 40 45
Ser Gly Lys Pro Leu His Tyr Lys Gly Ser Thr Phe His Arg Val Ile
50 55 60
Pro Xaa Phe Met Cys Gln Gly Gly Asp Phe
65 70
(2) INFORMATION FOR SEQ ID NO:1397:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..65
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500167
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397:
Met Thr Val Gly Gly Ala Pro Ala Gly Arg Ile Val Met Glu Leu Tyr
1 5 10 15
Ala Asn Glu Val Pro Lys Thr Ala Glu Asn Phe Arg Ala Leu Cys Thr
20 25 30
Gly Glu Lys Gly Val Gly Lys Ser Gly Lys Pro Leu His Tyr Lys Gly
35 40 45
Ser Thr Phe His Arg Val Ile Pro Xaa Phe Met Cys Gln Gly Gly Asp
50 55 60
Phe
65

(2) INFORMATION FOR SEQ ID NO:1398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:

Met Glu Leu Tyr Ala Asn Glu Val Pro Lys Thr Ala Glu Asn Phe Arg
1 5 10 15
Ala Leu Cys Thr Gly Glu Lys Gly Val Gly Lys Ser Gly Lys Pro Leu
20 25 30
His Tyr Lys Gly Ser Thr Phe His Arg Val Ile Pro Xaa Phe Met Cys
35 40 45
Gln Gly Gly Asp Phe
50

(2) INFORMATION FOR SEQ ID NO:1399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..507
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:

acgatatttaa ccgacacaaaa taagctagtgt gtagcagttg gaggggtaac agcacttgct 60
gcagggatat acacaacaag ggaggggtgca agagtgtct ggggctatgt tgatcgtatt 120
ctgggtcagc catcactgat aaggagtgca tcacgtggga aatatccctg gtctggtttc 180
ctctcacgtg ctacaagtac cctgactagc aaactgaaga atggaagcaa cctagggaag 240
gacagaaatg gggttggtgga tgttattcta aatccttctc tccagaagag agtgaagcag 300
cttgctaatt ccacagccaa tacaaaaact catcaagctc ctttcaggaa catgcttttc 360
tatgggcctc ctggcacagg gaaaaccatg gcagcacgag aacttgctcg caattctgga 420
ttagattatg cactaatgac tgggtggagat gttgcaccat tgggatcaca agcagtcacc 480
aagattcatc agttgtttga ctgggag

(2) INFORMATION FOR SEQ ID NO:1400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..169
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:

Thr Ile Leu Thr Asp Gln Asn Lys Leu Val Val Ala Val Gly Gly Val
1 5 10 15
Thr Ala Leu Ala Ala Gly Ile Tyr Thr Thr Arg Glu Gly Ala Arg Val
20 25 30
Val Trp Gly Tyr Val Asp Arg Ile Leu Gly Gln Pro Ser Leu Ile Arg
35 40 45
Glu Ser Ser Arg Gly Lys Tyr Pro Trp Ser Gly Phe Leu Ser Arg Ala
50 55 60

Thr	Ser	Thr	Leu	Thr	Ser	Lys	Leu	Lys	Asn	Gly	Ser	Asn	Leu	Gly	Lys
65				70					75					80	
Asp	Arg	Asn	Gly	Phe	Gly	Asp	Val	Ile	Leu	Asn	Pro	Ser	Leu	Gln	Lys
			85						90					95	
Arg	Val	Lys	Gln	Leu	Ala	Asn	Ala	Thr	Ala	Asn	Thr	Lys	Leu	His	Gln
			100					105					110		
Ala	Pro	Phe	Arg	Asn	Met	Leu	Phe	Tyr	Gly	Pro	Pro	Gly	Thr	Gly	Lys
			115					120				125			
Thr	Met	Ala	Ala	Arg	Glu	Leu	Ala	Arg	Asn	Ser	Gly	Leu	Asp	Tyr	Ala
	130				135						140				
Leu	Met	Thr	Gly	Gly	Asp	Val	Ala	Pro	Leu	Gly	Ser	Gln	Ala	Val	Thr
145					150					155				160	
Lys	Ile	His	Gln	Leu	Phe	Asp	Trp	Ala							

(2) INFORMATION FOR SEQ ID NO:1401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..536
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:

aaaagccagg	attcctctgc	tcttctctgtt	tagggtttcc	ccctctctct	gtcctctgccg	60
gatgcatgg	cgattccgcc	gcggactcct	tccccgccgc	catcgttggtc	gcgctctgta	120
accgagaccg	ttcgggggtc	ccaccagtgc	accgtacggg	gctactccct	cgccaaggcc	180
atggggcccc	gcgcctacct	cgccagcgac	gtcttcgccg	tcggaggata	ccactggggc	240
gtctacctct	accgccagcg	caagaacgcc	gaggacaact	ccaactacgt	ctccgttttc	300
gtcgccctct	cttcgcagcg	catcgacgtc	cgagccctct	tcgagctcac	cttcctcgac	360
cagtycgccg	gcggctgcma	caaggttcac	tcgcactttg	accgctcgct	caagtctggc	420
ccatacacc	tcaagtacag	gggatccatg	tggggttaca	agcgcttcta	caaaagaaca	480
ctcttggaag	aactctgatt	cttaaagaat	gattgcttag	tgatgaactg	cacagt	

(2) INFORMATION FOR SEQ ID NO:1402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:

Lys	Pro	Gly	Phe	Leu	Cys	Ser	Ser	Cys	Leu	Gly	Phe	Pro	Pro	Leu	Ser
1				5				10				15			
Ala	Pro	Ala	Gly	Cys	Asp	Gly	Asp	Ser	Ala	Ala	Asp	Ser	Phe	Pro	Ala
			20					25				30			
Ala	Ile	Val	Val	Ala	Leu	Cys	Asn	Arg	Asp	Arg	Ser	Gly	Val	Pro	Pro
	35						40					45			
Val	His	Arg	Thr	Gly	Leu	Leu	Pro	Arg	Gln	Gly	His	Gly	Pro	Arg	Pro
	50					55					60				
Leu	Pro	Arg	Gln	Arg	Arg	Leu	Arg	Arg	Arg	Arg	Ile	Pro	Leu	Gly	Arg
65					70					75				80	
Leu	Pro	Leu	Pro	Arg	Arg	Gln	Glu	Arg	Arg	Gly	Gln	Leu	Gln	Leu	Arg
			85					90						95	
Leu	Arg	Phe	Arg	Arg	Pro	Arg	Phe	Arg	Arg	His	Arg	Arg	Pro	Ser	Pro
			100					105						110	

Leu Arg Ala His Pro Pro Arg Pro Xaa Arg Xaa Arg Leu Xaa Gln Gly
115 120 125
Ser Leu Ala Leu
130

(2) INFORMATION FOR SEQ ID NO:1403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1500181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:

Met	Ala	Ile	Pro	Pro	Arg	Thr	Pro	Ser	Pro	Pro	Ser	Trp	Ser	Arg
1			5					10					15	
Ser	Val	Thr	Glu	Thr	Val	Arg	Gly	Ser	His	Gln	Phe	Thr	Val	Arg
			20				25					30		Gly
Tyr	Ser	Leu	Ala	Lys	Gly	Met	Gly	Pro	Gly	Arg	Tyr	Leu	Ala	Ser
			35				40					45		Asp
Val	Phe	Ala	Val	Gly	Gly	Tyr	His	Trp	Ala	Val	Tyr	Leu	Tyr	Pro
			50				55				60			Asp
Gly	Lys	Asn	Ala	Glu	Asp	Asn	Ser	Asn	Tyr	Val	Ser	Val	Phe	Val
			65				70				75			Ala
Leu	Ala	Ser	Asp	Gly	Ile	Asp	Val	Arg	Ala	Leu	Phe	Glu	Leu	Thr
			85					90					95	
Leu	Asp	Gln	Xaa	Gly	Xaa	Gly	Cys	Xaa	Lys	Val	His	Ser	His	Phe
			100				105						110	
Arg	Ser	Leu	Lys	Phe	Gly	Pro	Tyr	Thr	Leu	Lys	Tyr	Arg	Gly	Ser
			115				120					125		Met
Trp	Gly	Tyr	Lys	Arg	Phe	Tyr	Lys	Arg	Thr	Leu	Leu	Glu	Glu	Ser
			130				135					140		Asp
Phe	Leu	Lys	Asn	Asp	Cys	Leu	Val	Met	Asn	Cys	Thr			
			145				150				155			

(2) INFORMATION FOR SEQ ID NO:1404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1500182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:

Met	Gly	Pro	Gly	Arg	Tyr	Leu	Ala	Ser	Asp	Val	Phe	Ala	Val	Gly	Gly
1			5					10						15	
Tyr	His	Trp	Ala	Val	Tyr	Leu	Tyr	Pro	Asp	Gly	Lys	Asn	Ala	Glu	Asp
			20					25				30			
Asn	Ser	Asn	Tyr	Val	Ser	Val	Phe	Val	Ala	Leu	Ala	Ser	Asp	Gly	Ile
			35					40				45			
Asp	Val	Arg	Ala	Leu	Phe	Glu	Leu	Thr	Leu	Leu	Asp	Gln	Xaa	Gly	Xaa
			50				55				60				
Gly	Cys	Xaa	Lys	Val	His	Ser	His	Phe	Asp	Arg	Ser	Leu	Lys	Phe	Gly
			65				70				75			80	
Pro	Tyr	Thr	Leu	Lys	Tyr	Arg	Gly	Ser	Met	Trp	Gly	Tyr	Lys	Arg	Phe
			85					90					95		
Tyr	Lys	Arg	Thr	Leu	Leu	Glu	Glu	Ser	Asp	Phe	Leu	Lys	Asn	Asp	Cys

110

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 540 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..540

(D) OTHER INFORMATION: / Ceres Seq. ID 1500186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:

(X1) SEQUENCE DESCRIPTION						
ggccacacac	tcgcgccccc	ggcctccgcg	cgcctgcgcg	cccgctgcgt	cctgtctgtc	60
tctctctctc	ctcgcgtgag	cgccgcgaac	catgaacac	ctctctcaag	attctcttga	120
cgccccccg	cgggactctc	caagagatgc	agacattgaa	atgggaatgc	atcaagctga	180
tgtctcagac	aacttaaaag	attctctgaa	gaaggtcgat	acaaattgca	gtttaattgc	240
aaagctgaca	aatctattga	atctctatca	gactgcaaat	gaggaaatga	aagcagctac	300
aaaagcaagt	tccatgaaag	caataatgca	gcggatggag	aaaagattgc	atgaagtggg	360
gaaattctgc	cgtcaggcga	agacaaataa	tgtatgaatt	gaaaaagata	actctacaaa	420
taggcaaaagt	ctcggatgtg	gaaaaaggtt	tgcctctggc	cgatcaagag	agcaaaamtac	480
tggacacata	aaaaagaaat	tgaaggagcg	gatgatgtac	tttcacagct	tgagaaagac	540

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1500187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:

(X1) SEQUENCE DESCRIPTION: 151																
Ala Thr	Pro Ser	Val Pro	Arg Pro	Pro Leu	Ala Ala	Ser Pro	Pro Pro	Ala Cys	15							
Pro Cys	Leu Ser	Leu Ser	Leu Leu	Ala Leu	Ala Ser	Pro Pro	Pro Ala	Met Asn	20							
Asn Leu	Leu Thr	Asp Ser	Phe Glu	Leu Leu	Ala Leu	Pro Arg	Arg Arg	Asp Ser	Ser Arg	25						
Asp Ala	Asp Ile	Glu Met	Gly Met	His Gln	Ala Asp	Ala Ser	Ala Ser	Asp Asn	30							
Leu Lys	Asp Phe	Leu Lys	Lys Val	Asp Thr	Ile Glu	Ser Leu	Ile Ala	Leu Ile	Ala Ala	35						
Lys Leu	Thr Asn	Leu Leu	Asn Lys	Leu Gln	Thr Thr	Ala Asn	Glu Glu	Leu Ser	Glu Ser	40						
Lys Ala	Val Thr	Lys Ala	Ser Ser	Met Lys	Ala Ile	Lys Gln	Arg Arg	Gln Arg	Met Thr	45						
Glu Lys	Asp Ile	Asp Glu	Val Gly	Lys Lys	Ile Ala	Arg Gln	Ala Arg	Gln Ala	Lys Thr	50						
Lys Leu	Thr Asn	Leu Leu	Asn Lys	Leu Gln	Thr Thr	Ala Asn	Glu Glu	Leu Ser	Glu Ser	55						
Lys Ala	Val Thr	Lys Ala	Ser Ser	Met Lys	Ala Ile	Lys Gln	Arg Arg	Gln Arg	Met Thr	60						
Glu Lys	Asp Ile	Asp Glu	Val Gly	Lys Lys	Ile Ala	Arg Gln	Ala Arg	Gln Ala	Lys Thr	65						
Lys Leu	Thr Asn	Leu Leu	Asn Lys	Leu Gln	Thr Thr	Ala Asn	Glu Glu	Leu Ser	Glu Ser	70						
Lys Ala	Val Thr	Lys Ala	Ser Ser	Met Lys	Ala Ile	Lys Gln	Arg Arg	Gln Arg	Met Thr	75						
Glu Lys	Asp Ile	Asp Glu	Val Gly	Lys Lys	Ile Ala	Arg Gln	Ala Arg	Gln Ala	Lys Thr	80						
Lys Leu	Thr Asn	Leu Leu	Asn Lys	Leu Gln	Thr Thr	Ala Asn	Glu Glu	Leu Ser	Glu Ser	85						
Lys Ala	Val Thr	Lys Ala	Ser Ser	Met Lys	Ala Ile	Lys Gln	Arg Arg	Gln Arg	Met Thr	90						
Glu Lys	Asp Ile	Asp Glu	Val Gly	Lys Lys	Ile Ala	Arg Gln	Ala Arg	Gln Ala	Lys Thr	95						
Lys Leu	Thr Asn	Leu Leu	Asn Lys	Leu Gln	Thr Thr	Ala Asn	Glu Glu	Leu Ser	Glu Ser	100						
Lys Ala	Val Thr	Lys Ala	Ser Ser	Met Lys	Ala Ile	Lys Gln	Arg Arg	Gln Arg	Met Thr	105						
Glu Lys	Asp Ile	Asp Glu	Val Gly	Lys Lys	Ile Ala	Arg Gln	Ala Arg	Gln Ala	Lys Thr	110						
Lys Leu	Thr Asn	Leu Leu	Asn Lys	Leu Gln	Thr Thr	Ala Asn	Glu Glu	Leu Ser	Glu Ser	115						
Lys Ala	Val Thr	Lys Ala	Ser Ser	Met Lys	Ala Ile	Lys Gln	Arg Arg	Gln Arg	Met Thr	120						
Glu Lys	Asp Ile	Asp Glu	Val Gly	Lys Lys	Ile Ala	Arg Gln	Ala Arg	Gln Ala	Lys Thr	125						
Lys Leu	Thr Asn	Leu Leu	Asn Lys	Leu Gln	Thr Thr	Ala Asn	Glu Glu	Leu Ser	Glu Ser	130						
Lys Ala	Val Thr	Lys Ala	Ser Ser	Met Lys	Ala Ile	Lys Gln	Arg Arg	Gln Arg	Met Thr	135						
Glu Lys	Asp Ile	Asp Glu	Val Gly	Lys Lys	Ile Ala	Arg Gln	Ala Arg	Gln Ala	Lys Thr	140						
Lys Leu	Thr Asn	Leu Leu	Asn Lys	Leu Gln	Thr Thr	Ala Asn	Glu Glu	Leu Ser	Glu Ser	145						

(2) INFORMATION FOR SEQ ID NO:1407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:

Met Asn Asn Leu Leu Thr Asp Ser Phe Glu Leu Pro Arg Arg Asp Ser
1 5 10 15
Ser Arg Asp Ala Asp Ile Glu Met Gly Met His Gln Ala Asp Ala Ser
20 25 30
Asp Asn Leu Lys Asp Phe Leu Lys Lys Val Asp Thr Ile Glu Ser Leu
35 40 45
Ile Ala Lys Leu Thr Asn Leu Leu Asn Lys Leu Gln Thr Ala Asn Glu
50 55 60
Glu Ser Lys Ala Val Thr Lys Ala Ser Ser Met Lys Ala Ile Lys Gln
65 70 75 80
Arg Met Glu Lys Asp Ile Asp Glu Val Gly Lys Ile Ala Arg Gln Ala
85 90 95
Lys Thr Lys Val Asp Glu Leu Glu Lys Asp Asn Leu Ser Asn Arg Gln
100 105 110
Lys Pro Gly Cys Gly Lys Gly Ser Ala Val Asp Arg Ser Arg Glu Gln
115 120 125
Xaa Thr Gly Ala Val Lys Lys Lys Leu Lys Glu Arg Met Asp Asp Phe
130 135 140
Gln Thr Leu Arg Glu
145

(2) INFORMATION FOR SEQ ID NO:1408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:

Met Gly Met His Gln Ala Asp Ala Ser Asp Asn Leu Lys Asp Phe Leu
1 5 10 15
Lys Lys Val Asp Thr Ile Glu Ser Leu Ile Ala Lys Leu Thr Asn Leu
20 25 30
Leu Asn Lys Leu Gln Thr Ala Asn Glu Glu Ser Lys Ala Val Thr Lys
35 40 45
Ala Ser Ser Met Lys Ala Ile Lys Gln Arg Met Glu Lys Asp Ile Asp
50 55 60
Glu Val Gly Lys Ile Ala Arg Gln Ala Lys Thr Lys Val Asp Glu Leu
65 70 75 80
Glu Lys Asp Asn Leu Ser Asn Arg Gln Lys Pro Gly Cys Gly Lys Gly
85 90 95
Ser Ala Val Asp Arg Ser Arg Glu Gln Xaa Thr Gly Ala Val Lys Lys
100 105 110
Lys Leu Lys Glu Arg Met Asp Asp Phe Gln Thr Leu Arg Glu
115 120 125

(2) INFORMATION FOR SEQ ID NO:1409:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1473 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1473

(D) OTHER INFORMATION: / Ceres Seq. ID 1500190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:

```
agaaagaaga agataacaca atgctcttct tcttattctt cttctactta ctcttatctt 60
catcctccga tctagtcttc gccgacgcgt ggtgactcca cgaacatttc ttccctatag 120
attgcgcacc accgtcacca ccatcaccac caccacttcc taaactacca ttctcttcaa 180
ccactcctcc atcttcatca gacccaaaatg cttctccttt cttcccttta tacccttcat 240
ctccaccacc acccttctca gccctccttg cttcttcttc ggogaatatc tcatctctaa 300
tcgtccctca gcgcactaaa tcccacccta actccaaaaa actcctttac gtgcctatct 360
ccgcgcgttc ctccgctgct ttagtcgctc tacttatcgc ttactctat tggcgaagaa 420
gcaaacgtta ccaagatctt aacttctccg atgatagcaa aacatacacc accgcacgta 480
gccgcgcgtg ctaccctctt cctccggcaa cggcgctccc aacacgacgc aatgcggagg 540
ctagaagtaa acagaggacc accacgagct ccaccaataa caacagctct gagttctctt 600
acttaggaac aatggtgaat caaagaggaa tcgatgaaca atctcttagt aataatggat 660
caagctcaag aaaaactgaa tctccagatc ttcaaccact tcctccattg atgaacgaa 720
gtttccgtht aatccagat gttggttcaa tcggagaaga agatgaagaa gatgagtttt 780
actctccacg tggctcacia agcgggcgag aaccgthtaa ccgggtcgga cttccgggtc 840
aaaatcctag atctgttaac aatgacacta tctctgtctc atcttcacga tctggttca 900
cagggaagat aacatttatc agtatctctc ctccaatgag tcttaagaga tctgaacca 960
aaccgcgcgt tatctccaca ccagaaccgg cggagthaac cgattataga ttgttctggt 1020
ctccgtcact ctgcttagct tctttatcgt cgggattgaa aaactccgat gaagttaggt 1080
tgaatcaaat ctttagatct ccgacgggta catctctaac aacttcaccg gagaataaca 1140
aaaaagagaa ctctccatta tcatctactt caacttcacc ggaacgacga ccaaatgata 1200
caccagaagc ttacttgaga tctccgtcgc attctctgc tctcatatca ccgtatagat 1260
gttttcagaa atctccggag gtcttacccg cgthtatgag taatctccgg caaggtttgc 1320
aatctcagtht actatctctt ccttcaact ctcattggag acaaggtttc ctttagcagt 1380
tagatgcatt acgttctcgt tcaccgtcgt cgtctctctc tctgtttgtt tcttcaccgg 1440
agaaagcttc tcataagta cagattacat etc
```

(2) INFORMATION FOR SEQ ID NO:1410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 490 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..490

(D) OTHER INFORMATION: / Ceres Seq. ID 1500191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:

```
Lys Glu Glu Asp Asn Thr Met Leu Phe Phe Leu Phe Phe Tyr Leu
1 5 10 15
Leu Leu Ser Ser Ser Asp Leu Val Phe Ala Asp Arg Arg Val Leu
20 25 30
His Glu Pro Phe Phe Pro Ile Asp Ser Pro Pro Pro Ser Pro Pro Ser
35 40 45
Pro Pro Pro Leu Pro Lys Leu Pro Phe Ser Ser Thr Thr Pro Pro Ser
50 55 60
Ser Ser Asp Pro Asn Ala Ser Pro Phe Phe Pro Leu Tyr Pro Ser Ser
65 70 75 80
Pro Pro Pro Pro Ser Pro Ala Ser Phe Ala Ser Phe Phe Ala Asn Ile
85 90 95
Ser Ser Leu Ile Val Pro His Ala Thr Lys Ser Pro Pro Asn Ser Lys
```

	100		105		110	
Lys	Leu	Leu	Ile	Val	Ala	Ile
	115		120		125	
Ala	Leu	Leu	Ile	Ala	Leu	Tyr
	130		135		140	
Asp	Leu	Asn	Phe	Ser	Asp	Asp
	145		150		155	
Arg	Arg	Val	Tyr	Pro	Pro	Pro
			165		170	
Asn	Ala	Glu	Ala	Arg	Ser	Lys
			180		185	
Asn	Asn	Ser	Ser	Glu	Phe	Leu
			195		200	
Gly	Ile	Asp	Glu	Gln	Ser	Leu
	210		215		220	
Leu	Glu	Ser	Pro	Asp	Leu	Gln
	225		230		235	
Phe	Arg	Leu	Asn	Pro	Asp	Val
			245		250	
Asp	Glu	Phe	Tyr	Ser	Pro	Arg
			260		265	
Asn	Arg	Val	Gly	Leu	Pro	Gly
			275		280	
Thr	Ile	Ser	Cys	Ser	Ser	Ser
	290		295		300	
Phe	Ile	Ser	Ile	Ser	Pro	Ser
	305		310		315	
Pro	Pro	Val	Ile	Ser	Thr	Pro
			325		330	
Phe	Val	Arg	Ser	Pro	Ser	Leu
			340		345	
Lys	Asn	Ser	Asp	Glu	Val	Gly
			355		360	
Val	Thr	Ser	Leu	Thr	Thr	Ser
	370		375		380	
Pro	Leu	Ser	Ser	Thr	Ser	Thr
	385		390		395	
Pro	Glu	Ala	Tyr	Leu	Arg	Ser
			405		410	
Pro	Tyr	Arg	Cys	Phe	Gln	Lys
			420		425	
Ser	Asn	Leu	Arg	Gln	Gly	Leu
			435		440	
Asn	Ser	His	Gly	Gly	Gln	Gly
			450		455	
Ser	Arg	Ser	Pro	Ser	Ser	Ser
	465		470		475	
Lys	Ala	Ser	His	Lys	Ser	Pro
			485		490	

(2) INFORMATION FOR SEQ ID NO:1411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 484 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..484

(D) OTHER INFORMATION: / Ceres Seq. ID 1500192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:

Met Leu Phe Phe Leu Phe Phe Phe Tyr Leu Leu Leu Ser Ser Ser Ser
1 5 10 15
Asp Leu Val Phe Ala Asp Arg Arg Val Leu His Glu Pro Phe Phe Pro
20 25 30
Ile Asp Ser Pro Pro Pro Ser Pro Pro Ser Pro Pro Leu Pro Lys
35 40 45
Leu Pro Phe Ser Ser Thr Thr Pro Pro Ser Ser Ser Asp Pro Asn Ala
50 55 60
Ser Pro Phe Phe Pro Leu Tyr Pro Ser Ser Pro Pro Pro Ser Pro
65 70 75 80
Ala Ser Phe Ala Ser Phe Pro Ala Asn Ile Ser Ser Leu Ile Val Pro
85 90 95
His Ala Thr Lys Ser Pro Pro Asn Ser Lys Lys Leu Leu Ile Val Ala
100 105 110
Ile Ser Ala Val Ser Ser Ala Ala Leu Val Ala Leu Leu Ile Ala Leu
115 120 125
Leu Tyr Trp Arg Arg Ser Lys Arg Asn Gln Asp Leu Asn Phe Ser Asp
130 135 140
Asp Ser Lys Thr Tyr Thr Thr Asp Ser Ser Arg Arg Val Tyr Pro Pro
145 150 155 160
Pro Pro Ala Thr Ala Pro Pro Thr Arg Arg Asn Ala Glu Ala Arg Ser
165 170 175
Lys Gln Arg Thr Thr Thr Ser Ser Thr Asn Asn Asn Ser Ser Glu Phe
180 185 190
Leu Tyr Leu Gly Thr Met Val Asn Gln Arg Gly Ile Asp Glu Gln Ser
195 200 205
Leu Ser Asn Asn Gly Ser Ser Ser Arg Lys Leu Glu Ser Pro Asp Leu
210 215 220
Gln Pro Leu Pro Pro Leu Met Lys Arg Ser Phe Arg Leu Asn Pro Asp
225 230 235 240
Val Gly Ser Ile Gly Glu Glu Asp Glu Glu Asp Glu Phe Tyr Ser Pro
245 250 255
Arg Gly Ser Gln Ser Gly Arg Glu Pro Leu Asn Arg Val Gly Leu Pro
260 265 270
Gly Gln Asn Pro Arg Ser Val Asn Asn Asp Thr Ile Ser Cys Ser Ser
275 280 285
Ser Ser Ser Gly Ser Pro Gly Arg Ser Thr Phe Ile Ser Ile Ser Pro
290 295 300
Ser Met Ser Pro Lys Arg Ser Glu Pro Lys Pro Pro Val Ile Ser Thr
305 310 315 320
Pro Glu Pro Ala Glu Leu Thr Asp Tyr Arg Phe Val Arg Ser Pro Ser
325 330 335
Leu Ser Leu Ala Ser Leu Ser Ser Gly Leu Lys Asn Ser Asp Glu Val
340 345 350
Gly Leu Asn Gln Ile Phe Arg Ser Pro Thr Val Thr Ser Leu Thr Thr
355 360 365
Ser Pro Glu Asn Asn Lys Lys Glu Asn Ser Pro Leu Ser Ser Thr Ser
370 375 380
Thr Ser Pro Glu Arg Arg Pro Asn Asp Thr Pro Glu Ala Tyr Leu Arg
385 390 395 400
Ser Pro Ser His Ser Ser Ala Ser Thr Ser Pro Tyr Arg Cys Phe Gln
405 410 415
Lys Ser Pro Glu Val Leu Pro Ala Phe Met Ser Asn Leu Arg Gln Gly
420 425 430
Leu Gln Ser Gln Leu Leu Ser Ser Pro Ser Asn Ser His Gly Gly Gln
435 440 445
Gly Phe Leu Lys Gln Leu Asp Ala Leu Arg Ser Arg Ser Pro Ser Ser
450 455 460
Ser Ser Ser Ser Val Cys Ser Ser Pro Glu Lys Ala Ser His Lys Ser
465 470 475 480
Pro Val Thr Ser

(2) INFORMATION FOR SEQ ID NO:1412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..287
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:

Met Val Asn Gln Arg Gly Ile Asp Glu Gln Ser Leu Ser Asn Asn Gly
1 5 10 15
Ser Ser Ser Arg Lys Leu Glu Ser Pro Asp Leu Gln Pro Leu Pro Pro
20 25 30
Leu Met Lys Arg Ser Phe Arg Leu Asn Pro Asp Val Gly Ser Ile Gly
35 40 45
Glu Glu Asp Glu Glu Asp Glu Phe Tyr Ser Pro Arg Gly Ser Gln Ser
50 55 60
Gly Arg Glu Pro Leu Asn Arg Val Gly Leu Pro Gly Gln Asn Pro Arg
65 70 75 80
Ser Val Asn Asn Asp Thr Ile Ser Cys Ser Ser Ser Ser Ser Gly Ser
85 90 95
Pro Gly Arg Ser Thr Phe Ile Ser Ile Ser Pro Ser Met Ser Pro Lys
100 105 110
Arg Ser Glu Pro Lys Pro Pro Val Ile Ser Thr Pro Glu Pro Ala Glu
115 120 125
Leu Thr Asp Tyr Arg Phe Val Arg Ser Pro Ser Leu Ser Leu Ala Ser
130 135 140
Leu Ser Ser Gly Leu Lys Asn Ser Asp Glu Val Gly Leu Asn Gln Ile
145 150 155 160
Phe Arg Ser Pro Thr Val Thr Ser Leu Thr Thr Ser Pro Glu Asn Asn
165 170 175
Lys Lys Glu Asn Ser Pro Leu Ser Ser Thr Ser Thr Ser Pro Glu Arg
180 185 190
Arg Pro Asn Asp Thr Pro Glu Ala Tyr Leu Arg Ser Pro Ser His Ser
195 200 205
Ser Ala Ser Thr Ser Pro Tyr Arg Cys Phe Gln Lys Ser Pro Glu Val
210 215 220
Leu Pro Ala Phe Met Ser Asn Leu Arg Gln Gly Leu Gln Ser Gln Leu
225 230 235 240
Leu Ser Ser Pro Ser Asn Ser His Gly Gly Gln Gly Phe Leu Lys Gln
245 250 255
Leu Asp Ala Leu Arg Ser Arg Ser Pro Ser Ser Ser Ser Ser Val
260 265 270
Cys Ser Ser Pro Glu Lys Ala Ser His Lys Ser Pro Val Thr Ser
275 280 285

(2) INFORMATION FOR SEQ ID NO:1413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..503
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413:

gccatttttr gtgartgcgc cctttccctt cctccccaga tccccgtccc cgttttccac 60
ttttgcctcc gccccaattc ggataacaaa cccctccgcc tcgtcgcgtc tcctcccagc 120
cgagccgcat cggtagagag agggagargg agggactgar ggaggaggag tctgggttccg 180
gtcccgcccg cccggccgnc ntgcgcgatt cgattgcagc tctcgtcccc gggcggcgctc 240
caggatggtg cgggggaaga cgcagatgaa gcggatagag aacccgacca gccgcaggtg 300
caccttctcc aagcgcgcga acggcctgct caagaaggcg ttcgarctct ccgtcctctg 360
cramgcgagc gtgcgcctcg tmtcttctc cmcgcgccgc aagctctacg aattcgccag 420
cggaagtrcg cagaaaacga ttgaacgtta tagaacatac acaaaggata atgtcagcaa 480
cagacagtg cagcaggata ttg

(2) INFORMATION FOR SEQ ID NO:1414:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1500199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

Ala Ile Phe Xaa Xaa Cys Ala Leu Ser Leu Pro Pro Gln Ile Pro Val
1 5 10 15
Pro Val Phe His Phe Cys Leu Arg Pro Asn Ser Asp Asn Lys Pro Leu
20 25 30
Arg Leu Val Ala Ser Pro Pro Ser Arg Ala Asp Pro Val Glu Arg Gly
35 40 45
Arg Xaa Arg Asp
50

(2) INFORMATION FOR SEQ ID NO:1415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1500200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

Met Val Arg Gly Lys Thr Gln Met Lys Arg Ile Glu Asn Pro Thr Ser
1 5 10 15
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala
20 25 30
Phe Xaa Leu Ser Val Leu Cys Xaa Ala Glu Val Ala Leu Xaa Val Phe
35 40 45
Ser Xaa Arg Gly Lys Leu Tyr Glu Phe Ala Ser Gly Ser Xaa Gln Lys
50 55 60
Thr Ile Glu Arg Tyr Arg Thr Tyr Thr Lys Asp Asn Val Ser Asn Lys
65 70 75 80
Thr Val Gln Gln Asp Ile
85

(2) INFORMATION FOR SEQ ID NO:1416:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..79
(D) OTHER INFORMATION: / Ceres Seq. ID 1500201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:

Met Lys Arg Ile Glu Asn Pro Thr Ser Arg Gln Val Thr Phe Ser Lys
1 5 10 15
Arg Arg Asn Gly Leu Leu Lys Lys Ala Phe Xaa Leu Ser Val Leu Cys
20 25 30
Xaa Ala Glu Val Ala Leu Xaa Val Phe Ser Xaa Arg Gly Lys Leu Tyr
35 40 45
Glu Phe Ala Ser Gly Ser Xaa Gln Lys Thr Ile Glu Arg Tyr Arg Thr
50 55 60
Tyr Thr Lys Asp Asn Val Ser Asn Lys Thr Val Gln Gln Asp Ile
65 70 75

(2) INFORMATION FOR SEQ ID NO:1417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 892 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..892
(D) OTHER INFORMATION: / Ceres Seq. ID 1500202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:

atcctcgcca tcgctccgc ttgtcccttg tttaattcca aaggtttcat tttctgcagg 60
gataacattt gtvvggggtg gtgagccgcg cgccctata gaatcctgct cctgctcctg 120
cgcccgcccc cttttcatgt tgctttccct ttccctcctc tcttctcctc cactcaccgc 180
gtcacctcc tatttagccg tcggaattgc ttgtcagcat cttcccagct tctttcttct 240
cttccaacgc cgtacgctgc tctgtccccc ggtgtcgtct tggattcttc tctcttca 300
ggaagggaag attggtacc gagatatcc tactagtcca gggctgtagt gcactcgtgc 360
cgcttggttt attctgcagc cataaccagt accagtaacc ccagcctgav ccggtgagga 420
gaggagatag agagagcgag cgggagcggg gagcagagga ggaggccat ggaaggcgac 480
agcttctcgc gcggcgccat ggccaaacggc ggcggcggcg gcggcagcgg cggcgggcag 540
gtggtggagc ggaagctgat ccacacgttc cacaggagct tctgtcaggt gcagagcctg 600
ctggaccaga accggatgct catcagcgag atcaaccaga accacgagtc ccgcgcgcgt 660
gntmstccgc tgcgtgtgct gcgggataga tatagcgctt ccacttaatt tcttctgtct 720
ttttcggttt cttcttcttc tctggttccc gctgcttgta ttgtattgta tctagtatgt 780
atcgtcgtcc atccctccgc cgggctctga gatgtacctc cattcctcct cgtgtaccgc 840
ctcgtacga gatgataccg gggcatgtga atgaacagag ctggttccga cc

(2) INFORMATION FOR SEQ ID NO:1418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..99
(D) OTHER INFORMATION: / Ceres Seq. ID 1500203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:

Ser Ser Ala Ser Val Pro Leu Cys Pro Cys Leu Ile Pro Lys Val Ser
1 5 10 15
Phe Ser Ala Gly Ile Thr Phe Xaa Gly Gly Glu Pro Ala Gly Pro
20 25 30
Ile Glu Ser Cys Ser Cys Ser Cys Ala Arg Pro Leu Phe Met Leu Leu
35 40 45
Ser Leu Ser Ser Ser Ser Ser Ser Ser Pro His Arg Leu Thr Ser Tyr
50 55 60

Leu Ala Val Arg Ile Ala Cys Gln His Leu Pro Ser Phe Phe Phe Phe
65 70 75 80
Phe Gln Pro Arg Tyr Ala Leu Leu Ser Pro Val Leu Ala Trp Ile Leu
85 90 95
Leu Ser Ser

(2) INFORMATION FOR SEQ ID NO:1419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1500204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:

Met Glu Gly Asp Ser Xaa Ser Gly Gly Ala Met Ala Asn Gly Gly Gly
1 5 10 15
Gly Gly Gly Ser Gly Gly Gly Gln Val Val Asp Gly Lys Leu Ile His
20 25 30
Thr Phe His Arg Ser Phe Val Gln Val Gln Ser Leu Leu Asp Gln Asn
35 40 45
Arg Met Leu Ile Ser Glu Ile Asn Gln Asn His Glu Ser Arg Ala Arg
50 55 60
Xaa Xaa Pro Leu Leu Leu Leu Arg Asp Arg Tyr Ser Ala Ser Thr
65 70 75

(2) INFORMATION FOR SEQ ID NO:1420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1500205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:

Met Ala Asn Gly Gly Gly Gly Gly Gly Ser Gly Gly Gln Val Val
1 5 10 15
Asp Gly Lys Leu Ile His Thr Phe His Arg Ser Phe Val Gln Val Gln
20 25 30
Ser Leu Leu Asp Gln Asn Arg Met Leu Ile Ser Glu Ile Asn Gln Asn
35 40 45
His Glu Ser Arg Ala Arg Xaa Xaa Pro Leu Leu Leu Arg Asp Arg
50 55 60
Tyr Ser Ala Ser Thr
65

(2) INFORMATION FOR SEQ ID NO:1421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..756
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:

atagggttct	aagcctcggc	cgtttcttcg	tctccacagc	tcccgcgcgc	gcggaccagc	60
gcgtcactct	acccgggttcc	ggcgtctccc	cgtacccgta	gcgcgggcatc	catggcgga	120
agacggaaaag	ggctttcttg	aagcagccca	agggtgtttct	ctgttccaa	aaggccacca	180
aggttaacaa	acctggcaag	ggaggaacaa	gattctggaa	gaacattggc	cttggtttca	240
agacaccag	ggaagccatt	gaaggaaacct	acattgataa	gaagtgtcca	ttcaccggca	300
ctgtgtctat	caggggctgc	atcatcgccg	gaacatgcca	cagtgtctaag	atgaatagga	360
ccatcattgt	tcgtaggaa	tatcttcact	tcgtcaagaa	gtaccagagg	tatgagaaga	420
gacactccaa	catccctgcg	cacatttcac	catgcttcgc	tgtaacagaa	ggagatcatg	480
tgatcattgg	ccagtgccag	ccagtgtcga	agactgntaa	ggttcaatgt	ggtcaaaagt	540
attctcgcaag	gttcgaagag	tgagacagtg	aagaaagctt	taactgcgcg	taaagatcat	600
gacgagttca	tcatccatgg	cccggaaaag	ctctgtgtta	taactgtttg	atgtgcctca	660
ttagcctttt	tcocccgtaa	tactatagt	gtacttggaa	ttggacttga	attacatcca	720
gaacttgaaa	tcttgaaaaa	aaatcataac	cccttg			

(2) INFORMATION FOR SEQ ID NO:1422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:

Met	Asn	Arg	Thr	Ile	Ile	Val	Arg	Arg	Asn	Tyr	Leu	His	Phe	Val	Lys	
1				5					10					15		
Lys	Tyr	Gln	Arg	Tyr	Glu	Lys	Arg	His	Ser	Asn	Ile	Pro	Ala	His	Ile	
				20					25				30			
Ser	Pro	Cys	Phe	Arg	Val	Lys	Glu	Gly	Asp	His	Val	Ile	Ile	Gly	Gln	
				35					40				45			
Cys	Arg	Pro	Val	Ser	Lys	Thr	Xaa	Lys	Val	Gln	Cys	Gly	Gln	Ser	Tyr	
				50					55				60			
Ser	Cys	Arg	Phe	Glu	Glu	Trp	Ser	Ser	Glu	Glu	Ser	Phe	His	Cys	Arg	
				70					75				80			
Leu	Arg	Ser														

(2) INFORMATION FOR SEQ ID NO:1423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1034
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:

gtgtctctta	ttcttttgg	tggtttggtg	ctggaaaggg	agtggacttt	tacaacttct	60
catgtcccta	ttgttgggag	ggttcggagt	ccggatcggg	atttgaccag	accagattgt	120
tcaacactcg	gaaggctcac	caaatcgctc	tacgctctctg	cttctcctctc	cacgaggtga	180
ggaaaccccta	gcgactgacc	atggcggttc	tcccgcgcac	cgacgggttg	gccttctctt	240
ctaccocgcg	gtgctactcc	gcgcgcgcgc	ctcgggcgcg	ctccccgacc	tcocccagcgc	300
catacggggg	cgcgccccc	ccggcgatgt	cgaagaggnc	cgatgtctgc	gtctccaaag	360
ttgatgacct	gatgaactgg	gcgcgtaagg	gctcgatttg	gcccatgacc	tttgggctcg	420
ctcgtgcrc	ggtcagagat	atgcacgcgc	gcgcgtcccg	ctacgacttc	gacccgggtc	480
ggcgctcatc	tcctgtccctc	gcgcgcgcgc	tccgatttga	tgatcgtcgc	cggcagagtc	540
accacaaaaa	ttggctccag	cctccgcaag	gtttatgacc	aaatgcctga	gctactagat	600
gttatttcaa	ttgggcagctg	tgccaaacgtt	ggtggatact	accattactc	ctactctggt	660

gtacgtggat	gtgacgctt	agtccccgtg	gacatctacg	tccctgggtg	cccacacaat	720
gctggaagac	tgctgtacgc	tgttcttcag	ctccaaaaga	agatcacatg	cgcgaaggat	780
ttcccttacc	ggttgaccaa	gtctctgtgt	gtctcgtcgt	gtctcgtcgt	ctacgthttct	840
ttgtcactga	ccaacctgtc	ttatctgaaa	taaggacgga	ttctctcgtg	attacacaaat	900
ttgtctgtcc	tctaaggatg	tgtcccgagc	ttgtgacgaa	catataaact	gtgtactatct	960
agtcagtgct	ctcgtaatgc	acaccagacc	tgctgtgaat	ctgtttttaa	gcttcatttg	1020
taatacaqca	atac					

(2) INFORMATION FOR SEQ ID NO:1424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..12

(D) OTHER INFORMATION: / Ceres Seq. ID 1500235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:

1	Cys	Leu	Leu	Phe	Leu	Cys	Val	Phe	Gly	Cys	Trp	Lys	Gly	Ser	Gly	Leu
				5						10					15	
1	Leu	Gln	Leu	Leu	Met	Ser	Leu	Leu	Leu	Gly	Gly	Phe	Gly	Val	Arg	Ile
				20					25					30		
Gly	Ile	Cys	His	Asn	Gln	Ile	Val	Gln	His	Ser	Glu	Gly	Ser	Pro	Asn	
		35					40					45				
Arg	Pro	Thr	Leu	Leu	Leu	Pro	Pro	Pro	Arg	Gly	Glu	Glu	Thr	Leu	Ala	
		50				55					60					
Thr	Asp	His	Gly	Val	Ala	Pro	Ala	His	Arg	Thr	Val	Gly	Leu	Pro	Leu	
65					70					75					80	
Tyr	Pro	Ala	Val	Val	Leu	Arg	Arg	Arg	Arg	Cys	Gly	Arg	Leu	Pro	Asp	
				85					90					95		
Leu	Pro	Ser	Ala	Ile	Arg	Gly	Arg	Ala	Pro	Thr	Gly	Asp	Val	Glu	Glu	
			100					105					110			
Xaa	Arg	Val	Arg	Gly	Leu	Gln	Gly									
		115					120									

(2) INFORMATION FOR SEQ ID NO:1425:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..10

(D) OTHER INFORMATION: / Ceres Seq. ID 1500236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:

```
Met Ala Leu Leu Pro Arg Thr Ala Arg Leu Ala Phe Leu Ser Thr Pro
1      5      10      15
Arg Ser Tyr Ser Ala Ala Ala Ala Gly Ala Ser Pro Thr Ser Pro
20      25      30
Ala Pro Tyr Gly Gly Ala Pro Pro Pro Ala Met Ser Lys Arg Xaa Glu
35      40      45
Phe Val Val Ser Lys Val Asp Asp Leu Met Asn Trp Ala Arg Lys Gly
50      55      60
Ser Ile Trp Pro Met Thr Phe Gly Leu Ala Cys Xaa Val Glu Met
65      70      75      80
Met His Ala Gly Ala Ser Arg Tyr Asp Phe Asp Arg Val Arg Arg His
85      90      95
Leu Pro Ser Leu Ala Ala Xaa Val Arg Leu His Asp Arg Arg Arg His
100     105     110
Xaa His Gln Gln Asn Gly Ser Ser Pro Pro Gln Gly Leu
115     120     125
```

(2) INFORMATION FOR SEQ ID NO:1427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..539
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:

```
aaccacacac ctcgavcgcg cgcgcagcgc caccgctccg ccgctgcccc cccgcccgcc 60
tgccgaggat cctctctctt tctctccgctc tctctccgccc agccggcgcc cagctctcgc 120
gcacggactc cagttagccc tcagcgctcc cgaactctcc tctccgcccgc tccctctctc 180
agaatgggaa aagagacaca ttttggttgc ttgggttcaa aggtcgttcg gtatcaacca 240
cagttgatat cgaattagac tatgagagtg atccccctct tgacgataca aaagctattg 300
agaaggagtc atcaactaat gtgtgctgtt ctcaactcgc aattgacttc gatagagact 360
ctaatttatg twtggagcga ttttcccggt caaggaaaagc atctgtagtc tctactgggt 420
ctcttaagct tgamctcgct ctcggcggtg gaggattacc gaaggtagaa tgggtggagat 480
atatgggaaa gaagcatctg gaaagacaac actcgcgctt catgttatta aggaagctc
```

(2) INFORMATION FOR SEQ ID NO:1428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:

Pro His His Ser Xaa Ala Arg Asp Gly Pro Pro Leu Arg Arg Cys Pro
1 5 10 15
Pro Ala Ala Met Arg Gly Ile Leu Ser Ser Ser Ala Leu Arg
20 25 30
Arg Ala Gly Ala Gln Leu Ser Arg Thr Asp Cys Ser Ser Pro Ser Ala
35 40 45
Ser Ala Thr Ser Pro Leu Arg Arg Ser Pro Leu Gln Asn Gly Lys Arg
50 55 60
Asp Thr Phe Cys Ser Leu Trp Phe Lys Gly Arg Ser Val Ser Thr Thr
65 70 75 80
Val Asp Met Gln Leu Asp Tyr Glu Ser Asp Pro Pro Leu Asp Asp Thr
85 90 95
Lys Ala Ile Glu Lys Glu Ser Ser Leu Asn Val Ala Val Ser Gln Leu
100 105 110
Ala Ile Asp Phe Asp Arg Asp Ser Asn Leu Cys Xaa Glu Arg Phe Ser
115 120 125
Arg Ala Arg Lys Ala Ser Val Val Ser Thr Gly Ser Leu Lys Leu Xaa
130 135 140
Leu Ala Leu Gly Val Gly Gly Leu Pro Lys Val Glu Trp Trp Arg Tyr
145 150 155 160
Met Gly Lys Lys His Leu Gly Arg Gln His Ser Arg Phe Met Leu Leu
165 170 175
Arg Lys Leu

(2) INFORMATION FOR SEQ ID NO:1429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1500248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

Met Arg Gly Ile Leu Ser Ser Ser Ser Ala Leu Leu Arg Arg Ala Gly
1 5 10 15
Ala Gln Leu Ser Arg Thr Asp Cys Ser Ser Pro Ser Ala Ser Ala Thr
20 25 30
Ser Pro Leu Arg Arg Ser Pro Leu Gln Asn Gly Lys Arg Asp Thr Phe
35 40 45
Cys Ser Leu Trp Phe Lys Gly Arg Ser Val Ser Thr Thr Val Asp Met
50 55 60
Gln Leu Asp Tyr Glu Ser Asp Pro Pro Leu Asp Asp Thr Lys Ala Ile
65 70 75 80
Glu Lys Glu Ser Ser Leu Asn Val Ala Val Ser Gln Leu Ala Ile Asp
85 90 95
Phe Asp Arg Asp Ser Asn Leu Cys Xaa Glu Arg Phe Ser Arg Ala Arg
100 105 110
Lys Ala Ser Val Val Ser Thr Gly Ser Leu Lys Leu Xaa Leu Ala Leu
115 120 125
Gly Val Gly Gly Leu Pro Lys Val Glu Trp Trp Arg Tyr Met Gly Lys
130 135 140
Lys His Leu Gly Arg Gln His Ser Arg Phe Met Leu Leu Arg Lys Leu
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:1430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..97
(D) OTHER INFORMATION: / Ceres Seq. ID 1500249
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:
Met Gln Leu Asp Tyr Glu Ser Asp Pro Pro Leu Asp Asp Thr Lys Ala
1 5 10 15
Ile Glu Lys Glu Ser Ser Leu Asn Val Ala Val Ser Gln Leu Ala Ile
20 25 30
Asp Phe Asp Arg Asp Ser Asn Leu Cys Xaa Glu Arg Phe Ser Arg Ala
35 40 45
Arg Lys Ala Ser Val Val Ser Thr Gly Ser Leu Lys Leu Xaa Leu Ala
50 55 60
Leu Gly Val Gly Gly Leu Pro Lys Val Glu Trp Trp Arg Tyr Met Gly
65 70 75 80
Lys Lys His Leu Gly Arg Gln His Ser Arg Phe Met Leu Leu Arg Lys
85 90 95
Leu

(2) INFORMATION FOR SEQ ID NO:1431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..749
(D) OTHER INFORMATION: / Ceres Seq. ID 1500250
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:

agccgactgg gactgagaag aaacctccaa acacctacct ctctacgaac tacctgccgc 60
cggaataacc tagagcgctc gaccatggat ccgcagcagc cggagcctgt cagttacctc 120
tgcgggagatt gcggactgag aacaccctga agcccgagga tgcataccag tgccgtgaat 180
gtggctacgc catcctctac aagaagcggt agccaattc acggcactgg aagacctctg 240
aggggtgaact gcgggccacc gccacctaga gatggatccg caccaagagc accaaggggt 300
ggtggtgggt gcggcgccgc Cagcagcttt gtcgattcag ggaacaaggt atacgtgggg 360
aaccttgcatt gggcggttga caactcgact ctgagaacc tattcagtga gcaaggacag 420
gtgctggatg ctaaggtcat ctacgacagg gatagcggca ggtcaagggg gtttggtttc 480
gtcacctatg gctctgcgga ggaggtcaac aatgccatat caaaccttga tggcatagac 540
ttggatggta gacagatccg agtcacgggt gcagaatcaa agcccaggcg tgaattttga 600
gattttgtta aggtggttta gaggtcaata gcgtgtgttc acaagttcta gttttagcga 660
tctattcttt ctctcgtatg agtaacaaga agatgtgatg aatgagagac tgggaagtga 720
acagtgctcc acaggaagat attttccc

(2) INFORMATION FOR SEQ ID NO:1432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..146
(D) OTHER INFORMATION: / Ceres Seq. ID 1500251
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:

Met Ser Ser Ala Val Asn Val Ala Thr Ala Ser Ser Thr Arg Ser

1	5	10	15
Gly Ser His Ile His Gly Thr Gly Arg Pro Leu Arg Val Asn Cys Gly			
	20	25	30
Pro Pro Pro Pro Arg Asp Gly Ser Ala Pro Arg Ala Pro Arg Gly Gly			
	35	40	45
Gly Gly Gly Gly Gly Ser Ser Phe Val Asp Ser Gly Asn Lys Val			
	50	55	60
Tyr Val Gly Asn Leu Ala Trp Gly Val Asp Asn Ser Thr Leu Glu Asn			
	65	70	75
Leu Phe Ser Glu Gln Gly Gln Val Leu Asp Ala Lys Val Ile Tyr Asp			
	85	90	95
Arg Asp Ser Gly Arg Ser Arg Gly Phe Gly Phe Val Thr Tyr Gly Ser			
	100	105	110
Ala Glu Glu Val Asn Asn Ala Ile Ser Asn Leu Asp Gly Ile Asp Leu			
	115	120	125
Asp Gly Arg Gln Ile Arg Val Thr Val Ala Glu Ser Lys Pro Arg Arg			
	130	135	140
Glu Phe			
145			

(2) INFORMATION FOR SEQ ID NO:1433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1500252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:

Met Asp Pro His Gln Glu His Gln Gly Val Val Val Ala Ala Ala			
	5	10	15
Ala Ala Ala Leu Ser Ile Gln Gly Thr Arg Tyr Thr Trp Gly Thr Leu			
	20	25	30
His Gly Ala Leu Thr Thr Arg Leu Trp Arg Thr Tyr Ser Val Ser Lys			
	35	40	45
Asp Arg Cys Trp Met Leu Arg Ser Ser Thr Thr Gly Ile Ala Ala Gly			
	50	55	60
Gln Gly Gly Leu Val Ser Ser Pro Met Ala Leu Pro Arg Arg Ser Thr			
	65	70	75
Met Pro Tyr Gln Thr Leu Met Ala			
	85		

(2) INFORMATION FOR SEQ ID NO:1434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1250

(D) OTHER INFORMATION: / Ceres Seq. ID 1500263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:

ctctctctct	ctctctcttc	tcgcttctct	tctctctcc	gatcttctct	gtgaccctct	60
tcttcttcga	tttcttttgg	gtttcttctc	cgaatcgccg	gagaaaaaaa	ccctctcttg	120
aatctaaaga	gactgttttt	ttgaagctat	tgactgattg	attgataaag	aagaataaag	180
attgatcgat	ctgaattttg	ggtacaagat	gtcgagattc	agagacagga	cggaggattt	240
caaggattct	gttcggaagt	ccgtgttttc	gataggttat	aatgagtcta	aagtggcatc	300
aacaatggcg	tcttttatta	tacataagcc	aaaggagaga	tcgcctttca	cgaaagctgc	360

tttcaaaacg	cttgatagca	tcaaggagtt	ggaactgttt	atgttgaagc	atcgaaggga	420
ttatgttgat	ctgcaccgga	ctacagaaca	ggaaaaggat	agtattgaac	aagaagttgc	480
tgcttttatt	aaagcttgca	aagaacagat	cgtatttctc	ataaacagta	ttagaaatga	540
agaagcaaac	tccaaaggat	ggcttggcct	ccccgcagat	aacttcaatg	ctgattctat	600
agcacacaaa	catggagtg	ttttgattct	gagtgagaaa	cttcattcag	tcactgcccc	660
gtttgatcag	cttagagcta	ctcgtttcca	agatattata	aacagagcta	tgccgagaag	720
aaaacctaag	agggtcataa	aggaagctac	cccaattaat	acaactctgg	gaatttcgga	780
gtccatagaa	ccggatgaaa	tccaggccca	acctcgtaga	ttacaacaac	aacaacttct	840
agacgatgaa	acacaagccc	ttcaggtaga	gctaagtaat	cttttagatg	gtgctagggc	900
gcagaaaact	aagatgggtg	agatgtctgc	attaaaccac	ttgatggcaa	ctcatgttct	960
gcagcaagcc	caacagatag	agtttcttta	tgaccaggca	gttgaggcaa	caaagaacct	1020
ggagcttgga	aacaaagagc	tttctcaagc	aatcccaaga	aacagcagca	gcgaacacct	1080
tcctctactg	ttttctctgc	tccttacttt	ctcgcctctg	ttcttggtat	ggtagacgta	1140
aaaaaccatt	ctccaaacaac	aacttcacac	agtttttgta	gattttgatt	gttaactata	1200
aattatgaaa	aattggaaat	gggtttaaat	gttaaaacaa	aaataatgag		

(2) INFORMATION FOR SEQ ID NO:1435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..310

(D) OTHER INFORMATION: / Ceres Seq. ID 1500264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

Met	Ser	Arg	Phe	Arg	Asp	Arg	Thr	Glu	Asp	Phe	Lys	Asp	Ser	Val	Arg
1				5				10						15	
Lys	Ser	Ala	Val	Ser	Ile	Gly	Tyr	Asn	Glu	Ser	Lys	Val	Ala	Ser	Thr
			20					25						30	
Met	Ala	Ser	Phe	Ile	Ile	His	Lys	Pro	Lys	Glu	Arg	Ser	Pro	Phe	Thr
			35					40						45	
Lys	Ala	Ala	Phe	Lys	Thr	Leu	Asp	Ser	Ile	Lys	Glu	Leu	Glu	Leu	Phe
			50					55						60	
Met	Leu	Lys	His	Arg	Lys	Asp	Tyr	Val	Asp	Leu	His	Arg	Thr	Thr	Glu
65								70						80	
Gln	Glu	Lys	Asp	Ser	Ile	Glu	Gln	Glu	Val	Ala	Ala	Phe	Ile	Lys	Ala
								85						95	
Cys	Lys	Glu	Gln	Ile	Asp	Ile	Leu	Ile	Asn	Ser	Ile	Arg	Asn	Glu	Glu
								100						110	
Ala	Asn	Ser	Lys	Gly	Trp	Leu	Gly	Leu	Pro	Ala	Asp	Asn	Phe	Asn	Ala
								115						125	
Asp	Ser	Ile	Ala	His	Lys	His	Gly	Val	Val	Leu	Ile	Leu	Ser	Glu	Lys
								130						140	
Leu	His	Ser	Val	Thr	Ala	Gln	Phe	Asp	Gln	Leu	Arg	Ala	Thr	Arg	Phe
								145						155	
Gln	Asp	Ile	Ile	Asn	Arg	Ala	Met	Pro	Arg	Arg	Lys	Pro	Lys	Arg	Val
								165						175	
Ile	Lys	Glu	Ala	Thr	Pro	Ile	Asn	Thr	Thr	Leu	Gly	Asn	Ser	Glu	Ser
								180						190	
Ile	Glu	Pro	Asp	Glu	Ile	Gln	Ala	Gln	Pro	Arg	Arg	Leu	Gln	Gln	Gln
								195						205	
Gln	Leu	Leu	Asp	Asp	Glu	Thr	Gln	Ala	Leu	Gln	Val	Glu	Leu	Ser	Asn
								210						220	
Leu	Leu	Asp	Gly	Ala	Arg	Gln	Thr	Glu	Thr	Lys	Met	Val	Glu	Met	Ser
								215						225	
Ala	Leu	Asn	His	Leu	Met	Ala	Thr	His	Val	Leu	Gln	Gln	Ala	Gln	Gln
								230						235	
Ile	Glu	Phe	Leu	Tyr	Asp	Gln	Ala	Val	Glu	Ala	Thr	Lys	Asn	Val	Glu
								245						255	
								260						270	

Leu Gly Asn Lys Glu Leu Ser Gln Ala Ile Gln Arg Asn Ser Ser Ser
275 280 285
Arg Thr Phe Leu Leu Leu Phe Phe Val Leu Thr Phe Ser Val Leu
290 295 300
Phe Leu Asp Trp Tyr Ser
305 310

(2) INFORMATION FOR SEQ ID NO:1436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..278
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

Met Ala Ser Phe Ile Ile His Lys Pro Lys Glu Arg Ser Pro Phe Thr
1 5 10 15
Lys Ala Ala Phe Lys Thr Leu Asp Ser Ile Lys Glu Leu Glu Leu Phe
20 25 30
Met Leu Lys His Arg Lys Asp Tyr Val Asp Leu His Arg Thr Thr Glu
35 40 45
Gln Glu Lys Asp Ser Ile Glu Gln Glu Val Ala Ala Phe Ile Lys Ala
50 55 60
Cys Lys Glu Gln Ile Asp Ile Leu Ile Asn Ser Ile Arg Asn Glu Glu
65 70 75 80
Ala Asn Ser Lys Gly Trp Leu Gly Leu Pro Ala Asp Asn Phe Asn Ala
85 90 95
Asp Ser Ile Ala His Lys His Gly Val Val Leu Ile Leu Ser Glu Lys
100 105 110
Leu His Ser Val Thr Ala Gln Phe Asp Gln Leu Arg Ala Thr Arg Phe
115 120 125
Gln Asp Ile Ile Asn Arg Ala Met Pro Arg Arg Lys Pro Lys Arg Val
130 135 140
Ile Lys Glu Ala Thr Pro Ile Asn Thr Thr Leu Gly Asn Ser Glu Ser
145 150 155 160
Ile Glu Pro Asp Glu Ile Gln Ala Gln Pro Arg Arg Leu Gln Gln Gln
165 170 175
Gln Leu Leu Asp Asp Glu Thr Gln Ala Leu Gln Val Glu Leu Ser Asn
180 185 190
Leu Leu Asp Gly Ala Arg Gln Thr Glu Thr Lys Met Val Glu Met Ser
195 200 205
Ala Leu Asn His Leu Met Ala Thr His Val Leu Gln Gln Ala Gln Gln
210 215 220
Ile Glu Phe Leu Tyr Asp Gln Ala Val Glu Ala Thr Lys Asn Val Glu
225 230 235 240
Leu Gly Asn Lys Glu Leu Ser Gln Ala Ile Gln Arg Asn Ser Ser Ser
245 250 255
Arg Thr Phe Leu Leu Phe Phe Phe Val Leu Thr Phe Ser Val Leu
260 265 270
Phe Leu Asp Trp Tyr Ser
275

(2) INFORMATION FOR SEQ ID NO:1437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1500266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

Met	Leu	Lys	His	Arg	Lys	Asp	Tyr	Val	Asp	Leu	His	Arg	Thr	Thr	Glu	
1					5					10					15	
Gln	Glu	Lys	Asp	Ser	Ile	Glu	Gln	Glu	Val	Ala	Ala	Phe	Ile	Lys	Ala	
			20					25					30			
Cys	Lys	Glu	Gln	Ile	Asp	Ile	Leu	Ile	Asn	Ser	Ile	Arg	Asn	Glu	Glu	
		35					40					45				
Ala	Asn	Ser	Lys	Gly	Trp	Leu	Gly	Leu	Pro	Ala	Asp	Asn	Phe	Asn	Ala	
		50				55					60					
Asp	Ser	Ile	Ala	His	Lys	His	Gly	Val	Val	Leu	Ile	Leu	Ser	Glu	Lys	
65					70					75				80		
Leu	His	Ser	Val	Thr	Ala	Gln	Phe	Asp	Gln	Leu	Arg	Ala	Thr	Arg	Phe	
			85						90					95		
Gln	Asp	Ile	Ile	Asn	Arg	Ala	Met	Pro	Arg	Arg	Lys	Pro	Lys	Arg	Val	
			100						105					110		
Ile	Lys	Glu	Ala	Thr	Pro	Ile	Asn	Thr	Thr	Leu	Gly	Asn	Ser	Glu	Ser	
		115					120					125				
Ile	Glu	Pro	Asp	Glu	Ile	Gln	Ala	Gln	Pro	Arg	Arg	Leu	Gln	Gln	Gln	
		130					135					140				
Gln	Leu	Leu	Asp	Asp	Glu	Thr	Gln	Ala	Leu	Gln	Val	Glu	Leu	Ser	Asn	
		145			150					155				160		
Leu	Leu	Asp	Gly	Ala	Arg	Gln	Thr	Glu	Thr	Lys	Met	Val	Glu	Met	Ser	
			165						170					175		
Ala	Leu	Asn	His	Leu	Met	Ala	Thr	His	Val	Leu	Gln	Gln	Ala	Gln	Gln	
		180						185					190			
Ile	Glu	Phe	Leu	Tyr	Asp	Gln	Ala	Val	Glu	Ala	Thr	Lys	Asn	Val	Glu	
		195					200					205				
Leu	Gly	Asn	Lys	Glu	Leu	Ser	Gln	Ala	Ile	Gln	Arg	Asn	Ser	Ser	Ser	
		210				215					220					
Arg	Thr	Phe	Leu	Leu	Phe	Phe	Phe	Val	Leu	Thr	Phe	Ser	Val	Leu		
225				230				235						240		
Phe	Leu	Asp	Trp	Tyr	Ser											
					245											

(2) INFORMATION FOR SEQ ID NO:1438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 529 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..529

(D) OTHER INFORMATION: / Ceres Seq. ID 1500283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:

agagtccag	cgacctgtag	cctcctctct	cgctcgacct	cgctctcgcc	tcgccgcctc	60
cgaccgcag	cagcgctccc	attgctctct	ctcaccagtc	ccggcggttc	agtggggggc	120
attcatggcg	ggcgagtcgc	accgcacct	ctccatcttc	tcgccctcgc	aggtggagtt	180
cgtggctgag	gatgagattg	tcgaaatcgt	cccccaacatc	cgcatggacg	ccctcaacat	240
gatctgcggg	gatttcgggc	ccttctctcc	ccagattccc	accaaggtgc	ctctctggct	300
cgctgtcggc	ctcaagaagc	gtasaagtgc	accatccgca	ccccggactg	gatgactgtt	360
gaccgcttga	cacagggtat	ggaagcggaa	agagagtcgc	cacgagaatt	ccagccatta	420
ccattccact	atattgaaat	ttctaagctt	ctgtttgatc	atgctcgtga	tgacatctca	480
gatgcatacc	tggtgaagtc	tctaattgag	gacatcagag	atgtcagat		

(2) INFORMATION FOR SEQ ID NO:1439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..62
(D) OTHER INFORMATION: / Ceres Seq. ID 1500284
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:
Arg Val Pro Ala Thr Cys Ser Leu Leu Ser Pro Ser Thr Ser Leu Ser
1 5 10 15
Pro Arg Arg Leu Arg Pro Ala Ala Ala Pro Pro Leu Leu Ser Leu Thr
20 25 30
Ser Pro Gly Val Pro Val Gly Gly Ile His Gly Gly Ala Val Arg Pro
35 40 45
Ala Pro Leu His Leu Leu Ala Leu Arg Gly Gly Val Arg Gly
50 55 60

(2) INFORMATION FOR SEQ ID NO:1440:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..117
(D) OTHER INFORMATION: / Ceres Seq. ID 1500285
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:
Glu Ser Gln Arg Pro Val Ala Ser Ser Leu Arg Arg Pro Arg Ser Arg
1 5 10 15
Leu Ala Ala Ser Asp Pro Gln Gln Arg Leu His Cys Ser Leu Ser Arg
20 25 30
Val Pro Ala Phe Gln Trp Gly Ala Phe Met Ala Gly Gln Ser Asp Pro
35 40 45
His Leu Ser Ile Phe Ser Pro Ser Glu Val Glu Phe Val Ala Glu Asp
50 55 60
Glu Ile Val Glu Ile Val Pro Asn Ile Arg Met Asp Ala Leu Asn Met
65 70 75 80
Ile Cys Gly Asp Phe Gly Pro Phe Phe Pro Gln Ile Pro Thr Lys Val
85 90 95
Pro Leu Trp Leu Ala Val Ala Leu Lys Lys Arg Xaa Ser Ala Pro Ser
100 105 110
Ala Pro Arg Thr Gly
115

(2) INFORMATION FOR SEQ ID NO:1441:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..76
(D) OTHER INFORMATION: / Ceres Seq. ID 1500286
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:
Met Ala Gly Gln Ser Asp Pro His Leu Ser Ile Phe Ser Pro Ser Glu
1 5 10 15
Val Glu Phe Val Ala Glu Asp Glu Ile Val Glu Ile Val Pro Asn Ile
20 25 30

Arg Met Asp Ala Leu Asn Met Ile Cys Gly Asp Phe Gly Pro Phe Phe
35 40 45
Pro Gln Ile Pro Thr Lys Val Pro Leu Trp Leu Ala Val Ala Leu Lys
50 55 60
Lys Arg Xaa Ser Ala Pro Ser Ala Pro Arg Thr Gly
65 70 75

(2) INFORMATION FOR SEQ ID NO:1442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..442

(D) OTHER INFORMATION: / Ceres Seq. ID 1500298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

tactacatgc aatttgggaa atgtaaat	60
ttt caatcagctt gtatatccaa tcattcaaaa	120
gacatacttt caagtvgrtg gcatccagca gaatgcccat	180
tctacatgaa aactaggaca tggccaatttg	240
gatcagcttg tgagttttat caccocaaaag	300
atcgvgvgtc ttccaagang rctgggaaca	360
ggcaggcgcc ctaccagccg ccgaabgcc	420
tgacgctgct tggcasacga catgtaccct	
gcrcctcgcc cagargcgcc ggcggcgga	
gggtctcgcc gctcgaracc ggcaccaagc	
tctacatctc caacctggac tttrgggtt	
cgaacgacga tatcaaggag ctgtctctcg	
agctagggtga tctgaagcgt ttttcgata	
tatatgadcg aagtrggagg tctaaaggaa	
caagctgaagt tg	

(2) INFORMATION FOR SEQ ID NO:1443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1500299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:

Tyr Tyr Met Gln Phe Gly Lys Cys Lys Phe Gln Ser Ala Cys Ile Phe	
1 5 10 15	
Asn His Ser Lys Asp Ile Leu Ser Ser Xaa Trp His Pro Ala Glu Cys	
20 25 30	
Pro Phe Tyr Met Lys Thr Arg Thr Cys Gln Phe Gly Ser Ala Cys Glu	
35 40 45	
Phe Tyr His Pro Lys Asp Arg Xaa Ser Phe Lys Xaa Xaa Gly Asn Arg	
50 55 60	
Gln Ala Pro Tyr Gln Pro Pro Xaa Ala Leu Thr Leu Arg Gly Xaa Arg	
65 70 75 80	
His Val Pro Cys Xaa Arg Arg Arg Xaa Gly Gly Gly Arg Val Ser	
85 90 95	
Ala Leu Xaa Thr Gly Thr Lys Leu Tyr Ile Ser Asn Leu Asp Phe Xaa	
100 105 110	
Val Ser Asn Asp Asp Ile Lys Glu Leu Phe Ser Glu Leu Gly Asp Leu	
115 120 125	
Lys Arg Phe Ser Ile Ile Tyr Xaa Arg Ser Xaa Arg Ser Lys Gly Thr	
130 135 140	
Ala Glu Val	
145	

(2) INFORMATION FOR SEQ ID NO:1444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..145
(D) OTHER INFORMATION: / Ceres Seq. ID 1500300
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:
Met Gln Phe Gly Lys Cys Lys Phe Gln Ser Ala Cys Ile Phe Asn His
1 5 10 15
Ser Lys Asp Ile Leu Ser Ser Xaa Trp His Pro Ala Glu Cys Pro Phe
20 25 30
Tyr Met Lys Thr Arg Thr Cys Gln Phe Gly Ser Ala Cys Glu Phe Tyr
35 40 45
His Pro Lys Asp Arg Xaa Ser Phe Lys Xaa Xaa Gly Asn Arg Gln Ala
50 55 60
Pro Tyr Gln Pro Pro Xaa Ala Leu Thr Leu Arg Gly Xaa Arg His Val
65 70 75 80
Pro Cys Xaa Arg Arg Arg Xaa Gly Gly Gly Arg Val Ser Ala Leu
85 90 95
Xaa Thr Gly Thr Lys Leu Tyr Ile Ser Asn Leu Asp Phe Xaa Val Ser
100 105 110
Asn Asp Asp Ile Lys Glu Leu Phe Ser Glu Leu Gly Asp Leu Lys Arg
115 120 125
Phe Ser Ile Ile Tyr Xaa Arg Ser Xaa Arg Ser Lys Gly Thr Ala Glu
130 135 140
Val
145

(2) INFORMATION FOR SEQ ID NO:1445:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..112
(D) OTHER INFORMATION: / Ceres Seq. ID 1500301
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

Met Lys Thr Arg Thr Cys Gln Phe Gly Ser Ala Cys Glu Phe Tyr His
1 5 10 15
Pro Lys Asp Arg Xaa Ser Phe Lys Xaa Xaa Gly Asn Arg Gln Ala Pro
20 25 30
Tyr Gln Pro Pro Xaa Ala Leu Thr Leu Arg Gly Xaa Arg His Val Pro
35 40 45
Cys Xaa Arg Arg Arg Xaa Gly Gly Gly Arg Val Ser Ala Leu Xaa
50 55 60
Thr Gly Thr Lys Leu Tyr Ile Ser Asn Leu Asp Phe Xaa Val Ser Asn
65 70 75 80
Asp Asp Ile Lys Glu Leu Phe Ser Glu Leu Gly Asp Leu Lys Arg Phe
85 90 95
Ser Ile Ile Tyr Xaa Arg Ser Xaa Arg Ser Lys Gly Thr Ala Glu Val
100 105 110

(2) INFORMATION FOR SEQ ID NO:1446:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 501 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..501
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500305
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

aacttgccccc	caaatcgtgg	agtggaacc	ctactcgtcc	ccttcgcgat	cgccgccccaa	60
ttcccccaac	caattccca	tctccgctcg	acagatccat	acatgatggg	agaggccaaag	120
gagaacgaag	tttatgagga	ggagctcctg	gactacgagg	aggacgacga	caagacgggtc	180
gatggctccg	ctgctaagcc	cacgggagag	gtcgcaaaag	agggctacgt	cgggatccac	240
agttccgggt	tcagagactt	cctgctcaag	ccagagctgc	tcctgtctat	ccaggattgt	300
gggttttrac	atccttcga	agtgcaaac	gagtgatcc	ctcaagccat	ctttggaatg	360
gatgtcatct	gtcaagctaa	atctgggatg	gggaaaactg	ctgtttttgt	cctttcatcc	420
ctccaacaaa	ttgacctgt	tgccgggtcag	gtagcagcac	ttgtactgtg	ccacacaarg	480
gaactggcgt	atcagatatg	c				

(2) INFORMATION FOR SEQ ID NO:1447:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..167
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500306
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

Asn	Leu	Ala	Pro	Asn	Arg	Gly	Val	Glu	Thr	Leu	Leu	Val	Pro	Phe	Arg
1				5				10						15	
Ile	Ala	Ala	Gln	Phe	Pro	His	Pro	Ile	Pro	Thr	Leu	Arg	Ser	Thr	Asp
			20					25					30		
Pro	Tyr	Met	Met	Gly	Glu	Ala	Lys	Glu	Asn	Asp	Val	Tyr	Glu	Glu	Glu
		35					40					45			
Leu	Leu	Asp	Tyr	Glu	Glu	Asp	Asp	Asp	Lys	Thr	Val	Asp	Gly	Ser	Ala
	50					55					60				
Ala	Lys	Pro	Thr	Gly	Glu	Val	Ala	Lys	Lys	Gly	Tyr	Val	Gly	Ile	His
	65				70					75				80	
Ser	Ser	Gly	Phe	Arg	Asp	Phe	Leu	Leu	Lys	Pro	Glu	Leu	Leu	Arg	Ala
			85					90					95		
Ile	Gln	Asp	Cys	Gly	Phe	Xaa	His	Pro	Ser	Glu	Val	Gln	His	Glu	Cys
		100						105					110		
Ile	Pro	Gln	Ala	Ile	Leu	Gly	Met	Asp	Val	Ile	Cys	Gln	Ala	Lys	Ser
		115					120						125		
Gly	Met	Gly	Lys	Thr	Ala	Val	Phe	Val	Leu	Ser	Ser	Leu	Gln	Gln	Ile
	130					135						140			
Asp	Pro	Val	Ala	Gly	Gln	Val	Ala	Ala	Leu	Val	Leu	Cys	His	Thr	Xaa
	145				150				155					160	
Glu	Leu	Ala	Tyr	Gln	Ile	Cys									
					165										

(2) INFORMATION FOR SEQ ID NO:1448:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 133 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1500307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:

```
Met Met Gly Glu Ala Lys Glu Asn Asp Val Tyr Glu Glu Glu Leu Leu
1      5      10      15
Asp Tyr Glu Glu Asp Asp Asp Lys Thr Val Asp Gly Ser Ala Ala Lys
20      25      30
Pro Thr Gly Glu Val Ala Lys Lys Gly Tyr Val Gly Ile His Ser Ser
35      40      45
Gly Phe Arg Asp Phe Leu Leu Lys Pro Glu Leu Leu Arg Ala Ile Gln
50      55      60
Asp Cys Gly Phe Xaa His Pro Ser Glu Val Gln His Glu Cys Ile Pro
65      70      75      80
Gln Ala Ile Leu Gly Met Asp Val Ile Cys Gln Ala Lys Ser Gly Met
85      90      95
Gly Lys Thr Ala Val Phe Val Leu Ser Ser Leu Gln Gln Ile Asp Pro
100      105      110
Val Ala Gly Gln Val Ala Ala Leu Val Leu Cys His Thr Xaa Glu Leu
115      120      125
Ala Tyr Gln Ile Cys
130
```

(2) INFORMATION FOR SEQ ID NO:1449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1500308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:

```
Met Gly Glu Ala Lys Glu Asn Asp Val Tyr Glu Glu Glu Leu Leu Asp
1      5      10      15
Tyr Glu Glu Asp Asp Asp Lys Thr Val Asp Gly Ser Ala Ala Lys Pro
20      25      30
Thr Gly Glu Val Ala Lys Lys Gly Tyr Val Gly Ile His Ser Ser Gly
35      40      45
Phe Arg Asp Phe Leu Leu Lys Pro Glu Leu Leu Arg Ala Ile Gln Asp
50      55      60
Cys Gly Phe Xaa His Pro Ser Glu Val Gln His Glu Cys Ile Pro Gln
65      70      75      80
Ala Ile Leu Gly Met Asp Val Ile Cys Gln Ala Lys Ser Gly Met Gly
85      90      95
Lys Thr Ala Val Phe Val Leu Ser Ser Leu Gln Gln Ile Asp Pro Val
100      105      110
Ala Gly Gln Val Ala Ala Leu Val Leu Cys His Thr Xaa Glu Leu Ala
115      120      125
Tyr Gln Ile Cys
130
```

(2) INFORMATION FOR SEQ ID NO:1450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1540 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1540

(D) OTHER INFORMATION: / Ceres Seq. ID 1500313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:

atcatcatg	tattcacgt	tgtccttct	ttcattgaca	cttgccagtt	tacatcgaca	60
aacaaaagaa	atcagaatgg	attttcag	gagattcttt	gtcatcttcg	ttaccttctt	120
ctttctccct	ctctgtctct	cagctgggag	ctacgatctc	ggttcgggtc	tcgagtcact	180
cgctcgcggg	atgcttcatt	cagccaagga	tcctgagttc	ttcagtgagg	tgagaggaa	240
taggagaaag	attcatgaga	acccagagac	agggtttcag	gagttcaaaa	cgagtcact	300
cgttcgagac	gagcttgact	cgcttggagt	gaagataaag	tatcctgtgg	cgaagcagtg	360
cgctgtcct	tgatcggagt	cctgttcgaa	acctgttttc	ggacttagag	cgacatgga	420
cgcaattccg	gttacaggga	attagtgaaa	tgggaatcga	aaagtaaaag	agatggaaa	480
atgcatgctt	tggtctatga	tactcatggt	gctatgcttc	ttgttgctgc	taagcttctt	540
caaaccacaa	aacacctcat	caaggggaca	gtaaaacttg	tgtttcaacc	aggcgaggaa	600
ggttatgcag	gtgcttatga	aatgctaaaa	gacgagattc	tagacgactt	msatgggata	660
ctcagtggtc	atgtctttcc	atcgatccca	tcagggtgga	ttggttctag	gctcgggacc	720
gttcttgca	gtcagagatt	gtttacagtc	acggttccag	gtcaaggtag	ccacgcagct	780
acacccgact	tctctaaara	cccggttctt	gcagcttctt	ccgctgttgt	tgctttcga	840
cagattgttt	cgccgggaact	ggatccactc	gaagctgggt	tggttacagt	tgatattatt	900
gaaggaggtc	atgctcaaaa	cgtaataacc	cagagtcgca	aatttggagg	tactttcaga	960
magcttaagc	aacgatgggc	tctctattat	ccaaagacgg	atcaaagaga	tttcagaggc	1020
acaagcagtc	gtataccgat	gcgaagcaga	agtaaaactc	gaagagaaaa	agccgtcgct	1080
tcacmccggt	aatgaataac	gacgagggct	tatacbgagc	acggtaaaaa	agtagcgga	1140
gcgatcatgt	gaagaataaa	cttccatgat	ttcccggtga	caatgggagg	agaggttttc	1200
cgntttcttc	actcaaaaaga	cntaaggctg	cgattttcgt	gctgggggata	aagaatgaga	1260
cgctagagcg	tggtaaagccg	cttactctgc	cttacttctt	tggtgatgaa	gaagctcttc	1320
ctgtttgggc	tgctcttccac	gcagctatgg	ccgtttctta	tttggacaaa	catgsgcaga	1380
gcatatgaaga	agaggtttaa	agtgaattat	agaaggtgtt	gggagaaaa	cagcttatat	1440
tagtcatcat	ctatttgtat	ttgaacttga	aagttaggtt	aggttaggtt	tcgggttggtg	1500
agaagatgtt	gttaatatgtc	acgagaaacc	aaccactttc			

(2) INFORMATION FOR SEQ ID NO:1451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..203

(D) OTHER INFORMATION: / Ceres Seq. ID 1500314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:

Met	His	Ala	Cys	Gly	His	Asp	Thr	His	Val	Ala	Met	Leu	Leu	Gly	Ala
1				5					10					15	
Ala	Lys	Leu	Leu	Gln	Thr	Thr	Lys	His	Leu	Ile	Lys	Gly	Thr	Val	Lys
				20					25					30	
Leu	Val	Phe	Gln	Pro	Gly	Glu	Glu	Gly	Tyr	Ala	Gly	Ala	Tyr	Glu	Met
				35					40					45	
Leu	Lys	Asp	Glu	Ile	Leu	Asp	Asp	Xaa	Xaa	Gly	Ile	Leu	Ser	Val	His
				50					55					60	
Val	Phe	Pro	Ser	Ile	Pro	Ser	Gly	Gly	Ile	Gly	Ser	Arg	Pro	Gly	Thr
				65					70					75	
Val	Leu	Ala	Gly	Ala	Gly	Leu	Phe	Thr	Val	Thr	Val	His	Gly	Gln	Gly
				85					90					95	
Ser	His	Ala	Ala	Thr	Pro	His	Phe	Ser	Lys	Xaa	Pro	Val	Leu	Ala	Ala
				100					105					110	
Ser	Ser	Ala	Val	Val	Ala	Leu	Gln	Gln	Ile	Val	Ser	Arg	Glu	Leu	Asp
				115					120					125	
Pro	Leu	Glu	Ala	Gly	Val	Val	Thr	Val	Gly	Tyr	Ile	Glu	Gly	Gly	His
				130					135					140	
Ala	Gln	Asn	Val	Ile	Pro	Gln	Ser	Ala	Lys	Phe	Gly	Gly	Thr	Phe	Arg
				145					150					155	
Xaa	Leu	Lys	Gln	Arg	Trp	Ala	Ser	Ile	Tyr	Pro	Lys	Thr	Asp	Gln	Arg
				165					170					175	

Asp Phe Arg Gly Thr Ser Ile Gly Ile Pro Met Gln Ser Arg Ser Lys
180 185 190
Leu Arg Arg Glu Lys Ala Val Ala Ser Xaa Arg
195 200

(2) INFORMATION FOR SEQ ID NO:1452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1500315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:

Met Leu Leu Gly Ala Ala Lys Leu Leu Gln Thr Thr Lys His Leu Ile
1 5 10 15
Lys Gly Thr Val Lys Leu Val Phe Gln Pro Gly Glu Glu Gly Tyr Ala
20 25 30
Gly Ala Tyr Glu Met Leu Lys Asp Glu Ile Leu Asp Asp Xaa Xaa Gly
35 40 45
Ile Leu Ser Val His Val Phe Pro Ser Ile Pro Ser Gly Gly Ile Gly
50 55 60
Ser Arg Pro Gly Thr Val Leu Ala Gly Ala Gly Leu Phe Thr Val Thr
65 70 75 80
Val His Gly Gln Gly Ser His Ala Ala Thr Pro His Phe Ser Lys Xaa
85 90 95
Pro Val Leu Ala Ala Ser Ser Ala Val Val Ala Leu Gln Gln Ile Val
100 105 110
Ser Arg Glu Leu Asp Pro Leu Glu Ala Gly Val Val Thr Val Gly Tyr
115 120 125
Ile Glu Gly Gly His Ala Gln Asn Val Ile Pro Gln Ser Ala Lys Phe
130 135 140
Gly Gly Thr Phe Arg Xaa Leu Lys Gln Arg Trp Ala Ser Ile Tyr Pro
145 150 155 160
Lys Thr Asp Gln Arg Asp Phe Arg Gly Thr Ser Ile Gly Ile Pro Met
165 170 175
Gln Ser Arg Ser Lys Leu Arg Arg Glu Lys Ala Val Ala Ser Xaa Arg
180 185 190

(2) INFORMATION FOR SEQ ID NO:1453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1500316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:

Met Leu Lys Asp Glu Ile Leu Asp Asp Xaa Xaa Gly Ile Leu Ser Val
1 5 10 15
His Val Phe Pro Ser Ile Pro Ser Gly Gly Ile Gly Ser Arg Pro Gly
20 25 30
Thr Val Leu Ala Gly Ala Gly Leu Phe Thr Val Thr Val His Gly Gln
35 40 45
Gly Ser His Ala Ala Thr Pro His Phe Ser Lys Xaa Pro Val Leu Ala

50	55	60
Ala Ser Ser Ala Val Val Ala Leu Gln Gln Ile Val Ser Arg Glu Leu		
65	70	75
Asp Pro Leu Glu Ala Gly Val Val Thr Val Gly Tyr Ile Glu Gly Gly		
	85	90
His Ala Gln Asn Val Ile Pro Gln Ser Ala Lys Phe Gly Gly Thr Phe		
	100	105
Arg Xaa Leu Lys Gln Arg Trp Ala Ser Ile Tyr Pro Lys Thr Asp Gln		
	115	120
Arg Asp Phe Arg Gly Thr Ser Ile Gly Ile Pro Met Gln Ser Arg Ser		
	130	135
Lys Leu Arg Arg Glu Lys Ala Val Ala Ser Xaa Arg		
145	150	155

(2) INFORMATION FOR SEQ ID NO:1454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..498
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

gcttgctcgc taacaatcag tgaactgaac accttcgcgc ctccggtctc ctccctgcc	60
ggtgctgaag aacctgtcca tcccgggaac tggatcgatc tgccgccaac tctgaaaatc	120
catccgatcc atctctgtcg tccaagtcta ctccccgatg gacattattt accaggacag	180
cagttgtctt gccttagagc aggcgctaca tgatgaagcg gtgggaccaa tgcacctacc	240
tttcatgttt ctcagggccca tcacaaaaga tttctctgat actcaactaa ttggcagggg	300
tgggttcgga gaggtttaca aggtatgcgt ggggtatttg gcacctgaat tcttgagcag	360
caatgcaatc acattcaagg cggacatatata cagtctargt gttataatca ctgagattct	420
gacgggggga taargratgc accartgttg acaaaggkgc ttgaaarctg gacggacatg	480
tttcagacat taggaagc	

(2) INFORMATION FOR SEQ ID NO:1455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

Ala Cys Ser Leu Thr Ile Ser Glu Leu Asn Thr Phe Arg Leu Pro Val	
1	5
Ser Ser Leu Pro Gly Ala Glu Glu Pro Cys His Pro Arg Asn Trp Ile	
	10
	15
	20
	25
Asp Leu Pro Pro Thr Leu Lys Ile His Pro Ile His Leu Cys Arg Pro	
	30
	35
	40
Ser Leu Leu Pro Asp Gly His Tyr Leu Pro Gly Gln Gln Leu Ser Cys	
	45
	50
	55
Pro Arg Ala Gly Ala Thr	
65	70

(2) INFORMATION FOR SEQ ID NO:1456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..91
(D) OTHER INFORMATION: / Ceres Seq. ID 1500323
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:
Met Asp Ile Ile Tyr Gln Asp Ser Ser Cys Leu Ala Leu Glu Gln Ala
1 5 10 15
Leu His Asp Glu Gly Val Gly Pro Ile Asp Leu Pro Phe Met Leu Leu
20 25 30
Arg Ala Ile Thr Lys Asp Phe Ser Asp Thr Gln Leu Ile Gly Arg Gly
35 40 45
Gly Phe Gly Glu Val Tyr Lys Val Cys Met Gly Tyr Leu Ala Pro Glu
50 55 60
Phe Leu Ser Ser Asn Ala Ile Thr Phe Lys Ala Asp Ile Tyr Ser Leu
65 70 75 80
Xaa Val Ile Ile Thr Glu Ile Leu Thr Gly Ala
85 90

(2) INFORMATION FOR SEQ ID NO:1457:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..62
(D) OTHER INFORMATION: / Ceres Seq. ID 1500324
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:
Met Leu Leu Arg Ala Ile Thr Lys Asp Phe Ser Asp Thr Gln Leu Ile
1 5 10 15
Gly Arg Gly Gly Phe Gly Glu Val Tyr Lys Val Cys Met Gly Tyr Leu
20 25 30
Ala Pro Glu Phe Leu Ser Ser Asn Ala Ile Thr Phe Lys Ala Asp Ile
35 40 45
Tyr Ser Leu Xaa Val Ile Ile Thr Glu Ile Leu Thr Gly Ala
50 55 60

(2) INFORMATION FOR SEQ ID NO:1458:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..368
(D) OTHER INFORMATION: / Ceres Seq. ID 1500367
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:
tcacactctg ccagctaa gctaagctccc tccgtccatc ggcattgcga ctaccactac 60
taccatctct ctctctctcc tctgtcgcagc cacagccgtc tcggcggcgc acctctccgt 120
gtaccacaac gtgcaccgc cgtccccgtc cccgctcgag tccatcatcg cgtcgcgcgc 180
cgccgacgac gcgcggctcc tcttctctct atccaaggcg gccctgctccg gcggcgctcac 240
ctccgtctcc gtcgctccg gccagactcc gcmctcgtag gtmgctccgc cggggctcgg 300
caccgccgtc cagcagctgc tctctgcgct cgacaccagc gccgacgccca cctggtcgca 360
ctgcgcgc

(2) INFORMATION FOR SEQ ID NO:1459:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..122
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500368
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:
Thr Leu Cys Pro Ala Lys Leu Ser Ser Leu Arg Pro Ser Ala Trp Arg
1 5 10 15
Leu Pro Leu Leu Pro Ser Ser Ser Ser Ser Ser Ser Gln Pro Gln Pro
 20 25 30
Ser Arg Arg Pro Thr Ser Pro Cys Thr Thr Thr Cys Thr Arg Arg Pro
 35 40 45
Arg Pro Arg Ser Ser Pro Ser Ser Arg Ser Pro Ala Pro Thr Thr Arg
 50 55 60
Gly Ser Ser Ser Ser His Pro Arg Arg Pro Arg Pro Ala Ala Ser Pro
65 70 75 80
Pro Leu Pro Ser Pro Pro Ala Arg Leu Arg Xaa Arg Thr Xaa Ser Ala
 85 90 95
Arg Gly Ser Ala Pro Arg Ser Ser Ser Cys Ser Ser Arg Ser Thr Pro
 100 105 110
Ala Pro Thr Pro Pro Gly Arg Thr Ala Arg
 115 120
(2) INFORMATION FOR SEQ ID NO:1460:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..108
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500369
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:
Met Ala Thr Thr Thr Thr Thr Ile Leu Leu Leu Leu Val Ala Ala
1 5 10 15
Thr Ala Val Ser Ala Ala Asp Leu Ser Val Tyr His Asn Val His Pro
 20 25 30
Pro Ser Pro Ser Pro Leu Glu Ser Ile Ile Ala Leu Ala Arg Ala Asp
 35 40 45
Asp Ala Arg Leu Leu Phe Leu Ser Ser Lys Ala Ala Ser Ser Gly Gly
 50 55 60
Val Thr Ser Ala Pro Val Ala Ser Gly Gln Thr Pro Xaa Ser Tyr Xaa
65 70 75 80
Val Arg Ala Gly Leu Gly Thr Pro Val Gln Gln Leu Leu Leu Ala Leu
 85 90 95
Asp Thr Ser Ala Asp Ala Thr Trp Ser His Cys Ala
 100 105
(2) INFORMATION FOR SEQ ID NO:1461:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 921 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..921

(D) OTHER INFORMATION: / Ceres Seq. ID 1500370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:

atcctctagc	tctctctctc	tctctctctc	cacacacaca	cacagtcaca	gacaccacct	60
tcacttagac	tgtgctagta	ggtagcgggc	gcgtaattga	gcaggagctc	agccttgagc	120
tcaccctctc	ccaccctctc	gcctcgccgc	cggagccacc	gggctacttc	gtctgcaagt	180
actgcgacgc	caagttcttc	agctcgcaag	ctctcggttg	ccaccagaac	gcgcacaagt	240
acgagcgcas	ctggccaagc	gcgcgagga	gatagccgcc	gccctcgccg	cgccaggggc	300
ggcgccccc	gcmacggg	cyccggagga	cgacgmcgyc	gccgcgatgg	gctctcgcca	360
tgtcccgccc	agggccaca	gcacgggtac	cggagtctgc	gtcgttgaag	atgagaggtg	420
aaccaggatg	atgggacaag	cagaaggctc	ctgctgctga	tgacgasstc	cgcgaccgcg	480
gtcgtcgagc	aacatgaaga	ggctcgctga	gtacggctac	ggcgctcgag	agctggatct	540
ctccctcagg	ctttgatggg	ttcctctctc	tcctccacyn	nnanataata	ttcgccccgt	600
tngctnagat	aattcgatct	ttgtggtcag	tgcaatcctc	tgtttcgcgt	gcgtgggtatc	660
tcagtgtcgtg	atccgtcact	ttcttctcca	tgtagttgtt	gtgcagttat	attcttccat	720
ccgatgatgg	aacctatgat	caagaactat	tgctggccca	tcctgctatc	caagggcgct	780
ggatatttgt	gtgctctttt	cggttttctg	ccttgagtct	tccttgcg	atctaaattc	840
gcagcttgtt	ttttccaaaa	cgcggaagac	agttttgcg	caatttcgtt	tggaactttt	900
tcaagtgact	ctaaattggg	c				

(2) INFORMATION FOR SEQ ID NO:1462:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1500371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:

Met	Glu	Gln	Glu	Leu	Ser	Leu	Glu	Leu	Thr	Leu	Leu	His	Pro	Ser	Ala
1		5					10					15			
Ser	Pro	Pro	Glu	Pro	Pro	Gly	Tyr	Phe	Val	Cys	Met	Tyr	Cys	Asp	Arg
		20					25					30			
Lys	Phe	Phe	Ser	Ser	Gln	Ala	Leu	Gly	Gly	His	Gln	Asn	Ala	His	Lys
		35					40					45			
Tyr	Glu	Arg	Xaa	Trp	Pro	Ser	Ala	Ala	Gly	Arg					
		50					55								

(2) INFORMATION FOR SEQ ID NO:1463:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..37

(D) OTHER INFORMATION: / Ceres Seq. ID 1500372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:

Met	Gly	Ser	Arg	Asp	Val	Pro	Ala	Arg	Pro	Gln	Gly	Thr	Gly	Thr	Gly
1		5					10					15			
Val	Val	Val	Val	Glu	Asp	Glu	Ser	Ala	Thr	Arg	Met	Met	Gly	Gln	Ala
		20					25					30			
Glu	Gly	Ser	Cys	Cys											
		35													

(2) INFORMATION FOR SEQ ID NO:1464:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..50
(D) OTHER INFORMATION: / Ceres Seq. ID 1500373
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:
Met Thr Xaa Ser Arg Asp Arg Val Val Glu Gln His Glu Val Val
1 5 10 15
Gly Val Arg Leu Arg Arg Arg Gly Ala Gly Ser Leu Pro Gln Ala Leu
20 25 30
Ile Gly Ser Ser Ser Ser Ser Xaa Xaa Tyr Asn Ser Pro Arg Xaa
35 40 45
Xaa Arg
50

(2) INFORMATION FOR SEQ ID NO:1465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..380

(D) OTHER INFORMATION: / Ceres Seq. ID 1500374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:

aaaatagagt tcacacgcac aacccgcgcg cgcacgccgg gatctcgata gactctggct 60
gcccggaagaa cggaagaaqaa ggcagggatc gtggccaaga tgcagatctt cgtgaagacg 120
ctgtcgtcga caaggacgat cacgctggag gttgagcctt cggacacggt ggcggagctr 180
aaggccaagg tgcacagatc ggaggggcgc ccgtacacct tggccttcca gaactagagc 240
gcggcagata gctaggtcgc ttctgtactcc ccccatattgc aatgacaaag cgtttttacc 300
tttctagata tgcacttatg tctagatata tagattatct tatacttttd wcgttctktt 360
ttatttatcg tgttttagtt

(2) INFORMATION FOR SEQ ID NO:1466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1500375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466:

Asn Arg Val His Thr His Asn Pro Pro His Ala Gly Ile Ser Ile
1 5 10 15
Asp Ser Gly Cys Arg Gly Lys Arg Lys Glu Gly Arg Asp Arg Gly Gln
20 25 30
Asp Ala Asp Leu Arg Glu Asp Ala Val Val Asp Lys Asp Asp His Ala
35 40 45
Gly Gly
50

(2) INFORMATION FOR SEQ ID NO:1467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..45

(D) OTHER INFORMATION: / Ceres Seq. ID 1500376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:

```
Met Gln Ile Phe Val Lys Thr Leu Ser Ser Thr Arg Thr Ile Thr Leu
1          5          10          15
Glu Val Glu Pro Ser Asp Thr Val Ala Asp Xaa Lys Ala Lys Val Tyr
20          25          30
Glu Ser Glu Gly Val Pro Tyr Thr Leu Ala Phe Gln Asn
35          40          45
```

(2) INFORMATION FOR SEQ ID NO:1468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..33

(D) OTHER INFORMATION: / Ceres Seq. ID 1500377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:

```
Met Thr Lys Arg Phe Tyr Leu Ser Arg Tyr Ala Leu Met Ser Arg Tyr
1          5          10          15
Ile Asp Tyr Leu Ile Leu Xaa Xaa Phe Xaa Phe Ile Tyr Arg Val Leu
20          25          30
Val
```

(2) INFORMATION FOR SEQ ID NO:1469:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1326 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1326

(D) OTHER INFORMATION: / Ceres Seq. ID 1500387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:

```
aaaaaaccaa atcgaagatc ttgtaaagt tcttttttc cgaatctga gcttggtat 60
tggttgataa gcttctcgga gattgagatt gaggattttg ataggtgagg agattgaaa 120
atttgatttt ttgggcggca aaaatgttga tgcagacgga agctagggtt ggtgtgagct 180
caggacatgg cgtagcttcg tcttctcatc gttttaacgca ggaccagaga tcacataatc 240
aatcgcgctc gcagctctta gCcgaggagac tcgctgggtc ttttagcaag aattgtactg 300
ctctctatct tcgtctcaac attctcttcc aggtgcaagg tatgcacaca aatgctcgag 360
ctttaagaaa gccaaagcata ttacacgagg ctccacggat attgaatgaa gaaggattga 420
aagctttttg gaaagggaaat ctagtacta ttgtccacgc gcttccatat tcttctgtta 480
atttctacgc atatgaacac tacaagaagt tcaatgtatat gtttactggg atgaaaaatc 540
acaagagagc tataaagttca aacctttttg tacattttgt agccggtggt ttggctggaa 600
tcacagctgc ttctgccaat tatccacttg atctctgttag aactcgtctt gctgctcaga 660
caaaagtaat ctactactcg ggtatctggc atactctgcg ctctattaca accgatgaag 720
gtatcttggg cctctacaag ggactaggaa caacgcttgt ggtgtgtggg ctagtattg 780
ccattagctt ttctgtgtat gaatcattga gatctattg gagggtcaact aggccccatg 840
attccctatc catggctcagt ctagcttgtg gaagtctttc aggaatagca tcttcaacag 900
ctacgtttcc attggaatct gtgagaagaa cgaagcagct ggaaggaata ggcgggcgag 960
cggtagtgtta caagacaggt ttgttaggca cattaaagcg tattgttcaa acggaaggag 1020
cgagagacct gtacagagga attcttccag agtactacaa agtggtaacct ggtgtaggga 1080
ttgtgcttat gacctacgag acactcaagc ttacttctaa ggaactttct tcgaactctat 1140
aacgggtttta aaggttggtg gatttgttta ggtctatttt tggtgagagg aaaaaactg 1200
```

taaaaaccaa acagcggaatg atgataatgt atacgaaatg tagaattata tatgtagttg 1260
ttggatgtag cttatagcag attaacattt gtattgggtac aatccttttc cattgttaca 1320
tggctt

(2) INFORMATION FOR SEQ ID NO:1470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..332
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:

Met	Val	Met	Gln	Thr	Glu	Ala	Arg	Val	Gly	Val	Ser	Ser	Gly	His	Gly
1			5					10						15	
Val	Ala	Ser	Ser	Ser	His	Arg	Leu	Thr	Gln	Asp	Gln	Arg	Ser	His	Ile
			20				25					30			
Glu	Ser	Ala	Ser	Gln	Leu	Leu	Ala	Gly	Gly	Leu	Ala	Gly	Ala	Phe	Ser
		35				40					45				
Lys	Thr	Cys	Thr	Ala	Pro	Leu	Ser	Arg	Leu	Thr	Ile	Leu	Phe	Gln	Val
	50					55					60				
Gln	Gly	Met	His	Thr	Asn	Ala	Ala	Ala	Leu	Arg	Lys	Pro	Ser	Ile	Leu
	65				70					75				80	
His	Glu	Ala	Ser	Arg	Ile	Leu	Asn	Glu	Glu	Gly	Leu	Lys	Ala	Phe	Trp
				85					90					95	
Lys	Gly	Asn	Leu	Val	Thr	Ile	Ala	His	Arg	Leu	Pro	Tyr	Ser	Ser	Val
				100				105					110		
Asn	Phe	Tyr	Ala	Tyr	Glu	His	Tyr	Lys	Lys	Phe	Met	Tyr	Met	Val	Thr
		115				120						125			
Gly	Met	Glu	Asn	His	Lys	Glu	Ser	Ile	Ser	Ser	Asn	Leu	Phe	Val	His
		130				135					140				
Phe	Val	Ala	Gly	Gly	Leu	Ala	Gly	Ile	Thr	Ala	Ala	Ser	Ala	Thr	Tyr
	145				150					155				160	
Pro	Leu	Asp	Leu	Val	Arg	Thr	Arg	Leu	Ala	Ala	Gln	Thr	Lys	Val	Ile
			165					170						175	
Tyr	Tyr	Ser	Gly	Ile	Trp	His	Thr	Leu	Arg	Ser	Ile	Thr	Thr	Asp	Glu
		180						185					190		
Gly	Ile	Leu	Gly	Leu	Tyr	Lys	Gly	Leu	Gly	Thr	Thr	Leu	Val	Gly	Val
		195				200						205			
Gly	Pro	Ser	Ile	Ala	Ile	Ser	Phe	Ser	Val	Tyr	Glu	Ser	Leu	Arg	Ser
		210				215					220				
Tyr	Trp	Arg	Ser	Thr	Arg	Pro	His	Asp	Ser	Pro	Ile	Met	Val	Ser	Leu
	225				230					235				240	
Ala	Cys	Gly	Ser	Leu	Ser	Gly	Ile	Ala	Ser	Ser	Thr	Ala	Thr	Phe	Pro
			245						250					255	
Leu	Asp	Leu	Val	Arg	Arg	Thr	Lys	Gln	Leu	Glu	Gly	Ile	Gly	Gly	Arg
			260					265					270		
Ala	Val	Val	Tyr	Lys	Thr	Gly	Leu	Leu	Gly	Thr	Leu	Lys	Arg	Ile	Val
		275				280						285			
Gln	Thr	Glu	Gly	Ala	Arg	Gly	Leu	Tyr	Arg	Gly	Ile	Leu	Pro	Glu	Tyr
		290				295					300				
Tyr	Lys	Val	Val	Pro	Gly	Val	Gly	Ile	Cys	Phe	Met	Thr	Tyr	Glu	Thr
			305			310				315				320	
Leu	Lys	Leu	Tyr	Phe	Lys	Asp	Leu	Ser	Ser	Asn	Leu				
			325					330							

(2) INFORMATION FOR SEQ ID NO:1471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..330
(D) OTHER INFORMATION: / Ceres Seq. ID 1500389
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:

Met	Gln	Thr	Glu	Ala	Arg	Val	Gly	Val	Ser	Ser	Gly	His	Gly	Val	Ala	
1			5				10				15					
Ser	Ser	Ser	His	Arg	Leu	Thr	Gln	Asp	Gln	Arg	Ser	His	Ile	Glu	Ser	
			20				25				30					
Ala	Ser	Gln	Leu	Leu	Ala	Gly	Gly	Leu	Ala	Gly	Ala	Phe	Ser	Lys	Thr	
			35				40				45					
Cys	Thr	Ala	Pro	Leu	Ser	Arg	Leu	Thr	Ile	Leu	Phe	Gln	Val	Gln	Gly	
			50				55				60					
Met	His	Thr	Asn	Ala	Ala	Ala	Leu	Arg	Lys	Pro	Ser	Ile	Leu	His	Glu	
65			70							75				80		
Ala	Ser	Arg	Ile	Leu	Asn	Glu	Glu	Gly	Leu	Lys	Ala	Phe	Trp	Lys	Gly	
			85						90					95		
Asn	Leu	Val	Thr	Ile	Ala	His	Arg	Leu	Pro	Tyr	Ser	Ser	Val	Asn	Phe	
			100						105					110		
Tyr	Ala	Tyr	Glu	His	Tyr	Lys	Lys	Phe	Met	Tyr	Met	Val	Thr	Gly	Met	
			115						120					125		
Glu	Asn	His	Lys	Glu	Ser	Ile	Ser	Ser	Asn	Leu	Phe	Val	His	Phe	Val	
			130						135					140		
Ala	Gly	Gly	Leu	Ala	Gly	Ile	Thr	Ala	Ala	Ser	Ala	Thr	Tyr	Pro	Leu	
145			150							155				160		
Asp	Leu	Val	Arg	Thr	Arg	Leu	Ala	Ala	Gln	Thr	Lys	Val	Ile	Tyr	Tyr	
			165						170					175		
Ser	Gly	Ile	Trp	His	Thr	Leu	Arg	Ser	Ile	Thr	Thr	Asp	Glu	Gly	Ile	
			180						185					190		
Leu	Gly	Leu	Tyr	Lys	Gly	Leu	Gly	Thr	Thr	Leu	Val	Gly	Val	Gly	Pro	
			195						200					205		
Ser	Ile	Ala	Ile	Ser	Phe	Ser	Val	Tyr	Glu	Ser	Leu	Arg	Ser	Tyr	Trp	
			210						215					220		
Arg	Ser	Thr	Arg	Pro	His	Asp	Ser	Pro	Ile	Met	Val	Ser	Leu	Ala	Cys	
225						230				235				240		
Gly	Ser	Leu	Ser	Gly	Ile	Ala	Ser	Ser	Thr	Ala	Thr	Phe	Pro	Leu	Asp	
						245				250				255		
Leu	Val	Arg	Arg	Thr	Lys	Gln	Leu	Glu	Gly	Ile	Gly	Gly	Arg	Ala	Val	
						260				265				270		
Val	Tyr	Lys	Thr	Gly	Leu	Leu	Gly	Thr	Leu	Lys	Arg	Ile	Val	Gln	Thr	
						275				280				285		
Glu	Gly	Ala	Arg	Gly	Leu	Tyr	Arg	Gly	Ile	Leu	Pro	Glu	Tyr	Tyr	Lys	
						290				295				300		
Val	Val	Pro	Gly	Val	Gly	Ile	Cys	Phe	Met	Thr	Tyr	Glu	Thr	Leu	Lys	
305						310				315				320		
Leu	Tyr	Phe	Lys	Asp	Leu	Ser	Ser	Asn	Leu							
						325				330						

- (2) INFORMATION FOR SEQ ID NO:1472:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..266
(D) OTHER INFORMATION: / Ceres Seq. ID 1500390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:

Met His Thr Asn Ala Ala Ala Leu Arg Lys Pro Ser Ile Leu His Glu
1 5 10 15
Ala Ser Arg Ile Leu Asn Glu Gly Leu Lys Ala Phe Trp Lys Gly
20 25 30
Asn Leu Val Thr Ile Ala His Arg Leu Pro Tyr Ser Ser Val Asn Phe
35 40 45
Tyr Ala Tyr Glu His Tyr Lys Lys Phe Met Tyr Met Val Thr Gly Met
50 55 60
Glu Asn His Lys Glu Ser Ile Ser Ser Asn Leu Phe Val His Phe Val
65 70 75 80
Ala Gly Gly Leu Ala Gly Ile Thr Ala Ala Ser Ala Thr Tyr Pro Leu
85 90 95
Asp Leu Val Arg Thr Arg Leu Ala Ala Gln Thr Lys Val Ile Tyr Tyr
100 105 110
Ser Gly Ile Trp His Thr Leu Arg Ser Ile Thr Thr Asp Glu Gly Ile
115 120 125
Leu Gly Leu Tyr Lys Gly Leu Gly Thr Thr Leu Val Gly Val Gly Pro
130 135 140
Ser Ile Ala Ile Ser Phe Ser Val Tyr Glu Ser Leu Arg Ser Tyr Trp
145 150 155 160
Arg Ser Thr Arg Pro His Asp Ser Pro Ile Met Val Ser Leu Ala Cys
165 170 175
Gly Ser Leu Ser Gly Ile Ala Ser Ser Thr Ala Thr Phe Pro Leu Asp
180 185 190
Leu Val Arg Arg Thr Lys Gln Leu Glu Gly Ile Gly Gly Arg Ala Val
195 200 205
Val Tyr Lys Thr Gly Leu Leu Gly Thr Leu Lys Arg Ile Val Gln Thr
210 215 220
Glu Gly Ala Arg Gly Leu Tyr Arg Gly Ile Leu Pro Glu Tyr Tyr Lys
225 230 235 240
Val Val Pro Gly Val Gly Ile Cys Phe Met Thr Tyr Glu Thr Leu Lys
245 250 255
Leu Tyr Phe Lys Asp Leu Ser Ser Asn Leu
260 265

(2) INFORMATION FOR SEQ ID NO:1473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..686
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:

tcccaagtga taatgcaagt aatgaaatgg aaaggcgctcc accccggaag cgaagatttc 60
aggaacttcc agctgattgt aaggttccag aaaaagacaa acagcaatcg gagttagcaa 120
tgacaggtga tgttactcca tcagcaataa gagtgcggtc gccgccttca ccaagatctg 180
taatgcctcc tcctccacca aagaccatcg caccacgcgc ttctaagacc atgtctcctc 240
catatcaaaa aagcatgctt cctccaccac cactttctaa gaccatgtct cctctaacat 300
caaaaagcat gcttctctcca ccaccgcgat ttacactgac aactcaacct tcaagattac 360
aggacaacca catcagtgta aagaaaccaa atccagttcc agatacgtta ataaaagtga 420
tggaatatgg agacgatgaa gacgatgatg acgatcctga tgagccattg acaactagat 480
cgtgacagtg tattagatta cagaaccttc ttatctggca acaaaatgtc aatttgtgtt 540
tgtaacaata gaagaatatg ttggtctctt actgatttgg aacttcattg cctaaggcta 600
ttagttaaat atttaagata ttagtacttt gtttgcgaag gcactgctcg ttttgttgta 660
tttcttatca ttaatacata atgggt

(2) INFORMATION FOR SEQ ID NO:1474:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..160
(D) OTHER INFORMATION: / Ceres Seq. ID 1500392
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:
Pro Ser Asp Asn Ala Ser Asn Glu Met Glu Arg Arg Pro Pro Arg Lys
1 5 10 15
Arg Lys Phe Gln Glu Leu Pro Ala Asp Cys Lys Val Pro Glu Lys Asp
20 25 30
Lys Gln Gln Ser Glu Leu Ala Met Thr Gly Asp Val Thr Pro Ser Ala
35 40 45
Asn Arg Val Arg Ser Pro Pro Ser Pro Arg Ser Val Met Pro Pro Pro
50 55 60
Pro Pro Lys Thr Ile Ala Pro Pro Pro Ser Lys Thr Met Ser Pro Pro
65 70 75 80
Ser Ser Lys Ser Met Leu Pro Pro Pro Pro Arg Ser Lys Thr Met Ser
85 90 95
Pro Leu Thr Ser Lys Ser Met Leu Pro Pro Pro Pro Arg Phe Thr Leu
100 105 110
Thr Thr Gln Pro Ser Arg Leu Gln Asp Asn His Ile Ser Val Lys Lys
115 120 125
Pro Asn Pro Val Pro Asp Thr Leu Ile Lys Leu Met Glu Tyr Gly Asp
130 135 140
Asp Glu Asp Asp Asp Asp Pro Asp Glu Pro Leu Thr Thr Arg Ser
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:1475:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1500393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:

Met Glu Arg Arg Pro Pro Arg Lys Arg Lys Phe Gln Glu Leu Pro Ala
1 5 10 15
Asp Cys Lys Val Pro Glu Lys Asp Lys Gln Gln Ser Glu Leu Ala Met
20 25 30
Thr Gly Asp Val Thr Pro Ser Ala Asn Arg Val Arg Ser Pro Pro Ser
35 40 45
Pro Arg Ser Val Met Pro Pro Pro Pro Lys Thr Ile Ala Pro Pro
50 55 60
Pro Ser Lys Thr Met Ser Pro Pro Ser Ser Lys Ser Met Leu Pro Pro
65 70 75 80
Pro Pro Arg Ser Lys Thr Met Ser Pro Leu Thr Ser Lys Ser Met Leu
85 90 95
Pro Pro Pro Pro Arg Phe Thr Leu Thr Thr Gln Pro Ser Arg Leu Gln
100 105 110
Asp Asn His Ile Ser Val Lys Lys Pro Asn Pro Val Pro Asp Thr Leu
115 120 125
Ile Lys Leu Met Glu Tyr Gly Asp Asp Glu Asp Asp Asp Asp Asp

130 135 140
Asp Glu Pro Leu Thr Thr Arg Ser
145 150
(2) INFORMATION FOR SEQ ID NO:1476:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..121
(D) OTHER INFORMATION: / Ceres Seq. ID 1500394
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:
Met Thr Gly Asp Val Thr Pro Ser Ala Asn Arg Val Arg Ser Pro Pro
1 5 10 15
Ser Pro Arg Ser Val Met Pro Pro Pro Pro Lys Thr Ile Ala Pro
20 25 30
Pro Pro Ser Lys Thr Met Ser Pro Pro Ser Ser Lys Ser Met Leu Pro
35 40 45
Pro Pro Pro Arg Ser Lys Thr Met Ser Pro Leu Thr Ser Lys Ser Met
50 55 60
Leu Pro Pro Pro Pro Arg Phe Thr Leu Thr Thr Gln Pro Ser Arg Leu
65 70 75
Gln Asp Asn His Ile Ser Val Lys Lys Pro Asn Pro Val Pro Asp Thr
85 90 95
Leu Ile Lys Leu Met Glu Tyr Gly Asp Asp Glu Asp Asp Asp Asp Asp
100 105 110
Pro Asp Glu Pro Leu Thr Thr Arg Ser
115 120

(2) INFORMATION FOR SEQ ID NO:1477:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..441
(D) OTHER INFORMATION: / Ceres Seq. ID 1500395
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:
ccagacttta ttcccaaaaa accaaaaataa tcgccaccgc tctccgcacg gaaccgaagc 60
ggcggcgatg gcggcgagaga agccgggtccc cgtgcgcgtg ctcactgcg gcgtctgcgg 120
cctcccggcc gactactgcg agttcggccc cgacttcgag cgctgcgaac cctggctgcg 180
cgcgcatgns ccggcgctcta cccgcacgaa ctgtgcgcg cmtctctctc ctcacccggm 240
ggcggcgaca aggacgtcga cagggtcggg gatcgcctcc agggcgctcg gatctccgac 300
ggctccacca gcgcgcgag gatgcttccg cgtctaagcc ccaagagggc aaacgcctgc 360
mtggtggtaa gctcaagaaa aaggagaagc aagaagtggc cattgagaag attgtccgta 420
acaagcgcaa atgtgttact g

(2) INFORMATION FOR SEQ ID NO:1478:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1500396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:

Gln	Thr	Leu	Phe	Pro	Lys	Asn	Gln	Asn	Arg	His	Arg	Ser	Pro	His
1				5					10					15
Gly	Thr	Ala	Ala	Ala	Ala	Met	Ala	Ala	Glu	Lys	Pro	Ala	Pro	Val
				20				25				30		Arg
Val	Leu	Tyr	Cys	Gly	Val	Cys	Gly	Leu	Pro	Ala	Glu	Tyr	Cys	Glu
				35			40				45			Phe
Gly	Pro	Asp	Phe	Glu	Arg	Cys	Lys	Pro	Trp	Leu	Arg	Ala	His	Xaa
				50			55				60			Pro
Ala	Ser	Thr	Pro	Thr	Asn	Leu	Ser	Pro	Xaa	Pro	Pro	Pro	His	Pro
				65			70				75			Xaa
Ala	Ala	Thr	Arg	Thr	Ser	Thr	Gly	Ser	Gly	Ile	Ala	Ser	Arg	Ala
				85			90							80
Gly	Ser	Pro	Thr	Ala	Pro	Pro	Ala	Pro	Gln	Gly	Cys	Phe	Arg	Val
				100			105						110	

(2) INFORMATION FOR SEQ ID NO:1479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1500397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

Arg	Leu	Tyr	Ser	Pro	Lys	Thr	Lys	Ile	Ile	Ala	Thr	Ala	Leu	Arg	Thr
1				5					10					15	
Glu	Pro	Lys	Arg	Arg	Arg	Trp	Arg	Arg	Arg	Ser	Arg	Leu	Pro	Cys	Ala
				20				25				30			
Cys	Ser	Thr	Ala	Ala	Ser	Ala	Ala	Ser	Arg	Pro	Ser	Thr	Ala	Ser	Ser
				35			40					45			
Ala	Pro	Thr	Ser	Ser	Ala	Ala	Ser	Pro	Gly	Cys	Ala	Arg	Met	Xaa	Arg
				50			55				60				
Arg	Leu	Pro	Arg	Arg	Thr	Cys	Arg	Arg	Xaa	Leu	Leu	Ile	Arg	Xaa	
				65			70				75			80	
Arg	Arg	Gln	Gly	Arg	Arg	Gln	Gly	Arg	Gly	Ser	Pro	Pro	Gly	Arg	Arg
				85			90						95		
Asp	Leu	Arg	Arg	Leu	His	Gln	Arg	Arg	Arg	Asp	Ala	Ser	Ala	Ser	Lys
				100			105					110			
Pro	Gln	Glu	Ala	Lys	Arg	Leu	Xaa	Gly	Gly	Lys	Leu	Lys	Lys	Lys	Glu
				115			120					125			
Lys	Gln	Glu	Val	Val	Ile	Glu	Lys	Ile	Val	Arg	Asn	Lys	Arg	Lys	Cys
				130			135					140			
Val	Thr														
145															

(2) INFORMATION FOR SEQ ID NO:1480:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1500398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

Met Ala Ala Glu Lys Pro Ala Pro Val Arg Val Leu Tyr Cys Gly Val

1 5 10 15
Cys Gly Leu Pro Ala Glu Tyr Cys Glu Phe Gly Pro Asp Phe Glu Arg
20 25 30
Cys Lys Pro Trp Leu Arg Ala His Xaa Pro Ala Ser Thr Pro Thr Asn
35 40 45
Leu Ser Pro Xaa Pro Pro Pro His Pro Xaa Ala Ala Thr Arg Thr Ser
50 55 60
Thr Gly Ser Gly Ile Ala Ser Arg Ala Ser Gly Ser Pro Thr Ala Pro
65 70 75 80
Pro Ala Pro Gln Gly Cys Phe Arg Val
85

(2) INFORMATION FOR SEQ ID NO:1481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..431
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:

atccctccct cctcatcg cgttttatatt tcccgctcctt cttcattcgg cccttcgccc 60
ctgctatatt tcgcgccgcg cttgcctcct aataatagcm gccgcggcag tggataccgc 120
caccgccatg ggagcgctcg aggagggccca cctcgcgccc gccgcgtgcg cgtgcgagga 180
ggaggaggaa agcgactaca tcggcctcct cgcaggggaa gccgcggcgg gcgacgcgct 240
ggagccggcc gtgcgcggcc tgctgctggg gctcggtgag gacgacggcc gcgarggcct 300
gctccggcag cccaagcgcg tcgccaaggc cttccgcgac gccaccgcag gctacaggca 360
aaaagtaaaa gacatagtc aaggtgctct gttccarag gttggtgtgg ataaaaggac 420
tggatctgct g

(2) INFORMATION FOR SEQ ID NO:1482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:

Ile Pro Pro Ser Leu Ile Ala Phe Tyr Tyr Ser Arg Pro Ser Ser Phe
1 5 10 15
Gly Pro Ser Pro Leu Leu Tyr Phe Ala Ala Leu Pro Pro Asn Asn
20 25 30
Ser Xaa Arg Gly Ser Gly Tyr Arg His Arg His Gly Ser Ala Arg Gly
35 40 45
Gly Pro Pro Arg Gly Arg Arg Val Arg Arg Gly Gly Gly Lys
50 55 60
Arg Leu His Arg Pro Pro Arg Arg Gly Ser Gly Gly Arg Arg Arg
65 70 75 80
Gly Ala Gly Arg Ala Arg Pro Ala Ala Gly Ala Arg
85 90

(2) INFORMATION FOR SEQ ID NO:1483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1500409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:

```
Ser Leu Pro Pro Ser Ser Arg Phe Ile Ile Pro Val Leu Leu His Ser
1      5      10      15
Ala Leu Arg Arg Cys Tyr Ile Ser Arg Pro Pro Cys Leu Leu Ile Ile
20      25      30
Xaa Ala Ala Ala Val Asp Thr Ala Thr Ala Met Gly Ala Leu Glu Glu
35      40      45
Ala His Leu Ala Ala Ala Ala Cys Ala Cys Glu Glu Glu Glu Ser
50      55      60
Asp Tyr Ile Gly Leu Leu Ala Gly Glu Ala Ala Ala Gly Asp Ala Val
65      70      75      80
Glu Pro Ala Val Arg Ala Leu Leu Leu Gly Leu Gly Glu Asp Asp Arg
85      90      95
Arg Xaa Gly Leu Leu Arg Thr Pro Lys Arg Val Ala Lys Ala Phe Arg
100      105      110
Asp Gly Thr Arg Gly Tyr Arg Gln Lys Val Lys Asp Ile Val Gln Gly
115      120      125
Ala Leu Phe Pro Xaa Val Gly Val Asp Lys Arg Thr Gly Ser Ala
130      135      140
```

(2) INFORMATION FOR SEQ ID NO:1484:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1500410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:

```
Met Gly Ala Leu Glu Glu Ala His Leu Ala Ala Ala Cys Ala Cys
1      5      10      15
Glu Glu Glu Glu Glu Ser Asp Tyr Ile Gly Leu Leu Ala Gly Glu Ala
20      25      30
Ala Ala Gly Asp Ala Val Glu Pro Ala Val Arg Ala Leu Leu Leu Gly
35      40      45
Leu Gly Glu Asp Asp Arg Arg Xaa Gly Leu Leu Arg Thr Pro Lys Arg
50      55      60
Val Ala Lys Ala Phe Arg Asp Gly Thr Arg Gly Tyr Arg Gln Lys Val
65      70      75      80
Lys Asp Ile Val Gln Gly Ala Leu Phe Pro Xaa Val Gly Val Asp Lys
85      90      95
Arg Thr Gly Ser Ala
100
```

(2) INFORMATION FOR SEQ ID NO:1485:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: ~

(B) LOCATION: 1..470

(D) OTHER INFORMATION: / Ceres Seq. ID 1500422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:
agcaaacct agcgcannc anccaccac ccactcgctt cagccgcctc cgccgcgcgt 60
acaagcaggt ggagacagga tgccggcttg ccacggcctg cgctcgcgga cgccgcgacct 120
cttcgcgcgc cccttcgcga agaagggtta catcccgctc accacctacc tccgcacctta 180
caagatcggc gattacgtcg atgtcaagggt gaacggcgcc gtccacaagg ggaatgccga 240
caagtcttac cagcgccgca cgggtcgctg ctggaacgtc accaagcgcg ccactggcgt 300
cgaggtcaac aagcaggttag acaacgcgga tcccttttc gcagaggcaa ttacgattag 360
tgcgctggcg catcttctga tcgtttcatt ctaggaaatg taacgattta atatagaatg 420
gsggctattt gctgacggtg ttgtttgatt tggatttata gaatttgtac

(2) INFORMATION FOR SEQ ID NO:1486:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1500423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:

Ala Asn Pro Ser Ala Xaa Xaa Pro Pro Thr His Ser Leu Gln Pro Pro
1 5 10 15
Pro Pro Arg Val Gln Ala Gly Gly Asp Arg Met Pro Ala Gly His Gly
20 25 30
Leu Arg Ser Arg Thr Arg Asp Leu Phe Ala Arg Pro Phe Arg Lys Lys
35 40 45
Gly Tyr Ile Pro Leu Thr Thr Tyr Leu Arg Thr Tyr Lys Ile Gly Asp
50 55 60
Tyr Val Asp Val Lys Val Asn Gly Ala Val His Lys Gly Met Pro His
65 70 75 80
Lys Phe Tyr His Gly Arg Thr Gly Arg Val Trp Asn Val Thr Lys Arg
85 90 95
Ala Ile Gly Val Glu Val Asn Lys Gln Val Asp Asn Ala Asp Pro Phe
100 105 110
Phe Ala Glu Ala Ile Thr Ile Ser Ala Leu Ala His Leu Leu Ile Val
115 120 125

Ser Phe
130

(2) INFORMATION FOR SEQ ID NO:1487:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1500424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

Gln Thr Leu Ala Xaa Xaa Xaa His Pro Pro Thr Arg Phe Ser Arg Leu
1 5 10 15
Arg Arg Ala Tyr Lys Gln Val Glu Thr Gly Cys Arg Leu Ala Thr Ala
20 25 30
Cys Ala Arg Gly Arg Ala Thr Ser Ser Arg Ala Pro Ser Ala Arg Arg
35 40 45
Ala Thr Ser Arg Ser Pro Pro Thr Ser Ala Pro Thr Arg Ser Ala Ile
50 55 60
Thr Ser Met Ser Arg
65

(2) INFORMATION FOR SEQ ID NO:1488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

Met Pro Ala Gly His Gly Leu Arg Ser Arg Thr Arg Asp Leu Phe Ala
1 5 10 15
Arg Pro Phe Arg Lys Lys Gly Tyr Ile Pro Leu Thr Thr Tyr Leu Arg
20 25 30
Thr Tyr Lys Ile Gly Asp Tyr Val Asp Val Lys Val Asn Gly Ala Val
35 40 45
His Lys Gly Met Pro His Lys Phe Tyr His Gly Arg Thr Gly Arg Val
50 55 60
Trp Asn Val Thr Lys Arg Ala Ile Gly Val Glu Val Asn Lys Gln Val
65 70 75 80
Asp Asn Ala Asp Pro Phe Phe Ala Glu Ala Ile Thr Ile Ser Ala Leu
85 90 95
Ala His Leu Leu Ile Val Ser Phe
100

(2) INFORMATION FOR SEQ ID NO:1489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: ~
- (B) LOCATION: 1..453
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

aatcggaaca attccgcgtt gccatccat cccggaaata tcccaagga aacctcgcc 60
cccctctctt cccgcgcgcg gtccgccagat ctccggtcat ggacgacgac ggcggggcct 120
cccggtcgcc ctgcgcgtcc ccgtcgcgct ctccgtcccc gtccccctgt gccgacctcc 180
tcacggtcgc ngcggcgccg cccggccacg tcgctcgctc tatccccctc cgcaagcact 240
cgcttctctc cgcgcgcgcc ggccggcgcg gcggccgna gggacgattg ggagcgacg 300
cgccacctcc acgctcatcg acgctctggg ggagcgcttc gtggcgctgg gccggggcag 360
cctccgcac ccgacgtggc aggaggtcgc cgaggtcgtc tcctctcgcg acagytactc 420
caaggcgccc caaatcgac gtcccagtgc aag

(2) INFORMATION FOR SEQ ID NO:1490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

Asn Arg Asn Asn Ser Ala Leu Pro Ile His Pro Gly Asn Ile Pro Lys
1 5 10 15
Glu Thr Leu Ala Pro Leu Leu Pro Arg Arg Arg Ser Pro Asp Leu Arg

	20						25						30					
Ser	Trp	Thr	Thr	Thr	Ala	Gly	Pro	Pro	Gly	Arg	Pro	Arg	Arg	Pro	Arg			
		35						40					45					
Arg	Ala	Leu	Arg	Pro	Arg	Ser	Pro	Trp	Pro	Thr	Pro	Ser	Arg	Ser	Xaa			
		50					55						60					
Arg	Arg	Arg	Pro	Ala	Thr	Ser	Pro	Ser	Leu	Ser	Pro	Ser	Ala	Ser	Thr			
		65			70					75				80				
Arg	Leu	Pro	Pro	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Xaa	Arg	Asp	Asp			
				85						90				95				
Trp	Glu	Arg	Arg	Arg	His	Leu	His	Ala	His	Arg	Arg	Leu	Gly	Gly	Ala			
			100						105					110				
Leu	Arg	Gly	Ala	Gly	Pro	Gly	Gln	Pro	Pro	Pro	Pro	Ala	Val	Ala	Gly			
		115					120						125					
Gly	Arg	Arg	Gly	Arg	Leu	Leu	Ser	Arg	Gln	Xaa	Leu	Gln	Gly	Ala	Pro			
		130					135					140						
Asn	Pro	Thr	Ser	Gln	Cys	Lys												
		145			150													

(2) INFORMATION FOR SEQ ID NO:1491:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1500466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

Ile	Gly	Thr	Ile	Pro	Arg	Cys	Pro	Ser	Ile	Pro	Glu	Ile	Ser	Pro	Arg			
				5					10					15				
Lys	Pro	Ser	Pro	Pro	Ser	Phe	Pro	Ala	Ala	Gly	Arg	Gln	Ile	Ser	Gly			
			20					25					30					
His	Gly	Arg	Arg	Arg	Arg	Gly	Leu	Pro	Val	Ala	Leu	Ala	Val	Pro	Val			
		35					40					45						
Ala	Leu	Ser	Val	Pro	Ala	Pro	Arg	Gly	Arg	Pro	Arg	His	Gly	Arg	Xaa			
		50				55					60							
Gly	Ala	Ala	Arg	Pro	Arg	Arg	Arg	Arg	Tyr	Pro	Pro	Pro	Gln	Ala	Leu			
		65			70				75					80				
Ala	Phe	Leu	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Pro	Xaa	Gly	Thr	Ile			
			85					90					95					
Gly	Ser	Asp	Gly	Ala	Thr	Ser	Thr	Leu	Ile	Asp	Ala	Trp	Gly	Glu	Arg			
			100					105					110					
Phe	Val	Ala	Leu	Gly	Arg	Gly	Ser	Leu	Arg	His	Pro	Gln	Trp	Gln	Glu			
		115					120					125						
Val	Ala	Glu	Val	Val	Ser	Ser	Arg	Asp	Xaa	Tyr	Ser	Lys	Ala	Pro	Gln			
		130					135					140						
Ile	Arg	Arg	Pro	Ser	Ala													
		145			150													

(2) INFORMATION FOR SEQ ID NO:1492:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1500467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

Ser Glu Gln Phe Arg Val Ala His Pro Ser Arg Lys Tyr Pro Gln Gly
1 5 10 15
Asn Pro Arg Pro Pro Ser Pro Pro Val Ala Arg Ser Pro Val
20 25 30
Met Asp Asp Asp Gly Gly Ala Ser Arg Ser Pro Ser Pro Ser
35 40 45
Arg Ser Pro Ser Pro Leu Pro Val Ala Asp Pro Val Thr Val Xaa Ala
50 55 60
Ala Pro Pro Gly His Val Ala Val Ala Ile Pro Leu Arg Lys His Ser
65 70 75 80
Pro Ser Ser Gly Gly Gly Gly Gly Gly Arg Xaa Gly Arg Leu
85 90 95
Gly Ala Thr Ala Pro Pro Pro Arg Ser Ser Thr Pro Gly Gly Ser Ala
100 105 110
Ser Trp Arg Trp Ala Gly Ala Ala Ser Ala Thr Arg Ser Gly Arg Arg
115 120 125
Ser Pro Arg Ser Ser Pro Leu Ala Thr Xaa Thr Pro Arg Arg Pro Lys
130 135 140
Ser Asp Val Pro Val Gln
145 150

(2) INFORMATION FOR SEQ ID NO:1493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..654
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

ggacctttct atcgcgcgca tttttcttcc gaccagccga vcgcccgcgc cctccggcag 60
gtttttcttc cggccaacgac caccacaagc aggtcttccc ggcccgaac gcgagcaccc 120
agccctcttc caggtcttcc ccggcgacga cgcgctagaa gaggggatcc ttagcacaat 180
ggaagaagga gcaccagggc cgtcgcaagc catcccggaat tctggagaca cgtaccgcga 240
cagctccacc gcgcccgtgg gcagcagctc accgtctgtc gcgaagctcc ggaagctgct 300
gttcggcggg atgctcatcg gcgtcaacga cggccgctac ttccacggcc tgttccactg 360
catcgacaag cagggcaaca tcatactcca ggacgcgcta gactaccgca gcgcccgcga 420
ctgctcgctc ccgacggagc agcggtgcct ggggctcatt ctgatcccg gcgctcgcc 480
gtcgtctgac caggtcgatt gctccgttga agagaagatg tcgctcctgt gttttgagt 540
aatcgtgctt caaagggaat acactacgca tgtactaagt tactggggct catctctgct 600
atctgaact gagaggcatg attgtgttt cctatttttg aaggattgtt tatt

(2) INFORMATION FOR SEQ ID NO:1494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:

Asp Leu Ser Ile Ala Arg Ile Phe Phe Pro Thr Ser Arg Xaa Pro Pro
1 5 10 15
Pro Ser Gly Arg Ser Ser Ser Arg Pro Arg Pro Thr Pro Gly Leu
20 25 30
Pro Gly Pro Glu Arg Glu His Pro Ala Leu Leu Gln Val Phe Pro Gly
35 40 45

Asp Glu Arg Val Glu Glu Gly Ile Leu Ser Thr Met Glu Glu Gly Ala
50 55 60
Pro Gly Pro Ser Gln Ala Ile Pro Asp Ser Gly Asp Thr Tyr Arg Asn
65 70 75 80
Ser Ser Thr Ala Pro Val Gly Ser Ser Ser Pro Ser Val Ala Lys Leu
85 90 95
Arg Lys Leu Leu Phe Arg Arg Met Leu Ile Gly Val Asn Asp Gly Arg
100 105 110
Tyr Phe His Gly Leu Phe His Cys Ile Asp Lys Gln Gly Asn Ile Ile
115 120 125
Leu Gln Asp Ala Val Glu Tyr Arg Ser Ala Arg His Cys Ser Pro Pro
130 135 140
Thr Glu Gln Arg Cys Leu Gly Leu Ile Leu Ile Pro Ala Ala Cys Arg
145 150 155 160
Ser Ser Cys Gln Val Asp Cys Ser Val Glu Lys Met Ser Leu Leu
165 170 175
Cys Phe Glu

(2) INFORMATION FOR SEQ ID NO:1495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:

Met Glu Glu Gly Ala Pro Gly Pro Ser Gln Ala Ile Pro Asp Ser Gly
1 5 10 15
Asp Thr Tyr Arg Asn Ser Ser Thr Ala Pro Val Gly Ser Ser Pro
20 25 30
Ser Val Ala Lys Leu Arg Lys Leu Phe Arg Arg Met Leu Ile Gly
35 40 45
Val Asn Asp Gly Arg Tyr Phe His Gly Leu Phe His Cys Ile Asp Lys
50 55 60
Gln Gly Asn Ile Ile Leu Gln Asp Ala Val Glu Tyr Arg Ser Ala Arg
65 70 75 80
His Cys Ser Pro Pro Thr Glu Gln Arg Cys Leu Gly Leu Ile Leu Ile
85 90 95
Pro Ala Ala Cys Arg Ser Ser Cys Gln Val Asp Cys Ser Val Glu Glu
100 105 110
Lys Met Ser Leu Leu Cys Phe Glu
115 120

(2) INFORMATION FOR SEQ ID NO:1496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..410
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:

gtgcttcaag aattgatccg ttccgggtgc gacctccagg tccaggagca gcaccaatcc 60
ccaagcgcg catggcgccc gaccccaacg tgcgtcttct cgtacctttc ctgcgcattc 120
ccctctactt ctctctggcc accagacgta ggaagcccaag cggggggcgcg cggctccccc 180

cgggcgccgtg ggcgctgccc gtggctgggc acctgcacac cctagccccc ggccctccgc 240
accgcgctcat ggcgcamctg ggcargcgcc acgcccgcct catgatgctc cggttcggcg 300
aggtcccggt ggtgggtggc tctcgccgg cmgrcgcgcg cgaggtgatg cggaccacag 360
acgcgcggtt crgctcgccg cccatcggtc ccgtgtmccg gctctggttc

(2) INFORMATION FOR SEQ ID NO:1497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

Val Leu Gln Glu Leu Ile Arg Ser Arg Cys Asp Leu Gln Leu Gln Glu
1 5 10 15
Gln His Gln Ser Pro Lys Pro Pro Trp Pro Pro Thr Pro Arg Cys Cys
20 25 30
Phe Ser Tyr Leu Ser Ser Pro Ser Thr Ser Ser Trp Pro Pro
35 40 45
Asp Val Gly Arg His Ala Gly Ala Arg Gly Ser Arg Gly Arg Gly
50 55 60
Arg Cys Pro Trp Ser Gly Thr Cys Ile Thr
65 70

(2) INFORMATION FOR SEQ ID NO:1498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:

Ala Ser Arg Ile Asp Pro Phe Ala Val Arg Pro Pro Ala Pro Gly Ala
1 5 10 15
Ala Pro Ile Pro Gln Ala Ala Met Ala Ala Asp Pro Thr Leu Leu Leu
20 25 30
Leu Val Pro Phe Leu Ala Ile Pro Leu Tyr Phe Phe Leu Ala Thr Arg
35 40 45
Arg Arg Thr Pro Arg Gly Gly Ala Arg Leu Pro Pro Gly Pro Trp Ala
50 55 60
Leu Pro Val Val Gly His Leu His His Leu Ala Arg Gly Leu Pro His
65 70 75 80
Arg Val Met Arg Xaa Leu Ala Xaa Arg His Gly Pro Leu Met Met Leu
85 90 95
Arg Phe Gly Gly Val Pro Val Val Val Ala Ser Ser Pro Xaa Xaa Ala
100 105 110
Arg Glu Val Met Arg Thr His Asp Ala Ala Phe Xaa Ser Arg Pro Ile
115 120 125
Gly Pro Val Xaa Arg Leu Trp Phe
130 135

(2) INFORMATION FOR SEQ ID NO:1499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..113
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500477
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:
Met Ala Ala Asp Pro Thr Leu Leu Leu Leu Val Pro Phe Leu Ala Ile
1 5 10 15
Pro Leu Tyr Phe Phe Leu Ala Thr Arg Arg Arg Thr Pro Arg Gly Gly
 20 25 30
Ala Arg Leu Pro Pro Gly Pro Trp Ala Leu Pro Val Val Gly His Leu
 35 40 45
His His Leu Ala Arg Gly Leu Pro His Arg Val Met Arg Xaa Leu Ala
50 55 60
Xaa Arg His Gly Pro Leu Met Met Leu Arg Phe Gly Glu Val Pro Val
65 70 75 80
Val Val Ala Ser Ser Pro Xaa Xaa Ala Arg Glu Val Met Arg Thr His
 85 90 95
Asp Ala Ala Phe Xaa Ser Arg Pro Ile Gly Pro Val Xaa Arg Leu Trp
 100 105 110
Phe

(2) INFORMATION FOR SEQ ID NO:1500:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 328 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..328
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500478
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:
cagatcttat cccttccagt tccaggcagc atccccagcc tgacgaagga attgaggacg 60
ctcgagctcg agctacgtca ggrtccaaca ccascatggt tacgggaaca agaggacgtt 120
cgtgctctac ccgtcgctgg gcgtgggcca cctgatcccg atggtggagc tggccaagca 180
ctctctgcgc caccggccacg gcgcgtctcat cgccgtggtc aaccgcgccg acascgagcg 240
cgtgtcgccc gcmgcggtkg agcgctctcgc ggcggycaac ccggccatcg cgttccgcct 300
cctgccggtc ccggccagcc cggagcgc

(2) INFORMATION FOR SEQ ID NO:1501:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..109
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500479
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501:
Gln Ile Leu Ser Leu Pro Val Pro Gly Ser Ile Pro Ser Leu Thr Lys
1 5 10 15
Glu Leu Arg Thr Leu Glu Leu Glu Leu Arg Gln Xaa Pro Thr Pro Xaa
 20 25 30
Trp Leu Arg Glu Gln Glu Asp Val Arg Ala Leu Pro Val Ala Gly Arg
 35 40 45
Gly Pro Pro Asp Pro Asp Gly Gly Ala Gly Gln Ala Pro Leu Ala Pro
50 55 60

Arg Pro Arg Arg Ala His Arg Arg Gly Gln Pro Ala Arg Xaa Arg Arg
65 70 75 80
Arg Val Gly Arg Xaa Gly Xaa Ala Pro Xaa Gly Xaa Gln Pro Gly His
85 90 95
Arg Val Pro Pro Pro Ala Gly Pro Gly Gln Pro Gly Arg
100 105

(2) INFORMATION FOR SEQ ID NO:1502:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1500480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502:

Met Val Glu Leu Ala Lys His Leu Leu Arg His Gly Ala Leu
1 5 10 15
Ile Ala Val Val Asn Pro Pro Asp Xaa Asp Ala Val Ser Ala Xaa Ala
20 25 30
Xaa Glu Arg Leu Xaa Ala Xaa Asn Pro Ala Ile Ala Phe Arg Leu Leu
35 40 45
Pro Val Pro Ala Ser Pro Asp Ala
50 55

(2) INFORMATION FOR SEQ ID NO:1503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 531 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..531

(D) OTHER INFORMATION: / Ceres Seq. ID 1500481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503:

atcaaaactgc acagcttctc ctgcattgcc cttccaggaa tatccacctg gaataaacact 60
tgtacctatg aagagttaga cactagcgcc attccgtaca actaatcttg tggtagtagc 120
atcaaccaat ggtgctgggt gatctacatg ttctgatttt ttgcttcgg gggaagctct 180
gcttatagat cctgtagtga gctctcaggt tcatgcagag cttgcagatc tcattgatgc 240
ctctccaaaa aggttattag ttcttggttac acatcatcat caggatcaca ttgagggtct 300
tcagtcgttt cagagatgca atcctgatgc tgttcttctg acacacccaa gtacaatgga 360
ttgcattggg aaaggaaact ggcagattga ctacacttca gtaactgggt gtgaaaagat 420
atgcataggt taccaagaac tacaaagtgt ttttgcacct ggtcatcacg atggtcatat 480
ggggcttctc catgtaata ccaatacatt gggtgttgga gatcattgtg t

(2) INFORMATION FOR SEQ ID NO:1504:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1500482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504:

Ser Asn Cys Thr Ala Ser Pro Ala Leu Pro Phe Gln Glu Tyr Pro Pro
1 5 10 15

Gly Ile Thr Leu Val Pro Met Lys Ser Arg Thr Leu Ala Pro Phe Arg
20 25 30
Thr Thr Asn Leu Val Val Val Arg Ser Thr Asn Gly Ala Gly Gly Ser
35 40 45
Thr Cys Ser Asp Phe Phe Ala Ser Gly Glu Ala Leu Leu Ile Asp Pro
50 55 60
Gly Cys Ser Ser Gln Val His Ala Glu Leu Ala Asp Leu Ile Asp Ser
65 70 75 80
Leu Pro Lys Arg Leu Leu Val Leu Val Thr His His His Gln Asp His
85 90 95
Ile Glu Gly Leu Ser Val Val Gln Arg Cys Asn Pro Asp Ala Val Leu
100 105 110
Leu Thr His Gln Ser Thr Met Asp Arg Ile Gly Lys Gly Thr Trp Gln
115 120 125
Ile Asp Tyr Thr Ser Val Thr Gly Gly Glu Lys Ile Cys Ile Gly Asp
130 135 140
Gln Glu Leu Gln Val Val Phe Ala Pro Gly His Thr Asp Gly His Met
145 150 155 160
Gly Leu Leu His Val Asn Thr Asn Thr Leu Val Val Gly Asp His Cys
165 170 175

(2) INFORMATION FOR SEQ ID NO:1505:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1500483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1505:

Met Lys Ser Arg Thr Leu Ala Pro Phe Arg Thr Thr Asn Leu Val Val
1 5 10 15
Val Arg Ser Thr Asn Gly Ala Gly Gly Ser Thr Cys Ser Asp Phe Phe
20 25 30
Ala Ser Gly Glu Ala Leu Leu Ile Asp Pro Gly Cys Ser Ser Gln Val
35 40 45
His Ala Glu Leu Ala Asp Leu Ile Asp Ser Leu Pro Lys Arg Leu Leu
50 55 60
Val Leu Val Thr His His His Gln Asp His Ile Glu Gly Leu Ser Val
65 70 75 80
Val Gln Arg Cys Asn Pro Asp Ala Val Leu Thr His Gln Ser Thr
85 90 95
Met Asp Arg Ile Gly Lys Gly Thr Trp Gln Ile Asp Tyr Thr Ser Val
100 105 110
Thr Gly Gly Glu Lys Ile Cys Ile Gly Asp Gln Glu Leu Gln Val Val
115 120 125
Phe Ala Pro Gly His Thr Asp Gly His Met Gly Leu Leu His Val Asn
130 135 140
Thr Asn Thr Leu Val Val Gly Asp His Cys
145 150

(2) INFORMATION FOR SEQ ID NO:1506:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 555 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..555

(D) OTHER INFORMATION: / Ceres Seq. ID 1500487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506:

gactccacgc	cgccagtcac	gaccacgccc	cgctccgcc	tggaaccctt	tagccgagcg	60
gasaagggaa	gaaatgggga	agggtagcgg	cagcttcggc	aagcgccgga	acaagacgca	120
cacgctctgc	atccgctgcg	cgcccgccgc	tggagcgggc	gcgtcaagaa	cccggatcta	180
aatcgggcgc	ccagcccgca	gagctccgac	gccgagtgac	atgagaagcg	agcgagcagc	240
agcagacgca	gccacgcgaa	aggctcaacg	acgacgacgt	ccgttggtgc	gacgcgcccc	300
agcgacagat	gcgctgtctg	tcttctgttc	tatccacgta	cgtacgacgg	cccagctgac	360
ccgcttgctc	acccgtccgt	tctgtgcgac	tggatgggtc	gtcggcgggc	gtcgcggcgca	420
gggctttcgg	taegtctgtg	ataagcacga	ggggagggcg	ggcagggcgg	aacggagggc	480
gagggcgccg	ccccaaagtg	cggtctttcc	aaatgtcaaa	aaggacagct	gtaacagtga	540
taagaaaaac	aagtc					

(2) INFORMATION FOR SEQ ID NO:1507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1500488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507:

Asp	Ser	Thr	Pro	Pro	Val	Thr	Thr	Pro	Arg	Leu	Arg	Leu	Glu	Pro
1				5				10					15	
Phe	Ser	Arg	Ala	Xaa	Lys	Gly	Arg	Asn	Gly	Glu	Gly	Tyr	Gly	Gln
								20					25	
Arg	Gln	Ala	Pro	Glu	Gln	Asp	Ala	His	Ala	Leu	His	Pro	Leu	Arg
				30				35					40	
Pro	Ala	Trp	Ser	Gly	Arg	Val	Lys	Asn	Pro	Asp	Leu	Asn	Arg	Ala
				45				50					55	
Ser	Pro	Glu	Ser	Ser	Asp	Ala	Glu						60	
65								70						

(2) INFORMATION FOR SEQ ID NO:1508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1500489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508:

Thr	Pro	Arg	Arg	Gln	Ser	Arg	Pro	Arg	Arg	Ala	Ser	Ala	Trp	Asn	Pro
1				5									10		
Leu	Ala	Glu	Arg	Xaa	Arg	Glu	Glu	Met	Gly	Lys	Gly	Thr	Gly	Ser	Phe
								20					25		
Gly	Lys	Arg	Arg	Asn	Lys	Thr	His	Thr	Leu	Cys	Ile	Arg	Cys	Gly	Gly
				30				35					40		
Arg	Arg	Gly	Ala	Gly	Ala	Ser	Arg	Thr	Arg	Ile					
				45				50					55		

(2) INFORMATION FOR SEQ ID NO:1509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..111
(D) OTHER INFORMATION: / Ceres Seq. ID 1500490
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509:
Met Arg Ser Glu Arg Ala Ala Ala Ala Ala Thr Ala Lys Ala Gln
1 5 10 15
Arg Arg Arg Arg Pro Leu Leu Arg Arg Arg Pro Ala Gln His Ala Ala
20 25 30
Val Val Phe Val Arg Ile His Val Arg Thr Thr Ala Gln Leu Thr Arg
35 40 45
Leu Pro Thr Arg Pro Phe Cys Ala Thr Gly Trp Ser Val Gly Gly Arg
50 55 60
Arg Gly Glu Gly Phe Arg Tyr Val Val Asp Lys His Glu Gly Arg Ala
65 70 75 80
Gly Arg Arg Glu Arg Arg Arg Arg Arg Pro Gln Val Ala Val Phe
85 90 95
Pro Asn Val Lys Lys Asp Ser Cys Asn Ser Asp Lys Lys Asn Lys
100 105 110

(2) INFORMATION FOR SEQ ID NO:1510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..825
(D) OTHER INFORMATION: / Ceres Seq. ID 1500491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510:

attaaaaagc taatatggct actaggaag agagagataa gtatagatca gtccttgaag 60
atgcatagaca ggttcaatgg aggtatgata accctccaga ctccaatagt gtgaaccagc 120
tctttgaaga aggccagact aaggtgtggc cagaagggtc gttagaagag acagtgcaaa 180
acgcatgcaa gtcattggag atggagtctt cacataagat ccgtttacag gacttcaaga 240
ctataaacc tgagaagttt aagctctttg tcaatgggtt atcagctgaa gagacgttta 300
ggcttgggag ttacaatgct ttgctcaaga actctttgcc tgaagagttt cagtactata 360
agcccgagga agagagcttt gactcatcac atgacgcctt tagatctgct ttaccacgag 420
gggttgggag ggaaatactc tctgtgtact cggggccgcc tggttatagc ttcaaattta 480
gacactgggg atactttgaa ggaactttca aaggtcatgc tcctactggg gaaatggttc 540
aattctctggg tctaggagtt ctaaaagttg acgaatcact tagagcagag gagattgaga 600
tttactatga tccaggagag ctgttccggg gactactcaa gggacctcct atatcagaga 660
ccaaaaccac agacagtggg gacaaacact cagagaaaca aagctgccca ttcacacact 720
aagataataa gaaaagcaga agtgtatttg accctttaa gaatatattg taacagtctc 780
ttggttattg atgcatggaa taaattataa gttatgttag gcgcgc

(2) INFORMATION FOR SEQ ID NO:1511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..173
(D) OTHER INFORMATION: / Ceres Seq. ID 1500492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1511:

Met Glu Phe Ser His Lys Lys Arg Leu Gln Asp Phe Lys Thr Ile Asn

1	5	10	15
Pro Glu Lys Phe Lys Leu Phe Val Asn Gly Leu Ser Ala Glu Glu Thr	20	25	30
Leu Arg Leu Gly Ser Tyr Asn Ala Leu Lys Asn Ser Leu Pro Glu	35	40	45
Glu Phe Gln Tyr Tyr Lys Pro Glu Glu Ser Phe Glu Ser Ser His	50	55	60
Asp Ala Phe Arg Ser Ala Leu Pro Arg Gly Phe Ala Trp Glu Ile Leu	65	70	75
Ser Val Tyr Ser Gly Pro Pro Val Ile Ala Phe Lys Phe Arg His Trp	85	90	95
Gly Tyr Phe Glu Gly Thr Phe Lys Gly His Ala Pro Thr Gly Glu Met	100	105	110
Val Gln Phe Leu Gly Leu Gly Val Leu Lys Val Asp Glu Ser Leu Arg	115	120	125
Ala Glu Glu Ile Glu Ile Tyr Tyr Asp Pro Gly Glu Leu Phe Gly Gly	130	135	140
Leu Leu Lys Gly Pro Pro Ile Ser Glu Thr Lys Thr Thr Asp Ser Gly	145	150	155
Asp Asn Thr Ala Glu Lys Gln Ser Cys Pro Phe Thr His	165	170	

(2) INFORMATION FOR SEQ ID NO:1512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 668 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..668

(D) OTHER INFORMATION: / Ceres Seq. ID 1500495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512:

agttacttact	cactctcccc	ccaccgcgc	caggccagac	agactaactg	agcaccgcgt	60
gcaaggagtc	cgcgcccatg	gcgagcacc	acatggcgct	ggccacctcg	cggttcacgc	120
tggccgcggg	cggtgccacc	ggcagcagcg	gcggcccgct	caacttcgcc	tcggcgccca	180
accgcgttgg	caggaggctc	gtggcccggg	ccgacaacga	ggccgcgcga	gctgaggcgg	240
cggaagggga	gggtgcgctg	gccaccaagc	ccaaggccga	gaagccgcgc	ccgatcgggc	300
ccaatagggg	cgccaagggt	aagatcccta	ggaggggatc	ctactgggtac	aacgggatcg	360
cgcaactcgat	caccgtcgat	caggatccca	acaccgccta	cccgggtggt	gtcggttcca	420
acaaggtgaa	ctacgcgcgc	gtgtccacca	acaactacgc	cttgagcagag	gctttagagg	480
tgaatagagt	ggggccggcc	ggctcaaggg	tcgcgcgtag	ctaccgtgtg	attgatttgt	540
agtagttgtg	aaataggctg	gtgaagctgc	atgctgtgct	ggctagcgctc	acaacatcga	600
tcctatgtgt	aatagcataa	tccacataat	catatcatgt	aattgcttgc	tttattcacc	660
gtgtactc						

(2) INFORMATION FOR SEQ ID NO:1513:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1500496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513:

Met Ala Ser Thr Asn Met Ala Ser Ala Thr Ser Arg Phe Met Leu Ala	5	10	15
Ala Gly Val Pro Thr Gly Ser Ser Gly Gly Arg Val Asn Phe Ala Ser	20	25	30

Ala Pro Asn Arg Leu Gly Arg Arg Leu Val Ala Arg Ala Asp Asn Glu
35 40 45
Ala Ala Ala Ala Glu Ala Ala Glu Gly Glu Gly Ala Val Ala Thr Lys
50 55 60
Pro Lys Ala Glu Lys Pro Pro Ile Gly Pro Asn Arg Gly Ala Lys
65 70 75 80
Val Lys Ile Leu Arg Arg Glu Ser Tyr Trp Tyr Asn Gly Ile Gly Asn
85 90 95
Val Val Thr Val Asp Gln Asp Pro Asn Thr Arg Tyr Pro Val Val Val
100 105 110
Arg Phe Asn Lys Val Asn Tyr Ala Gly Val Ser Thr Asn Asn Tyr Ala
115 120 125
Leu Asp Glu Val Leu Glu Val Lys
130 135

(2) INFORMATION FOR SEQ ID NO:1514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514:

Met Ala Ser Ala Thr Ser Arg Phe Met Leu Ala Ala Gly Val Pro Thr
1 5 10 15
Gly Ser Ser Gly Gly Arg Val Asn Phe Ala Ser Ala Pro Asn Arg Leu
20 25 30
Gly Arg Arg Leu Val Ala Arg Ala Asp Asn Glu Ala Ala Ala Glu
35 40 45
Ala Ala Glu Gly Glu Gly Ala Val Ala Thr Lys Pro Lys Ala Glu Lys
50 55 60
Pro Pro Pro Ile Gly Pro Asn Arg Gly Ala Lys Val Lys Ile Leu Arg
65 70 75 80
Arg Glu Ser Tyr Trp Tyr Asn Gly Ile Gly Asn Val Val Thr Val Asp
85 90 95
Gln Asp Pro Asn Thr Arg Tyr Pro Val Val Val Arg Phe Asn Lys Val
100 105 110
Asn Tyr Ala Gly Val Ser Thr Asn Asn Tyr Ala Leu Asp Glu Val Leu
115 120 125
Glu Val Lys
130

(2) INFORMATION FOR SEQ ID NO:1515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515:

Met Leu Ala Ala Gly Val Pro Thr Gly Ser Ser Gly Arg Val Asn
1 5 10 15
Phe Ala Ser Ala Pro Asn Arg Leu Gly Arg Arg Leu Val Ala Arg Ala
20 25 30
Asp Asn Glu Ala Ala Ala Ala Glu Ala Ala Glu Gly Glu Ala Val

35	40	45
Ala Thr Lys Pro Lys Ala Glu Lys Pro Pro Pro Ile Gly Pro Asn Arg		
50	55	60
Gly Ala Lys Val Lys Ile Leu Arg Arg Glu Ser Tyr Trp Tyr Asn Gly		
65	70	75
Ile Gly Asn Val Val Thr Val Asp Gln Asp Pro Asn Thr Arg Tyr Pro		
85	90	95
Val Val Val Arg Phe Asn Lys Val Asn Trp Ala Gly Val Ser Thr Asn		
100	105	110
Asn Tyr Ala Leu Asp Glu Val Leu Glu Val Lys		
115	120	

(2) INFORMATION FOR SEQ ID NO:1516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..425
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516:

gacaacacccg cgcgcgcaat acacgggaca cacacgcaga tccgagctaa ccaccatcga	60
cgagcgccas cgccagcagc cgagccggag cgacccctttc tttttctttt tacacagcgg	120
gcggagaaaa ggagtcacatc agccaaagcc acccaccgct ttaccaccac gatcggcggt	180
gccgcgcgcta ccattgtcgg ctccagctcc atccaaatcc accgccagca agcaagcaag	240
caagccggcg ccattgggtct gccgatgagg agggagaggg acgcggaggg ggagctgaac	300
ctgcgcgcgg ggttccggtt ccaccccacc gacgacgagc tgggtggagca ctacctgtgc	360
cgcaaggggc ggggcagcgc ctccccgtgc ccatcatgc cgaggtggac ctgtacaggt	420
tcgac	

(2) INFORMATION FOR SEQ ID NO:1517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517:

Asp Asn Thr Ala Arg Ala Ile His Gly Thr His Thr Gln Ile Arg Ala	
1	15
Asn His His Arg Arg Ala Pro Xaa Pro Ala Ala Glu Pro Asp Arg Pro	
20	30
Phe Leu Phe Ser Phe Thr Gln Arg Asp Gly Glu Arg Ser Gln Ser Ala	
35	45
Lys Ala Thr His Arg Phe Tyr Pro Pro Ile Gly Val Ala Ala Ala Ser	
50	60
Ile Val Gly Phe Ser Ser Ile Gln Ile His Arg Gln Gln Ala Ser Lys	
65	80
Gln Ala Gly Ala Met Gly Leu Pro Met Arg Arg Glu Arg Asp Ala Glu	
85	95
Ala Glu Leu Asn Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Asp	
100	110
Glu Leu Val Glu His Tyr Leu Xaa Arg Lys Gly Arg Gly Ser Ala Ser	
115	125
Pro Cys Pro Ser Ser Pro Arg Trp Thr Cys Thr Gly Ser	
130	140

(2) INFORMATION FOR SEQ ID NO:1518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518:

Thr	Thr	Pro	Arg	Ala	Gln	Tyr	Thr	Gly	His	Thr	Arg	Arg	Ser	Glu	Leu
1				5				10						15	
Thr	Thr	Ile	Asp	Glu	Arg	Xaa	Arg	Gln	Gln	Pro	Ser	Arg	Thr	Asp	Leu
			20					25					30		
Phe	Phe	Phe	Leu	Leu	His	Ser	Gly	Thr	Glu	Lys	Gly	Val	Asn	Gln	Pro
		35					40					45			
Lys	Pro	Pro	Thr	Ala	Phe	Thr	His	Arg	Ser	Ala	Leu	Pro	Pro	Leu	Ala
		50				55					60				
Leu	Ser	Ala	Ser	Ala	Pro	Ser	Lys	Ser	Thr	Ala	Ser	Lys	Gln	Ala	Ser
		65			70				75					80	
Lys	Pro	Ala	Pro	Trp	Val	Cys	Arg								
						85									

(2) INFORMATION FOR SEQ ID NO:1519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..493
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519:

atttctcttg	ctctctccct	ccaccagcat	ccctgagtct	gccatgggca	actgctgggg	60
aaccaagatt	agctctgaca	cgcgcgcctc	cccttccaca	tcaccgttcc	ctcgcagcga	120
gggtgagatt	ctccgggtgtg	ccaatgtcag	gagcttcacc	ttgacggagc	tgatgacctc	180
cacccggaac	ttccggcccg	acagcgtcct	cggcgaggga	ggcttcggct	ccgtcttcaa	240
ggggtggatc	gacgagacca	ctctcgcccc	ggccaggccc	ggcacaggga	tggctcatcg	300
tgtcaagaag	ctcaaccagc	agggattgca	ggggcacagg	gagtggtgtg	ctgaagtcaa	360
ctacctgggc	cagttgtctc	amcccgatct	cgtaargctc	gtagggtact	gcctccaaga	420
cgagcagcgc	cttctcgctc	acgagttcat	gccgcgarga	agcttkgaga	accatctttt	480
caggacctca	cgt					

(2) INFORMATION FOR SEQ ID NO:1520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1520:

Phe	Phe	Leu	Pro	Pro	Ser	Thr	Ser	Ile	Pro	Glu	Ser	Ala	Met	Gly
1				5				10					15	
Asn	Cys	Trp	Gly	Thr	Lys	Ile	Ser	Ser	Asp	Thr	Ala	Ala	Ser	Pro
			20					25					30	

Thr Ser Pro Phe Pro Arg Ser Glu Gly Glu Ile Leu Arg Cys Ala Asn
35 40 45
Val Arg Ser Phe Thr Leu Thr Glu Leu Met Thr Ser Thr Arg Asn Phe
50 55 60
Arg Pro Asp Ser Val Leu Gly Glu Gly Gly Phe Gly Ser Val Phe Lys
65 70 75 80
Gly Trp Ile Asp Glu Thr Thr Phe Ala Pro Ala Arg Pro Gly Thr Gly
85 90 95
Met Val Ile Ala Val Lys Lys Leu Asn Gln Gln Gly Leu Gln Gly His
100 105 110
Arg Glu Trp Leu Ala Glu Val Asn Tyr Leu Gly Gln Leu Ser Xaa Pro
115 120 125
Ser Leu Val Xaa Leu Val Gly Tyr Cys Leu Gln Asp Glu Gln Arg Leu
130 135 140
Leu Val Tyr Glu Phe Met Pro Arg Xaa Ser Xaa Glu Asn His Leu Phe
145 150 155 160
Arg Thr Ser Arg

(2) INFORMATION FOR SEQ ID NO:1521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1500506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1521:

Met Gly Asn Cys Trp Gly Thr Lys Ile Ser Ser Asp Thr Ala Ala Ser
1 5 10 15
Pro Ser Thr Ser Pro Phe Pro Arg Ser Glu Gly Glu Ile Leu Arg Cys
20 25 30
Ala Asn Val Arg Ser Phe Thr Leu Thr Glu Leu Met Thr Ser Thr Arg
35 40 45
Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly Gly Phe Gly Ser Val
50 55 60
Phe Lys Gly Trp Ile Asp Glu Thr Thr Phe Ala Pro Ala Arg Pro Gly
65 70 75 80
Thr Gly Met Val Ile Ala Val Lys Lys Leu Asn Gln Gln Gly Leu Gln
85 90 95
Gly His Arg Glu Trp Leu Ala Glu Val Asn Tyr Leu Gly Gln Leu Ser
100 105 110
Xaa Pro Ser Leu Val Xaa Leu Val Gly Tyr Cys Leu Gln Asp Glu Gln
115 120 125
Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Xaa Ser Xaa Glu Asn His
130 135 140
Leu Phe Arg Thr Ser Arg
145 150

(2) INFORMATION FOR SEQ ID NO:1522:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1500507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1522:
Met Thr Ser Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly
1 5 10 15
Gly Phe Gly Ser Val Phe Lys Gly Trp Ile Asp Glu Thr Thr Phe Ala
20 25 30
Pro Ala Arg Pro Gly Thr Gly Met Val Ile Ala Val Lys Lys Leu Asn
35 40 45
Gln Gln Gly Leu Gln Gly His Arg Glu Trp Leu Ala Glu Val Asn Tyr
50 55 60
Leu Gly Gln Leu Ser Xaa Pro Ser Leu Val Xaa Leu Val Gly Tyr Cys
65 70 75 80
Leu Gln Asp Glu Gln Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Xaa
85 90 95
Ser Xaa Glu Asn His Leu Phe Arg Thr Ser Arg
100 105

(2) INFORMATION FOR SEQ ID NO:1523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523:

acgaacccaa	ccacgtcgaa	ccacctcgcc	agtgagcgcc	ccctcccgct	cctctttccc	60
tgctggccac	aactccgaat	gaatcgcgtg	ctccaccagc	ttcttttacc	ttcagcaagc	120
gagccggtag	catcaagcta	gatcgcgagg	aagctcctcg	ttcccccat	cgcgctgctg	180
ctggcgggga	gaagcgtcct	ctcacgcggg	cggggaagac	caatccgcgc	cgccagtcce	240
tgccgcggtc	tcgctgaggt	ggctctggct	cctggggcgg	cgtgttcgtg	gcggccggcg	300
agatgagcac	ccacgcggtt	ggaacaagca	acggcgcgatc	cggtgatcgc	gcgcgggggg	360
gcgcggcgac	gaggaaacac	aggatgccca	aatattccaa	gttcacacag	caggagctgc	420
ccgcttkcaa	gcgattcttt	actccaaaat	gggttgtctc	tgt		

(2) INFORMATION FOR SEQ ID NO:1524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524:

Thr Asn Pro Thr Gln Ser Asn His Leu Ala Ser Glu Arg Pro Pro Pro
1 5 10 15
Val Leu Phe Pro Cys Trp Pro Glu Leu Arg Met Lys Ser Leu Leu His
20 25 30
Gln Leu Ser Leu Pro Ser Ala Ser Glu Pro Val Ala Ser Ser
35 40 45

(2) INFORMATION FOR SEQ ID NO:1525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..53
(D) OTHER INFORMATION: / Ceres Seq. ID 1500518
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525:
Met Ser Ser His Ala Val Gly Thr Ser Asn Gly Gly Ser Gly Asp Ala
1 5 10 15
Ala Ala Gly Gly Ala Ala Arg Arg Asn Thr Arg Met Pro Lys Tyr Ser
20 25 30
Lys Phe Thr Gln Gln Glu Leu Pro Ala Xaa Lys Pro Ile Leu Thr Pro
35 40 45
Lys Trp Val Val Ser
50

(2) INFORMATION FOR SEQ ID NO:1526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..39

(D) OTHER INFORMATION: / Ceres Seq. ID 1500519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1526:

Met Arg Pro Pro Gly Ala Arg Pro Gly Gly Thr Pro Gly Cys Pro Asn
1 5 10 15
Ile Pro Ser Ser His Ser Arg Ser Cys Pro Leu Xaa Ser Arg Phe Leu
20 25 30
Leu Gln Asn Gly Leu Ser Leu
35

(2) INFORMATION FOR SEQ ID NO:1527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..535

(D) OTHER INFORMATION: / Ceres Seq. ID 1500539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1527:

tgggatgaaag ccgtggttat gttaccgtga ctacgactgt aacttcaact ccgacatatt 60
cggttgagttt gctaccgata tcgcatcgaa aatggtggat ggtccacgac gccatgccac 120
aggaaacttca ccaattctgt tacttgcat ccaagcaaaa ggcacagctg gaatatgac 180
gccggcaagc agaggccgca aattatgccg acggtcattg gaaaataaga gtaaaggacc 240
cgagattcaa aatttgcatc gacaaattat gtaattggaa aagtatgctg cggcattggg 300
gcgaatacaaa ttggactgac tacgagtcct ttgttccac ccaccagcc attaccgtag 360
accggagatc atcaattccc ggccataact tgtgacgcaa taattataca tactatttaa 420
tggatttcac gagttttttg gtttgaattg ttgctgcgag attagtgaa tatcagttgt 480
gtaactatat ctttttccta tagttttgtc aaattgaata aaacattttt ttgcg

(2) INFORMATION FOR SEQ ID NO:1528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1500540
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1528:
Gly Met Lys Pro Trp Leu Cys Tyr Arg Asp Tyr Asp Cys Asn Phe Asn
1 5 10 15
Ser Asp Ile Phe Val Glu Phe Ala Thr Asp Ile Ala Ser Lys Met Val
20 25 30
Asp Gly Pro Arg Arg His Ala Thr Gly Thr Ser Pro Ile Leu Leu Leu
35 40 45
Ala Ile Gln Ala Lys Gly Thr Ala Gly Ile
50 55
(2) INFORMATION FOR SEQ ID NO:1529:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 98 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..98
(D) OTHER INFORMATION: / Ceres Seq. ID 1500541
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1529:
Met Val His Asp Ala Met Pro Gln Glu Leu His Gln Phe Cys Tyr Leu
1 5 10 15
Arg Ser Lys Gln Lys Ala Gln Leu Glu Tyr Asp Arg Arg Gln Ala Glu
20 25 30
Ala Ala Asn Tyr Ala Asp Gly His Trp Lys Ile Arg Val Lys Asp Pro
35 40 45
Arg Phe Lys Ile Cys Ile Asp Lys Leu Cys Asn Trp Lys Ser Met Leu
50 55 60
Arg His Trp Gly Glu Ser Asn Trp Thr Asp Tyr Glu Ser Phe Val Pro
65 70 75 80
Thr Pro Pro Ala Ile Thr Val Asp Arg Arg Ser Ser Leu Pro Gly His
85 90 95
Asn Leu

(2) INFORMATION FOR SEQ ID NO:1530:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..93
(D) OTHER INFORMATION: / Ceres Seq. ID 1500542
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530:
Met Pro Gln Glu Leu His Gln Phe Cys Tyr Leu Arg Ser Lys Gln Lys
1 5 10 15
Ala Gln Leu Glu Tyr Asp Arg Arg Gln Ala Glu Ala Ala Asn Tyr Ala
20 25 30
Asp Gly His Trp Lys Ile Arg Val Lys Asp Pro Arg Phe Lys Ile Cys
35 40 45
Ile Asp Lys Leu Cys Asn Trp Lys Ser Met Leu Arg His Trp Gly Glu
50 55 60
Ser Asn Trp Thr Asp Tyr Glu Ser Phe Val Pro Thr Pro Pro Ala Ile
65 70 75 80
Thr Val Asp Arg Arg Ser Ser Leu Pro Gly His Asn Leu
85 90
(2) INFORMATION FOR SEQ ID NO:1531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1530 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1530
(D) OTHER INFORMATION: / Ceres Seq. ID 1500554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531:

atcgctgctt	tctatttttt	cttctttctt	cgatttcata	ccaaaacaag	aactctctgt	60
tttcgacaaa	aacgaaacct	tgagatctat	tttgattgac	ttttaagaaa	gagagagatc	120
tttcttagaa	gattttgtct	cgctcgccatt	gaagatccag	ggtttgtctt	tcgaaattca	180
gagagaaaaa	gggtgatgag	cgagagatca	aggaacattt	aaagccacaa	gcttcatctg	240
aaacaatgga	caagaaacat	aattgtgaaag	ggaagaggtt	atggcagaaa	gtcaagtata	300
aattggtgga	gtttcatcca	ttgcctgctt	atttaagaga	caatgagtag	atcatctggc	360
attaccagct	cgaatggccg	atcaaacaga	ttctcttcag	catctttacc	attcataatg	420
agactttgaa	tgtttgagcg	cacttgattg	ggtttttcct	gtttttggcg	ctcaactata	480
acactgcaac	gaaagtaccg	agtgctcggtg	atcttcatct	gcttcaacac	cgtttaccgc	540
atttgttgag	gaaaaacagat	ctccacaaaac	ttcattctga	gctcatggct	cgcttctctt	600
ctagtcacat	tagttggcat	gtgatggacc	ttctttataa	ctgtttgcct	gaaagatttt	660
ctcatggcaa	ctacactgac	atgtgtgttc	tgcatctctg	gagggaaagt	cttgcaaaact	720
tgatagctcc	tttgatcttc	aggccaatta	ctcgatggcc	gttttatgca	tttctagggt	780
gtgctatgtt	ctgtctatta	gcaagcagca	cgctgcaacct	ctctctatgt	catcccgagc	840
gagctctcta	cataatgctt	aggctttatt	acgcgcggcat	cgcagctctat	atagcgcatt	900
ctcttcaacc	tcgggtttat	tactctctta	tgtgtgatcc	ttcttcttgc	aacctctact	960
taggattcat	aaccacttta	ggaatcgcca	ctgtgcttgt	ttctctctcc	ccggtttctc	1020
aaagcccgga	gtttcggttg	gtgaggcgct	ctctgttctt	tggaatggga	ttctctggtt	1080
tagctccgat	ttctcaacag	ctgataatct	tttgggacca	acctgaagcc	cttccacaga	1140
caggttatga	gattttgatg	ggtttgcctt	atgggttagg	agctctgtgt	tatgcaacta	1200
ggatcccgca	gagatggatg	ccgggtaaat	tcgatatagc	aggacatagc	catcagttgt	1260
ttcatgttct	ggttgttctg	gtgcgttcaac	gcactataga	gctgggctag	tgtatcttaa	1320
gtggagagat	atygaagatg	gttgaagatg	aagattgaag	attagatgga	atctttgaat	1380
cttggtttgta	gtagcttcat	ataaaaagttg	gattatgtaa	agtcctatat	gtaatcaaac	1440
gtttaattgt	ttcctttatt	caacaaaagga	tttatattgt	taatccacat	atgtattact	1500
gggttaagaa	gctggaaggt	tcataatttt				

(2) INFORMATION FOR SEQ ID NO:1532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..373
(D) OTHER INFORMATION: / Ceres Seq. ID 1500555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532:

Met	Gly	Asp	Glu	Ala	Glu	Ile	Lys	Glu	His	Leu	Lys	Pro	Gln	Ala	Ser
1			5					10					15		
Ser	Glu	Thr	Met	Asp	Lys	Lys	His	Asn	Val	Lys	Gly	Lys	Arg	Leu	Trp
			20					25					30		
Gln	Lys	Val	Lys	Tyr	Gln	Leu	Val	Glu	Phe	His	Ser	Leu	Pro	Ala	Tyr
			35					40					45		
Leu	Arg	Asp	Asn	Glu	Tyr	Ile	Ile	Gly	His	Tyr	Arg	Ser	Glu	Trp	Pro
			50					55					60		
Ile	Lys	Gln	Ile	Leu	Leu	Ser	Ile	Phe	Thr	Ile	His	Asn	Glu	Thr	Leu
			65					70					75		
Asn	Val	Trp	Thr	His	Leu	Ile	Gly	Phe	Phe	Leu	Phe	Leu	Ala	Leu	Thr
			85					90					95		

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Ile Tyr Thr Ala Thr Lys Val Pro Ser Val Val Asp Leu His Ser Leu
      100                      105                      110
Gln His Arg Leu Pro Asp Leu Leu Arg Lys Thr Asp Leu His Lys Leu
      115                      120                      125
His Ser Glu Leu Met Ala Arg Leu Pro Ser Ser Pro Ser Ser Trp His
      130                      135                      140
Val Met Asp Leu Leu Tyr Asn Cys Leu Pro Glu Arg Phe Ser His Gly
145                      150                      155                      160
Asn Tyr Thr Asp Met Cys Val Leu His Ser Val Arg Glu Asp Leu Ala
      165                      170                      175
Asn Leu Ile Ala Pro Leu Ile Phe Arg Pro Ile Thr Arg Trp Pro Phe
      180                      185                      190
Tyr Ala Phe Leu Gly Gly Ala Met Phe Cys Leu Leu Ala Ser Ser Thr
      195                      200                      205
Cys His Leu Leu Ser Cys His Ser Glu Arg Val Ser Tyr Ile Met Leu
210                      215                      220
Arg Leu Tyr Tyr Ala Gly Ile Ala Ala Leu Ile Ala Thr Ser Phe Tyr
225                      230                      235                      240
Pro Pro Val Tyr Tyr Ser Phe Met Cys Asp Pro Phe Phe Cys Asn Leu
      245                      250                      255
Tyr Leu Gly Phe Ile Thr Ile Leu Gly Ile Ala Thr Val Leu Val Ser
260                      265                      270
Leu Leu Pro Val Phe Gln Ser Pro Glu Phe Arg Val Val Arg Ala Ser
275                      280                      285
Leu Phe Phe Gly Met Gly Phe Ser Gly Leu Ala Pro Ile Leu His Lys
290                      295                      300
Leu Ile Ile Phe Trp Asp Gln Pro Glu Ala Leu His Thr Thr Gly Tyr
305                      310                      315                      320
Glu Ile Leu Met Gly Leu Leu Tyr Gly Leu Gly Ala Leu Val Tyr Ala
      325                      330                      335
Thr Arg Ile Pro Glu Arg Trp Met Pro Gly Lys Phe Asp Ile Ala Gly
340                      345                      350
His Ser His Gln Leu Phe His Val Leu Val Val Leu Val Arg Ser Arg
355                      360                      365
Thr Ile Glu Leu Gly
370

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(2) INFORMATION FOR SEQ ID NO:1533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1500556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533:

```

Met Asp Lys Lys His Asn Val Lys Gly Lys Arg Leu Trp Gln Lys Val
1      5      10      15
Lys Tyr Gln Leu Val Glu Phe His Ser Leu Pro Ala Tyr Leu Arg Asp
      20      25      30
Asn Glu Tyr Ile Ile Gly His Tyr Arg Ser Glu Trp Pro Ile Lys Gln
35      40      45
Ile Leu Leu Ser Ile Phe Thr Ile His Asn Glu Thr Leu Asn Val Trp
50      55      60
Thr His Leu Ile Gly Phe Phe Leu Phe Leu Ala Leu Thr Ile Tyr Thr
65      70      75      80
Ala Thr Lys Val Pro Ser Val Val Asp Leu His Ser Leu Gln His Arg
      85      90      95
Leu Pro Asp Leu Leu Arg Lys Thr Asp Leu His Lys Leu His Ser Glu

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Met	Ala	Arg	Leu	Pro	Ser	Ser	Pro	Ser	Ser	Trp	His	Val	Met	Asp	Leu
1			5						10					15	
Leu	Tyr	Asn	Cys	Leu	Pro	Glu	Arg	Phe	Ser	His	Gly	Asn	Tyr	Thr	Asp
		20						25					30		
Met	Cys	Val	Leu	His	Ser	Val	Arg	Glu	Asp	Leu	Ala	Asn	Leu	Ile	Ala
		35					40					45			
Pro	Leu	Ile	Phe	Arg	Pro	Ile	Thr	Arg	Trp	Pro	Phe	Tyr	Ala	Phe	Leu
		50				55					60				
Gly	Gly	Ala	Met	Phe	Cys	Leu	Leu	Ala	Ser	Ser	Thr	Cys	His	Leu	Leu
65					70					75				80	
Ser	Cys	His	Ser	Glu	Arg	Val	Ser	Tyr	Ile	Met	Leu	Arg	Leu	Tyr	Tyr
			85					90						95	
Ala	Gly	Ile	Ala	Ala	Leu	Ile	Ala	Thr	Ser	Phe	Tyr	Pro	Pro	Val	Tyr
			100					105					110		
Tyr	Ser	Phe	Phe	Cys	Asp	Pro	Phe	Phe	Cys	Asn	Leu	Tyr	Leu	Gly	Phe
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:1535:

(A) LENGTH: 660 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY: -
(B) LOCATION: 1..660
(D) OTHER INFORMATION:

(X1) SEQUENCE DEPENDENT						
atccaattat	tctatggagt	catctttctt	actcctctat	caactctcat	tctcttaact	60
taatccaaaa	tttggaaaaa	gaccttttgg	ttcttatcca	ttaatgcaga	gtctgcgaaa	120
atgcaaacaa	actcgcattt	gttctaacaa	gagtatgtgt	cccggctttg	gagaagcttc	180
accggagagt	aaggcagcga	agcatcttca	tgactcttct	actactgctg	cagtggagat	240
agtgtctgct	cagctttgaga	gttataatac	tgaggcttat	atggagttga	gagaaatttc	300
agatacaaac	tctgtaagtgt	accggtgata	attctgcgc	actctcatgc	gtctgccttc	360
acgtcacatg	acttgatgcc	tctgaattat	agaggtaacg	tctgtctatg	gtaaaacaag	420
tttgtaattg	gataatatga	agcgcctcgc	cttcaagaac	gtagatgatt	ccaacacaa	480
actcatgctc	gtagactcgt	ttggagactc	ccaatgcgaa	actgactgct	ataaagtgaa	540
ccgaaatctc	ctctgaatca	cattcatata	tatagagtct	tgtagagata	cacacttgaa	600
acgttttata	catcataata	catacattat	tgtatgttta	ctccgaagtt	ttgatacctt	660

(A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(A) NAME/KEY: peptide
(B) LOCATION: 1..178
(D) OTHER INFORMATION

Ser	Asn	Ile	Ser	Met	Glu	Ser	Ser	Ser	Ser	Leu	Leu	His	His	Ser	Tyr
1				5					10					15	
Leu	Ser	Tyr	Leu	Asn	Pro	Lys	Phe	Gly	Lys	Arg	Pro	Leu	Val	Ser	Tyr
			20					25					30		
Pro	Leu	Met	Gln	Ser	Ser	Arg	Lys	Cys	Lys	Gln	Thr	Arg	Ile	Cys	Ser
			35				40					45			
Asn	Lys	Met	Tyr	Val	Pro	Gly	Phe	Gly	Glu	Ala	Ser	Pro	Glu	Ala	Lys
			50			55					60				
Ala	Ala	Lys	His	Leu	His	Asp	Phe	Phe	Thr	Tyr	Val	Val	Ala	Arg	Ile

65					70					75					80
Val	Ser	Ala	Gln	Leu	Glu	Ser	Tyr	Asn	Pro	Glu	Ala	Tyr	Met	Glu	Leu
				85					90					95	
Arg	Glu	Phe	Leu	Asp	Thr	Asn	Ser	Val	Ser	Asp	Gly	Asp	Lys	Phe	Cys
			100					105					110		
Ala	Thr	Leu	Met	Arg	Arg	Ser	Ser	Arg	His	Met	Asn	Leu	Ala	Leu	Arg
		115					120					125			
Ile	Leu	Glu	Val	Arg	Ser	Ala	Tyr	Cys	Lys	Asn	Asp	Phe	Glu	Trp	Asp
		130				135					140				
Asn	Met	Lys	Arg	Leu	Ala	Phe	Lys	Asn	Val	Asp	Asp	Ser	Asn	Thr	Arg
		145			150					155				160	
Leu	Met	Arg	Glu	Tyr	Val	Leu	Glu	Thr	Ser	His	Val	Glu	Thr	Asp	Ser
			165					170						175	

Asp Lys

(2) INFORMATION FOR SEQ ID NO:1537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174

(D) OTHER INFORMATION: / Ceres Seq. ID 1500560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1537:

Met	Glu	Ser	Ser	Ser	Ser	Leu	Leu	His	His	Ser	Tyr	Leu			
				5				10			15				
1															
Asn	Pro	Lys	Phe	Gly	Lys	Arg	Pro	Leu	Val	Ser	Tyr	Pro	Leu	Met	Gln
			20				25					30			
Ser	Ser	Arg	Lys	Cys	Lys	Gln	Thr	Arg	Ile	Cys	Ser	Asn	Lys	Met	Tyr
		35				40					45				
Val	Pro	Gly	Phe	Gly	Glu	Ala	Ser	Pro	Glu	Ala	Lys	Ala	Ala	Lys	His
		50			55					60					
Leu	His	Asp	Phe	Phe	Thr	Tyr	Val	Ala	Val	Arg	Ile	Val	Ser	Ala	Gln
	65				70				75					80	
Leu	Glu	Ser	Tyr	Asn	Pro	Glu	Ala	Tyr	Met	Glu	Leu	Arg	Glu	Phe	Leu
			85					90					95		
Asp	Thr	Asn	Ser	Val	Ser	Asp	Gly	Asp	Lys	Phe	Cys	Ala	Thr	Leu	Met
		100					105						110		
Arg	Arg	Ser	Ser	Arg	His	Met	Asn	Leu	Ala	Leu	Arg	Ile	Leu	Glu	Val
		115					120					125			
Arg	Ser	Ala	Tyr	Cys	Lys	Asn	Asp	Phe	Glu	Trp	Asp	Asn	Met	Lys	Arg
		130				135					140				
Leu	Ala	Phe	Lys	Asn	Val	Asp	Asp	Ser	Asn	Thr	Arg	Leu	Met	Arg	Glu
		145			150					155				160	
Tyr	Val	Leu	Glu	Thr	Ser	His	Val	Glu	Thr	Asp	Ser	Asp	Lys		
			165					170							

(2) INFORMATION FOR SEQ ID NO:1538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1500561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1538:

```

Met Gln Ser Ser Arg Lys Cys Lys Gln Thr Arg Ile Cys Ser Asn Lys
1          5          10          15
Met Tyr Val Pro Gly Phe Gly Glu Ala Ser Pro Glu Ala Lys Ala Ala
          20          25          30
Lys His Leu His Asp Phe Phe Thr Tyr Val Ala Val Arg Ile Val Ser
          35          40          45
Ala Gln Leu Glu Ser Tyr Asn Pro Glu Ala Tyr Met Glu Leu Arg Glu
          50          55          60
Phe Leu Asp Thr Asn Ser Val Ser Asp Gly Asp Lys Phe Cys Ala Thr
65          70          75          80
Leu Met Arg Arg Ser Ser Arg His Met Asn Leu Ala Leu Arg Ile Leu
          85          90          95
Glu Val Arg Ser Ala Tyr Cys Lys Asn Asp Phe Glu Trp Asp Asn Met
          100          105          110
Lys Arg Leu Ala Phe Lys Asn Val Asp Asp Ser Asn Thr Arg Leu Met
          115          120          125
Arg Glu Tyr Val Leu Glu Thr Ser His Val Glu Thr Asp Ser Asp Lys
          130          135          140

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(2) INFORMATION FOR SEQ ID NO:1539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1616
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1539:

```

atcgataacc aaataaaaaa tggcgatctc ttctctctgt gttttttctc tcacctctgt      60
ttcgtaaatc ttittttgcc aaaaaatacaa acgatcaaaa tggaaatctc ctccaagccc      120
tcccaagttt cgggctcatcg ggaacttaca tcagattgga gaattgcctc acaggctact      180
tcaacatctc gcgaaaagat accgacactgt gatgcttctt cactttgggt ttgtccctat      240
aactgtggtc tcatcgagag aagccgctga agaagtgctt agaactcatg acctagactg      300
ttgcagcagg cctaagcttg tcgggacaag gttactctcg gcgggatatt aaagatatcg      360
gttttacgcc atacggtaac gaggtggaag gcgcggcgta aggtttgcc ttgctgagac      420
ttttctggtt gaaaaaggtt cagtccttta ggcataatcg agagaaagaa tgtaactctc      480
tggtcaagca actgtcgaaa tccgcggttg atcgctctcc ggtcgatttg agcaaatccc      540
ttttctggct aaccgctagt atccttttta gattgtcctt aggcagaaat ttccacgaga      600
gcgattttat cgataaagaa aagatcgaag agctcgtgtt cgaagctgag actgccttag      660
caagtttccat ttgtctgat tcttccctgt ttgcgggact tggatggctc gttgatttgt      720
tttcgggaca acacaagaga ctcaacgatg ttttttcaaa gctcgatgct ctgtttcaat      780
atgtcataga tgatcattta aatcctggaa gatcaaaaga gcacgaagac atcatgcttt      840
caatgttgga ttgtattcat aaacaaggag aggatagttc cttagagctc acatagatc      900
atgtcaaggg gtttctcgcg aatatatttc ttgcagggat agacacaggg gccataccaca      960
tgatatgggc agtgacggag ctogttaaaa acccgaaact gataaaagaa gttcaaggcg      1020
atatcgaga acaacttggc agcaataaag agagaatcac cgaggaagat atcgagaagat      1080
ttccttactt gaagatggta atcaaaagaaa cattcagggtt acacccagca gctcctctta      1140
tacttccaag ggaacaatg gctcacatca aagttcaagg gtatgatatt cctcccaaga      1200
ggaggatctt ggtaaatggt tcggcaaatg gaagagatcc caaactctgg acaaacccga      1260
aagagtttga cctcgagagg ttatatggata gctttgttga ttatagggga caacattacg      1320
agctcttacc atttgggtcc ggtcgaagga tatgtcccgg gatgccaatg gggattgctg      1380
ccgtcgaaat gggactcttg aacttaactt actctctoga tttatcttga ttggatggga      1440
tgacacataa agatatcgat actgaagaa ctgggtactct tacaatagtc aagaaagtat      1500
ctctcaagct cgttccagtt cgagttcagt gatcagacca aactccaacac cttttgaata      1560
aatatacatg gaaatcagtt taagctttct tcatgatgta tgaagtatat ttttcc

```

(2) INFORMATION FOR SEQ ID NO:1540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..229
(D) OTHER INFORMATION: / Ceres Seq. ID 1500563
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1540:
Met Leu Asp Val Ile His Lys Gln Gly Glu Asp Ser Ser Leu Glu Leu
1 5 10 15
Thr Ile Asp His Ile Lys Gly Phe Leu Ala Asn Ile Phe Leu Ala Gly
20 25 30
Ile Asp Thr Gly Ala Ile Thr Met Ile Trp Ala Val Thr Glu Leu Val
35 40 45
Lys Asn Pro Lys Leu Ile Lys Lys Val Gln Gly Asp Ile Arg Glu Gln
50 55 60
Leu Gly Ser Asn Lys Glu Arg Ile Thr Glu Glu Asp Ile Glu Lys Val
65 70 75 80
Pro Tyr Leu Lys Met Val Ile Lys Glu Thr Phe Arg Leu His Pro Ala
85 90 95
Ala Pro Leu Ile Leu Pro Arg Glu Thr Met Ala His Ile Lys Val Gln
100 105 110
Gly Tyr Asp Ile Pro Pro Lys Arg Arg Ile Leu Val Asn Val Ser Ala
115 120 125
Ile Gly Arg Asp Pro Lys Leu Trp Thr Asn Pro Lys Glu Phe Asp Pro
130 135 140
Glu Arg Phe Met Asp Ser Phe Val Asp Tyr Arg Gly Gln His Tyr Glu
145 150 155 160
Leu Leu Pro Phe Gly Ser Gly Arg Arg Ile Cys Pro Gly Met Pro Met
165 170 175
Gly Ile Ala Ala Val Glu Leu Gly Leu Leu Asn Leu Leu Tyr Phe Phe
180 185 190
Asp Trp Lys Leu Pro Asp Gly Met Thr His Lys Asp Ile Asp Thr Glu
195 200 205
Glu Ala Gly Thr Leu Thr Ile Val Lys Lys Val Pro Leu Lys Leu Val
210 215 220
Pro Val Arg Val Gln
225

(2) INFORMATION FOR SEQ ID NO:1541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..190
(D) OTHER INFORMATION: / Ceres Seq. ID 1500564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1541:

Met Ile Trp Ala Val Thr Glu Leu Val Lys Asn Pro Lys Leu Ile Lys
1 5 10 15
Lys Val Gln Gly Asp Ile Arg Glu Gln Leu Gly Ser Asn Lys Glu Arg
20 25 30
Ile Thr Glu Glu Asp Ile Glu Lys Val Pro Tyr Leu Lys Met Val Ile
35 40 45
Lys Glu Thr Phe Arg Leu His Pro Ala Ala Pro Leu Ile Leu Pro Arg
50 55 60
Glu Thr Met Ala His Ile Lys Val Gln Gly Tyr Asp Ile Pro Pro Lys

65					70					75					80
Arg	Arg	Ile	Leu	Val	Asn	Val	Ser	Ala	Ile	Gly	Arg	Asp	Pro	Lys	Leu
					85				90					95	
Trp	Thr	Asn	Pro	Lys	Glu	Phe	Asp	Pro	Glu	Arg	Phe	Met	Asp	Ser	Phe
					100				105					110	
Val	Asp	Tyr	Arg	Gly	Gln	His	Tyr	Glu	Leu	Leu	Pro	Phe	Gly	Ser	Gly
					115				120					125	
Arg	Arg	Ile	Cys	Pro	Gly	Met	Pro	Met	Gly	Ile	Ala	Ala	Val	Glu	Leu
									135					140	
Gly	Leu	Leu	Asn	Leu	Leu	Tyr	Phe	Phe	Asp	Trp	Lys	Leu	Pro	Asp	Gly
									150					155	
Met	Thr	His	Lys	Asp	Ile	Asp	Thr	Glu	Glu	Ala	Gly	Thr	Leu	Thr	Ile
					165				170					175	
Val	Lys	Lys	Val	Pro	Leu	Lys	Leu	Val	Pro	Val	Arg	Val	Gln		
					180				185				190		

(2) INFORMATION FOR SEQ ID NO:1542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542:

Met	Val	Ile	Lys	Glu	Thr	Phe	Arg	Leu	His	Pro	Ala	Ala	Pro	Leu	Ile
1														15	
Leu	Pro	Arg	Glu	Thr	Met	Ala	His	Ile	Lys	Val	Gln	Gly	Tyr	Asp	Ile
									25					30	
Pro	Pro	Lys	Arg	Arg	Ile	Leu	Val	Asn	Val	Ser	Ala	Ile	Gly	Arg	Asp
									40				45		
Pro	Lys	Leu	Trp	Thr	Asn	Pro	Lys	Glu	Phe	Asp	Pro	Glu	Arg	Phe	Met
									55				60		
Asp	Ser	Phe	Val	Asp	Tyr	Arg	Gly	Gln	His	Tyr	Glu	Leu	Leu	Pro	Phe
									70					80	
Gly	Ser	Gly	Arg	Arg	Ile	Cys	Pro	Gly	Met	Pro	Met	Gly	Ile	Ala	Ala
									85				95		
Val	Glu	Leu	Gly	Leu	Leu	Asn	Leu	Leu	Tyr	Phe	Phe	Asp	Trp	Lys	Leu
									105				110		
Pro	Asp	Gly	Met	Thr	His	Lys	Asp	Ile	Asp	Thr	Glu	Glu	Ala	Gly	Thr
									115				125		
Leu	Thr	Ile	Val	Lys	Lys	Val	Pro	Leu	Lys	Leu	Val	Pro	Val	Arg	Val
									135				140		

Gln
145

(2) INFORMATION FOR SEQ ID NO:1543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1928 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1928
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543:

tttctctctt ttctatctcc acaaatccca aacatctctc tctctttctc tctcacacac
aaaattgcag aagaagaaga gtcatgaatg gtgaagaaga cttttagtaga gattgtctctg

60
120

tttttgttga	gattgaccc	tctggaagat	atggaagata	cgatgaaata	cttgccaaag	180
gagcttcaaa	gacagatatac	agagcatttg	atgagtata	aggtatagaa	gtagcatgga	240
accaagtata	gcttcgaaat	ttcacaaaga	atcctgagga	attagagaag	tttttcagag	300
agattcatct	tctcaagact	ttgaatcatc	aaaacattat	gaaattctac	acttcttggt	360
ttgataccaa	caattttatca	atcaattttg	tcactgaact	cttcacctct	gggtactctca	420
gacagtatag	gttgagacat	agaagagatga	atattagagc	agtgaagcaa	tggtgcaagc	480
agattttaaa	agggctctct	tatttacata	gtcgttctcc	accaattata	catagagatc	540
tcaaatgtga	taacattttc	atcaatggaa	accaaggtga	agtcaagatc	gggtgacctg	600
gactcgctgc	gattcttcgt	aaatcacatg	ccgttctggt	cggttggaacc	cctgagttta	660
tggtctcaga	agtgtatgat	gaggaatata	atgagttggt	tgatgtatat	gcttttggca	720
tggtgtgtgt	ggagatggtt	acttttgatt	atccttacag	tgaatgtact	caccgggac	780
aaatctacaa	gaaagttaac	tcggggaaaa	agcctgaagc	tttttactta	gtgaaggatc	840
ctgagggttcg	tgagtttgtt	gagaagtgtt	tagctaactg	gaegtgtagg	ctaaccggat	900
tgagagcttt	acaagaccct	ttctacaaag	atgataatat	ggatgggatt	gttatggagac	960
ctattgatta	tcacaatggt	tatgatgaaa	ctgggtgtgt	ccttagacat	ccttttgattg	1020
atgatctctct	ttaccatgat	cagtttgagt	cgctcacagat	atgtgagatc	gattcttttcg	1080
ctaacgatga	tgaagatcat	gtcgacattt	cgattaaagg	gaagagaaaac	gggtgatgatg	1140
ggatattctt	gagacttaga	atatctgatg	ctgaaggacg	gataagggaac	atttactctc	1200
cgtttgagac	ggctattgat	actgcattga	gtgtagcgtg	tgagatgggt	tcagagctcg	1260
acataacgaa	tcaagatggt	gcgaaaaatc	cgagatgatg	cgatgcagag	attgtctgat	1320
tggtgcttga	ttgaaaaaat	gatacacgaa	gttcccaaaa	tgtaaaacaac	aaacaagaaca	1380
acaacactgc	aggattctctg	ggagagtggt	cttcaaacgg	tgatatataca	gagacttgtat	1440
catcaggaga	aaaatctcat	cataatcatc	atgagttcga	tagttctgaa	gacaagagct	1500
gttcttcggt	tcacggttag	tttgccgata	tggtgggtgt	gcgagaataca	tattctcgatg	1560
gtggagaaaa	acagagctca	aggaaggtta	gaagtggagc	gtggctcgag	aatgagatga	1620
gacgagaact	gagatggctt	aaggcaaggg	acaagattca	acttatgaaa	atgagaggtc	1680
aaacgatctg	cgagacaccc	atagagatct	ctcttaacac	gggaacttca	gtttcgttac	1740
ctctctctta	caaggctata	tcacttctct	tgagtcgctg	ggatattgtg	catattgtga	1800
aagtctgatg	atagttatca	cttatatttg	tatgtttcga	catttttaac	ttttgttaag	1860
ttaaagattta	atgacatagt	gtactttatt	aagagagaag	aagagtaaac	gaaaaacata	1920
aattagtc						

(2) INFORMATION FOR SEQ ID NO:1544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..595
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544:

Ser	Ser	Ser	Ser	Ile	Ser	Thr	Asn	Ser	Lys	His	Leu	Ser	Leu	Phe	Leu
1				5					10					15	
Ser	His	Thr	Gln	Asn	Cys	Arg	Arg	Arg	Arg	Val	Met	Asn	Gly	Glu	Glu
				20					25					30	
Ser	Phe	Val	Glu	Asp	Cys	Ser	Val	Phe	Val	Glu	Ile	Asp	Pro	Ser	Gly
				35					40					45	
Arg	Tyr	Gly	Arg	Tyr	Asp	Glu	Ile	Leu	Gly	Lys	Gly	Ala	Ser	Lys	Thr
				50					55					60	
Val	Tyr	Arg	Ala	Phe	Asp	Glu	Tyr	Glu	Gly	Ile	Glu	Val	Ala	Trp	Asn
				65					70					75	
Gln	Val	Lys	Leu	Arg	Asn	Phe	Thr	Arg	Asn	Pro	Glu	Glu	Leu	Glu	Lys
				85					90					95	
Phe	Phe	Arg	Glu	Ile	His	Leu	Leu	Lys	Thr	Leu	Asn	His	Gln	Asn	Ile
				100					105					110	
Met	Lys	Phe	Thr	Thr	Ser	Trp	Val	Asp	Thr	Asn	Asn	Leu	Ser	Ile	Asn
				115					120					125	
Phe	Val	Thr	Glu	Leu	Phe	Thr	Ser	Gly	Thr	Leu	Arg	Gln	Tyr	Arg	Leu
				130					135					140	

Arg	His	Arg	Arg	Val	Asn	Ile	Arg	Ala	Val	Lys	Gln	Trp	Cys	Lys	Gln	
145					150					155					160	
Ile	Leu	Lys	Gly	Leu	Tyr	Leu	His	Ser	Arg	Ser	Pro	Pro	Ile	Ile		
				165				170						175		
His	Arg	Asp	Leu	Lys	Cys	Asp	Asn	Ile	Phe	Ile	Asn	Gly	Asn	Gln	Gly	
			180					185					190			
Glu	Val	Lys	Ile	Gly	Asp	Leu	Gly	Leu	Ala	Ala	Ile	Leu	Arg	Lys	Ser	
			195				200					205				
His	Ala	Val	Arg	Cys	Val	Gly	Thr	Pro	Glu	Phe	Met	Ala	Pro	Glu	Val	
	210					215					220					
Tyr	Asp	Glu	Glu	Tyr	Asn	Glu	Leu	Val	Asp	Val	Tyr	Ala	Phe	Gly	Met	
225					230					235					240	
Cys	Val	Leu	Glu	Met	Val	Thr	Phe	Asp	Tyr	Pro	Tyr	Ser	Glu	Cys	Thr	
				245					250					255		
His	Pro	Ala	Gln	Ile	Tyr	Lys	Lys	Val	Thr	Ser	Gly	Lys	Lys	Pro	Glu	
			260					265					270			
Ala	Phe	Tyr	Leu	Val	Lys	Asp	Pro	Glu	Val	Arg	Glu	Phe	Val	Glu	Lys	
			275				280					285				
Cys	Leu	Ala	Asn	Val	Thr	Cys	Arg	Leu	Thr	Ala	Leu	Glu	Leu	Leu	Gln	
	290					295					300					
Asp	Pro	Phe	Leu	Gln	Asp	Asp	Asn	Met	Asp	Gly	Phe	Val	Met	Arg	Pro	
305					310					315					320	
Ile	Asp	Tyr	Tyr	Asn	Gly	Tyr	Asp	Glu	Thr	Gly	Val	Phe	Leu	Arg	His	
				325				330						335		
Pro	Leu	Ile	Asp	Asp	Pro	Leu	Tyr	His	Asp	Gln	Phe	Glu	Ser	Ser	Gln	
			340				345						350			
Ile	Cys	Glu	Ile	Asp	Leu	Phe	Ala	Asn	Asp	Asp	Glu	Asp	His	Val	Asp	
			355				360					365				
Ile	Ser	Ile	Lys	Gly	Lys	Arg	Asn	Gly	Asp	Asp	Gly	Ile	Phe	Leu	Arg	
	370					375					380					
Leu	Arg	Ile	Ser	Asp	Ala	Glu	Gly	Arg	Ile	Arg	Asn	Ile	Tyr	Phe	Pro	
385					390					395					400	
Phe	Glu	Thr	Ala	Ile	Asp	Thr	Ala	Trp	Ser	Val	Ala	Val	Glu	Met	Val	
				405					410					415		
Ser	Glu	Leu	Asp	Ile	Thr	Asn	Gln	Asp	Val	Ala	Lys	Ile	Ala	Glu	Met	
			420				425						430			
Ile	Asp	Ala	Glu	Ile	Ala	Ala	Leu	Val	Pro	Asp	Trp	Lys	Asn	Asp	Thr	
			435				440					445				
Glu	Ser	Ser	Gln	Asn	Val	Asn	Asn	Asn	Lys	Asn	Asn	Asn	Thr	Ala	Gly	
			450			455					460					
Phe	Cys	Gly	Glu	Cys	Ala	Ser	Asn	Gly	Tyr	Ile	Gln	Glu	Thr	Val	Ser	
465					470					475					480	
Ser	Gly	Glu	Lys	Ser	His	His	Asn	His	His	Glu	Phe	Asp	Ser	Ser	Glu	
				485					490					495		
Asp	Lys	Ser	Cys	Ser	Ser	Val	His	Gly	Arg	Phe	Ala	Asp	Met	Trp	Gly	
			500				505						510			
Leu	Arg	Glu	Ser	Tyr	Ser	Asp	Asp	Gly	Glu	Lys	Gln	Ser	Ser	Arg	Lys	
			515				520					525				
Val	Arg	Ser	Gly	Arg	Trp	Ser	Glu	Asn	Glu	Met	Arg	Arg	Glu	Leu	Arg	
	530					535					540					
Trp	Leu	Lys	Ala	Arg	His	Lys	Ile	Gln	Leu	Met	Lys	Met	Arg	Gly	Gln	
545					550					555					560	
Thr	Ile	Cys	Glu	Thr	Pro	Ile	Glu	Ile	Ser	Leu	Thr	Pro	Gly	Thr	Ser	
				565					570					575		
Val	Ser	Leu	Pro	Leu	Leu	Tyr	Arg	Ala	Ile	Ser	Leu	Pro	Val	Asp	Ala	
			580					585					590			
Val	Asp	Met														
			595													

- (2) INFORMATION FOR SEQ ID NO:1545:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 568 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..568
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500616
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1545:

Met	Asn	Gly	Glu	Glu	Ser	Phe	Val	Glu	Asp	Cys	Ser	Val	Phe	Val	Glu	1	5	10	15
Ile	Asp	Pro	Ser	Gly	Arg	Tyr	Gly	Arg	Tyr	Asp	Glu	Ile	Leu	Gly	Lys	20	25	30	35
Gly	Ala	Ser	Lys	Thr	Val	Tyr	Arg	Ala	Phe	Asp	Glu	Tyr	Glu	Gly	Ile	40	45	50	55
Glu	Val	Ala	Trp	Asn	Gln	Val	Lys	Leu	Arg	Asn	Phe	Thr	Arg	Asn	Pro	60	65	70	75
Glu	Glu	Leu	Glu	Lys	Phe	Phe	Arg	Glu	Ile	His	Leu	Leu	Lys	Thr	Leu	80	85	90	95
Asn	His	Gln	Asn	Ile	Met	Lys	Phe	Tyr	Thr	Ser	Trp	Val	Asp	Thr	Asn	100	105	110	115
Asn	Leu	Ser	Ile	Asn	Phe	Val	Thr	Glu	Leu	Phe	Thr	Ser	Gly	Thr	Leu	120	125	130	135
Arg	Gln	Tyr	Arg	Leu	Arg	His	Arg	Arg	Val	Asn	Ile	Arg	Ala	Val	Lys	140	145	150	155
Gln	Trp	Cys	Lys	Gln	Ile	Leu	Lys	Gly	Leu	Leu	Tyr	Leu	His	Ser	Arg	160	165	170	175
Ser	Pro	Pro	Ile	Ile	His	Arg	Asp	Leu	Lys	Cys	Asp	Asn	Ile	Phe	Ile	180	185	190	195
Asn	Gly	Asn	Gln	Gly	Glu	Val	Lys	Ile	Gly	Asp	Leu	Gly	Leu	Ala	Ala	200	205	210	215
Ile	Leu	Arg	Lys	Ser	His	Ala	Val	Arg	Cys	Val	Gly	Thr	Pro	Glu	Phe	220	225	230	235
Met	Ala	Pro	Glu	Val	Tyr	Asp	Glu	Glu	Tyr	Asn	Glu	Leu	Val	Asp	Val	240	245	250	255
Tyr	Ala	Phe	Gly	Met	Cys	Val	Leu	Glu	Met	Val	Thr	Phe	Asp	Tyr	Pro	260	265	270	275
Tyr	Ser	Glu	Cys	Thr	His	Pro	Ala	Gln	Ile	Tyr	Lys	Lys	Val	Thr	Ser	280	285	290	295
Gly	Lys	Lys	Pro	Glu	Ala	Phe	Tyr	Leu	Val	Lys	Asp	Pro	Glu	Val	Arg	300	305	310	315
Glu	Phe	Val	Glu	Lys	Cys	Leu	Ala	Asn	Val	Thr	Cys	Arg	Leu	Thr	Ala	320	325	330	335
Leu	Glu	Leu	Leu	Gln	Asp	Pro	Phe	Leu	Gln	Asp	Asp	Asn	Met	Asp	Gly	340	345	350	355
Phe	Val	Met	Arg	Pro	Ile	Asp	Tyr	Tyr	Asn	Gly	Tyr	Asp	Glu	Thr	Gly	360	365	370	375
Val	Phe	Leu	Arg	His	Pro	Leu	Ile	Asp	Asp	Pro	Leu	Tyr	His	Asp	Gln	380	385	390	395
Phe	Glu	Ser	Ser	Gln	Ile	Cys	Glu	Ile	Asp	Leu	Phe	Ala	Asn	Asp	Asp	400	405	410	415
Glu	Asp	His	Val	Asp	Ile	Ser	Ile	Lys	Gly	Lys	Arg	Asn	Gly	Asp	Asp				
Gly	Ile	Phe	Leu	Arg	Leu	Arg	Ile	Ser	Asp	Ala	Glu	Gly	Arg	Ile	Arg				
Asn	Ile	Tyr	Phe	Pro	Phe	Glu	Thr	Ala	Ile	Asp	Thr	Ala	Trp	Ser	Val				
Ala	Val	Glu	Met	Val	Ser	Glu	Leu	Asp	Ile	Thr	Asn	Gln	Asp	Val	Ala				
Lys	Ile	Ala	Glu	Met	Ile	Asp	Ala	Glu	Ile	Ala	Ala	Leu	Val	Pro	Asp				

Trp Lys Asn Asp Thr Glu Ser Ser Gln Asn Val Asn Asn Asn Lys Asn
420 425 430
Asn Asn Thr Ala Gly Phe Cys Gly Glu Cys Ala Ser Asn Gly Tyr Ile
435 440 445
Gln Glu Thr Val Ser Ser Gly Glu Lys Ser His His Asn His His Glu
450 455 460
Phe Asp Ser Ser Glu Asp Lys Ser Cys Ser Ser Val His Gly Arg Phe
465 470 475 480
Ala Asp Met Trp Gly Leu Arg Glu Ser Tyr Ser Asp Asp Gly Glu Lys
485 490 495
Gln Ser Ser Arg Lys Val Arg Ser Gly Arg Trp Ser Glu Asn Glu Met
500 505 510
Arg Arg Glu Leu Arg Trp Leu Lys Ala Arg His Lys Ile Gln Leu Met
515 520 525
Lys Met Arg Gly Gln Thr Ile Cys Glu Thr Pro Ile Glu Ile Ser Leu
530 535 540
Thr Pro Gly Thr Ser Val Ser Leu Pro Leu Leu Tyr Arg Ala Ile Ser
545 550 555 560
Leu Pro Val Asp Ala Val Asp Met
565

(2) INFORMATION FOR SEQ ID NO:1546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..483
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1546:

Met Lys Phe Tyr Thr Ser Trp Val Asp Thr Asn Asn Leu Ser Ile Asn
1 5 10 15
Phe Val Thr Glu Leu Phe Thr Ser Gly Thr Leu Arg Gln Tyr Arg Leu
20 25 30
Arg His Arg Arg Val Asn Ile Arg Ala Val Lys Gln Trp Cys Lys Gln
35 40 45
Ile Leu Lys Gly Leu Leu Tyr Leu His Ser Arg Ser Pro Ile Ile
50 55 60
His Arg Asp Leu Lys Cys Asp Asn Ile Phe Ile Asn Gly Asn Gln Gly
65 70 75 80
Glu Val Lys Ile Gly Asp Leu Gly Leu Ala Ala Ile Leu Arg Lys Ser
85 90 95
His Ala Val Arg Cys Val Gly Thr Pro Glu Phe Met Ala Pro Glu Val
100 105 110
Tyr Asp Glu Glu Tyr Asn Glu Leu Val Asp Val Tyr Ala Phe Gly Met
115 120 125
Cys Val Leu Glu Met Val Thr Phe Asp Tyr Pro Tyr Ser Glu Cys Thr
130 135 140
His Pro Ala Gln Ile Tyr Lys Lys Val Thr Ser Gly Lys Lys Pro Glu
145 150 155 160
Ala Phe Tyr Leu Val Lys Asp Pro Glu Val Arg Glu Phe Val Glu Lys
165 170 175
Cys Leu Ala Asn Val Thr Cys Arg Leu Thr Ala Leu Glu Leu Leu Gln
180 185 190
Asp Pro Phe Leu Gln Asp Asp Asn Met Asp Gly Phe Val Met Arg Pro
195 200 205
Ile Asp Tyr Tyr Asn Gly Tyr Asp Glu Thr Gly Val Phe Leu Arg His
210 215 220
Pro Leu Ile Asp Asp Pro Leu Tyr His Asp Gln Phe Glu Ser Ser Gln

225 230 235 240
Ile Cys Glu Ile Asp Leu Phe Ala Asn Asp Asp Glu Asp His Val Asp
245 250 255
Ile Ser Ile Lys Gly Lys Arg Asn Gly Asp Asp Gly Ile Phe Leu Arg
260 265 270
Leu Arg Ile Ser Asp Ala Glu Gly Arg Ile Arg Asn Ile Tyr Phe Pro
275 280 285
Phe Glu Thr Ala Ile Asp Thr Ala Trp Ser Val Ala Val Glu Met Val
290 295 300
Ser Glu Leu Asp Ile Thr Asn Gln Asp Val Ala Lys Ile Ala Glu Met
305 310 315 320
Ile Asp Ala Glu Ile Ala Ala Leu Val Pro Asp Trp Lys Asn Asp Thr
325 330 335
Glu Ser Ser Gln Asn Val Asn Asn Asn Lys Asn Asn Thr Ala Gly
340 345 350
Phe Cys Gly Glu Cys Ala Ser Asn Gly Tyr Ile Gln Glu Thr Val Ser
355 360 365
Ser Gly Glu Lys Ser His His Asn His His Glu Phe Asp Ser Ser Glu
370 375 380
Asp Lys Ser Cys Ser Ser Val His Gly Arg Phe Ala Asp Met Trp Gly
385 390 395 400
Leu Arg Glu Ser Tyr Ser Asp Asp Gly Glu Lys Gln Ser Ser Arg Lys
405 410 415
Val Arg Ser Gly Arg Trp Ser Glu Asn Glu Met Arg Arg Glu Leu Arg
420 425 430
Trp Leu Lys Ala Arg His Lys Ile Gln Leu Met Lys Met Arg Gly Gln
435 440 445
Thr Ile Cys Glu Thr Pro Ile Glu Ile Ser Leu Thr Pro Gly Thr Ser
450 455 460
Val Ser Leu Pro Leu Leu Tyr Arg Ala Ile Ser Leu Pro Val Asp Ala
465 470 475 480
Val Asp Met

(2) INFORMATION FOR SEQ ID NO:1547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1512
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1547:

attctgaata	agatcaagaa	tttacaggtt	ctctctcttc	tctctctcaaa	gttctgtttt	60
gtttatataca	attacaactt	tagtttcgt	aataggtact	cattagtgtga	tcattgtctt	120
ctatgctcttg	ctatgcaatt	caataggcga	gtgtatcacc	aatcacagat	ccgggatccc	180
ggcttagtaaa	acattataaaa	gcttgcatat	acactttatt	tggatttgga	tttagtaaaa	240
aaatttcattt	tacagtatttt	gaaaaaatac	aaaatggcga	aaatctaccg	gaagttgaca	300
ggctacgggtg	gtgaaggagg	gcgtgaattg	gacgatgatg	tatatgaggg	tgtaaagaaa	360
gtgtatgtag	gacaagatat	caatcgatc	acttacgtca	aattcgagta	tgtgaaggaa	420
gacggccaag	tagtaacaac	tgaatatggg	aaaatcattc	aacaacccaa	agagtgttga	480
cttcaatatc	cggacgaaca	tatcatagcg	gtggaaggaa	actatcgcg	agtggctcta	540
tgtgccacag	aggtgatcac	aaacctgcct	ttcaagacct	caaagggtag	aaagtcacca	600
ctgtttgtgtc	caaacttgct	tggaaattac	accgggtaca	agttcgttat	tggagtagga	660
ggaagaagaa	tcgtagggtt	tcattggacg	tcgggttaag	ctctcgacgc	gcttggaggt	720
tactttgtac	atggctctct	acaacgctct	ccgctctgtt	acaagctgga	tgcccaaggt	780
gggtacagac	ggcgtgtttg	ggatgatggt	tcttacgacg	gcgttaaatc	gctgcgtatt	840
gggtcaagata	atbctcgtat	tacttattta	gagttcaggt	acgagaagag	cggtgaagta	900
gagacatgtc	gcaatggggt	gaaacaagaa	agatcacgta	agtttgagct	taaccgggat	960

gaatacatca	aatcggtgga	agcaacccat	gataaacccg	acattttccg	caatgtcgtc	1020
attacatcgc	tmcatttga	aacatcgaa	gggagmacgt	cattctctcg	gtataaggga	1080
ggtaaagaat	ttaaagctaga	gcaaaaggg	cgtaggcttg	tcgggttcca	tggaaggaa	1140
gggttcagcta	ttgatgcctt	tgagacatat	tttgcacctt	ttctactccc	gactccata	1200
attccagaag	aaactaccag	caataggcgg	cagcggagga	gttgcattgg	atgatgtgtg	1260
ctacgatggt	gtaaggaaga	tactgttagg	acaaggtaac	gatggtgtag	cctttgtcaa	1320
gtttgaatac	aataaaggaa	aagatcttgt	atctggagat	gaccatggga	agatgacatt	1380
actcggaact	gaagagtttg	tgcttgaaga	tggtgaatat	ctcacggcca	tagatggcta	1440
ttacgataag	attttcggag	tcgagacacc	aatgattatc	tgctttcagt	taaagacgaa	1500
caaaagggag	tc					

(2) INFORMATION FOR SEQ ID NO:1548:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 417 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..417

(D) OTHER INFORMATION: / Ceres Seq. ID 1500619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1548:

Ile	Leu	Asn	Lys	Ile	Lys	Asn	Leu	Gln	Val	Leu	Ser	Ser	Leu	Ser	Leu
1			5					10					15		
Lys	Phe	Cys	Phe	Val	Tyr	Thr	Asn	Tyr	Asn	Phe	Ser	Phe	Val	Asn	Arg
			20					25				30			
Tyr	Ser	Leu	Val	Asp	His	Cys	Ser	Leu	Cys	Leu	Ala	Met	Gln	Phe	Asn
		35					40				45				
Arg	Leu	Val	Tyr	His	Gln	Ser	Gln	Ile	Arg	Asp	Pro	Gly	Leu	Val	Asn
	50					55				60					
Ile	Ile	Lys	Leu	Ala	Tyr	Thr	Leu	Tyr	Leu	Asp	Leu	Asp	Leu	Val	Lys
			70						75				80		
Lys	Phe	Ile	Leu	Gln	Tyr	Leu	Lys	Lys	Tyr	Lys	Met	Ala	Lys	Ile	Tyr
			85					90					95		
Arg	Lys	Leu	Thr	Gly	Tyr	Gly	Gly	Glu	Gly	Gly	Arg	Glu	Trp	Asp	Asp
		100						105					110		
Asp	Val	Tyr	Glu	Gly	Val	Arg	Lys	Val	Tyr	Val	Gly	Gln	Asp	Ile	Asn
		115					120				125				
Arg	Ile	Thr	Tyr	Val	Lys	Phe	Glu	Tyr	Val	Lys	Glu	Asp	Gly	Gln	Val
	130					135					140				
Val	Thr	Thr	Glu	Tyr	Gly	Lys	Ile	Ile	Gln	Gln	Pro	Lys	Glu	Phe	Val
			150						155				160		
Leu	Gln	Tyr	Pro	Asp	Glu	His	Ile	Ile	Ala	Val	Glu	Gly	Asn	Tyr	Arg
			165						170				175		
Gly	Val	Ala	Leu	Cys	Ala	Thr	Glu	Val	Ile	Thr	Asn	Leu	Val	Phe	Lys
			180					185					190		
Thr	Ser	Lys	Gly	Arg	Lys	Ser	Pro	Leu	Phe	Gly	Pro	Asn	Leu	Leu	Gly
		195					200					205			
Ile	Thr	Thr	Gly	Thr	Lys	Phe	Val	Ile	Glu	Asp	Gly	Gly	Lys	Lys	Ile
	210					215					220				
Val	Gly	Phe	His	Gly	Arg	Ser	Gly	Asn	Ala	Leu	Asp	Ala	Leu	Gly	Val
	225				230					235			240		
Tyr	Phe	Val	His	Gly	Ser	Leu	Thr	Thr	Ser	Pro	Pro	Val	Tyr	Lys	Leu
			245						250				255		
Asp	Ala	Gln	Gly	Gly	Thr	Asp	Gly	Arg	Val	Trp	Asp	Asp	Gly	Ser	Tyr
		260					265						270		
Asp	Gly	Val	Lys	Ser	Leu	Arg	Ile	Gly	Gln	Asp	Asn	Ser	Arg	Ile	Thr
	275					280					285				
Tyr	Leu	Glu	Phe	Glu	Tyr	Glu	Lys	Gly	Gly	Lys	Leu	Glu	Thr	Cys	Arg
	290					295					300				
His	Gly	Val	Lys	Gln	Glu	Arg	Ser	Leu	Lys	Phe	Glu	Leu	Asn	Pro	Asp

305		310		315		320
Glu Tyr Ile Lys Ser Val Glu Ala Thr Tyr Asp Lys Pro Asp Ile Phe						
	325			330		335
Arg Asn Val Val Ile Thr Ser Leu Xaa Phe Glu Thr Ser Lys Gly Xaa						
	340			345		350
Thr Ser Phe Ser Gly Tyr Lys Gly Gly Lys Lys Phe Lys Leu Glu Gln						
	355			360		365
Lys Gly Arg Arg Leu Val Gly Phe His Gly Lys Glu Gly Ser Ala Ile						
	370			375		380
Asp Ala Leu Gly Ala Tyr Phe Ala Pro Ile Pro Thr Pro Thr Ile						
	385			390		400
Ile Pro Glu Glu Thr Thr Ser Asn Arg Arg Gln Arg Arg Ser Cys Met						
	405			410		415

Gly

(2) INFORMATION FOR SEQ ID NO:1549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..373
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1549:

Met	Gln	Phe	Asn	Arg	Leu	Val	Tyr	His	Gln	Ser	Gln	Ile	Arg	Asp	Pro
1			5					10						15	
Gly	Leu	Val	Asn	Ile	Ile	Lys	Leu	Ala	Tyr	Thr	Leu	Tyr	Leu	Asp	Leu
			20					25					30		
Asp	Leu	Val	Lys	Lys	Phe	Ile	Leu	Gln	Tyr	Leu	Lys	Lys	Tyr	Lys	Met
			35					40					45		
Ala	Lys	Ile	Tyr	Arg	Lys	Leu	Thr	Gly	Tyr	Gly	Gly	Glu	Gly	Gly	Arg
			50					55				60			
Glu	Trp	Asp	Asp	Asp	Val	Tyr	Glu	Gly	Val	Arg	Lys	Val	Tyr	Val	Gly
			65					70				75			80
Gln	Asp	Ile	Asn	Arg	Ile	Thr	Tyr	Val	Lys	Phe	Glu	Tyr	Val	Lys	Glu
			85					90						95	
Asp	Gly	Gln	Val	Val	Thr	Thr	Glu	Tyr	Gly	Lys	Ile	Ile	Gln	Gln	Pro
			100					105					110		
Lys	Glu	Phe	Val	Leu	Gln	Tyr	Pro	Asp	Glu	His	Ile	Ile	Ala	Val	Glu
			115					120					125		
Gly	Asn	Tyr	Arg	Gly	Val	Ala	Leu	Cys	Ala	Thr	Glu	Val	Ile	Thr	Asn
			130					135					140		
Leu	Val	Phe	Lys	Thr	Ser	Lys	Gly	Arg	Lys	Ser	Pro	Leu	Phe	Gly	Pro
			145					150					155		160
Asn	Leu	Leu	Gly	Ile	Thr	Thr	Gly	Thr	Lys	Phe	Val	Ile	Glu	Asp	Gly
			165					170					175		
Gly	Lys	Lys	Ile	Val	Gly	Phe	His	Gly	Arg	Ser	Gly	Asn	Ala	Leu	Asp
			180					185					190		
Ala	Leu	Gly	Val	Tyr	Phe	Val	His	Gly	Ser	Leu	Thr	Thr	Ser	Pro	Pro
			195					200					205		
Val	Tyr	Lys	Leu	Asp	Ala	Gln	Gly	Gly	Thr	Asp	Gly	Arg	Val	Trp	Asp
			210					215					220		
Asp	Gly	Ser	Tyr	Asp	Gly	Val	Lys	Ser	Leu	Arg	Ile	Gly	Gln	Asp	Asn
			225					230				235			240
Ser	Arg	Ile	Thr	Tyr	Leu	Glu	Phe	Glu	Tyr	Glu	Lys	Gly	Gly	Lys	Leu
			245					250					255		
Glu	Thr	Cys	Arg	His	Gly	Val	Lys	Gln	Glu	Arg	Ser	Leu	Lys	Phe	Glu
			260					265					270		

Leu Asn Pro Asp Glu Tyr Ile Lys Ser Val Glu Ala Thr Tyr Asp Lys
275 280
Pro Asp Ile Phe Arg Asn Val Ile Thr Ser Leu Xaa Phe Glu Thr
290 295 300
Ser Lys Gly Xaa Thr Ser Phe Ser Gly Tyr Lys Gly Gly Lys Lys Phe
305 310 315 320
Lys Leu Glu Gln Lys Gly Arg Arg Leu Val Gly Phe His Gly Lys Glu
325 330 335
Gly Ser Ala Ile Asp Ala Leu Gly Ala Tyr Phe Ala Pro Ile Pro Thr
340 345 350
Pro Thr Pro Ile Ile Pro Glu Glu Thr Thr Ser Asn Arg Arg Gln Arg
355 360 365
Arg Ser Cys Met Gly
370

(2) INFORMATION FOR SEQ ID NO:1550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1550:

Met Ala Lys Ile Tyr Arg Lys Leu Thr Gly Tyr Gly Gly Glu Gly Gly
1 5 10 15
Arg Glu Trp Asp Asp Val Tyr Glu Gly Val Arg Lys Val Tyr Val
20 25 30
Gly Gln Asp Ile Asn Arg Ile Thr Tyr Val Lys Phe Glu Tyr Val Lys
35 40 45
Glu Asp Gly Gln Val Val Thr Thr Glu Tyr Gly Lys Ile Ile Gln Gln
50 55 60
Pro Lys Glu Phe Val Leu Gln Tyr Pro Asp Glu His Ile Ile Ala Val
65 70 75 80
Glu Gly Asn Tyr Arg Gly Val Ala Leu Cys Ala Thr Glu Val Ile Thr
85 90 95
Asn Leu Val Phe Lys Thr Ser Lys Gly Arg Lys Ser Pro Leu Phe Gly
100 105 110
Pro Asn Leu Leu Gly Ile Thr Thr Gly Thr Lys Phe Val Ile Glu Asp
115 120 125
Gly Gly Lys Lys Ile Val Gly Phe His Gly Arg Ser Gly Asn Ala Leu
130 135 140
Asp Ala Leu Gly Val Tyr Phe Val His Gly Ser Leu Thr Thr Ser Pro
145 150 155 160
Pro Val Tyr Lys Leu Asp Ala Gln Gly Gly Thr Asp Gly Arg Val Trp
165 170 175
Asp Asp Gly Ser Tyr Asp Gly Val Lys Ser Leu Arg Ile Gly Gln Asp
180 185 190
Asn Ser Arg Ile Thr Tyr Leu Glu Phe Glu Tyr Glu Lys Gly Gly Lys
195 200 205
Leu Glu Thr Cys Arg His Gly Val Lys Gln Glu Arg Ser Leu Lys Phe
210 215 220
Glu Leu Asn Pro Asp Glu Tyr Ile Lys Ser Val Glu Ala Thr Tyr Asp
225 230 235 240
Lys Pro Asp Ile Phe Arg Asn Val Val Ile Thr Ser Leu Xaa Phe Glu
245 250 255
Thr Ser Lys Gly Xaa Thr Ser Phe Ser Gly Tyr Lys Gly Gly Lys Lys
260 265 270
Phe Lys Leu Glu Gln Lys Gly Arg Arg Leu Val Gly Phe His Gly Lys

275	280	285
Glu Gly Ser Ala Ile Asp	Ala Leu Gly Ala Tyr	Phe Ala Pro Ile Pro
290	295	300
Thr Pro Thr Pro Ile Ile	Pro Glu Glu Thr Thr	Ser Asn Arg Arg Gln
305	310	315
Arg Arg Ser Cys Met Gly		320
	325	

(2) INFORMATION FOR SEQ ID NO:1551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 721 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..721

(D) OTHER INFORMATION: / Ceres Seq. ID 1500622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1551:

aaacttaaaact	cttttagtaa	caatgggttct	ttcttcttta	accagacttg	tggttttttg	60
ttgtctcctc	ctgctcacat	tcacggacaa	ccttggtggt	ggaaaatctg	gcaaaagtga	120
gctcaaatct	tactacgaat	cactttgtcc	cggtgtgtcg	gaattcatcg	tcgatgacct	180
aggtaaaaac	tttgactacg	atctctacac	aatacactgat	ctcaagctgt	ttccaatttg	240
taatgcccga	ctctccgata	atctgactgt	cacttgccag	catgggtgaag	aggaatgcga	300
actaaacgcc	cttgaagctt	ggcgattaag	aacttgcccc	gatcagaaat	cacaatactc	360
gttcatacgg	tcgcgtcgaa	ggcgatacga	aggctgggaa	tcattgtgta	aaaaactctg	420
acgtgagaaa	gacgcaagtg	aagaagactg	ataattctga	agctatttgg	gtaaaatacca	480
attctcttca	tctttacttg	agggtttta	ttctttgatg	ttcttttttt	ctttcttagt	540
tcttatgtgt	attgttgtta	ttagtgttgt	gttggtgtgt	ttggtgatgt	tggtgttcta	600
atcatctctt	gtttctttta	ctctggtctt	gattatttga	ataaaggata	tctagagatt	660
gtgtgtgtgt	tggttttgta	ataattagag	tttgataaaa	graaatwaaa	tatttaaggt	720

(2) INFORMATION FOR SEQ ID NO:1552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1500623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1552:

Met Val Ser Ser Ser Leu Thr Lys Leu Val Phe Phe Gly Cys Leu Leu	
1 5 10 15	
Leu Leu Thr Phe Thr Asp Asn Leu Val Ala Gly Lys Ser Gly Lys Val	
20 25 30	
Lys Leu Asn Leu Tyr Tyr Glu Ser Leu Cys Pro Gly Cys Gln Glu Phe	
35 40 45	
Ile Val Asp Asp Leu Gly Lys Ile Phe Asp Tyr Asp Leu Tyr Thr Ile	
50 55 60	
Thr Asp Leu Lys Leu Phe Pro Phe Gly Asn Ala Glu Leu Ser Asp Asn	
65 70 75 80	
Leu Thr Val Thr Cys Gln His Gly Glu Glu Cys Lys Leu Asn Ala	
85 90 95	
Leu Glu Ala Cys Ala Leu Arg Thr Trp Pro Asp Gln Lys Ser Gln Tyr	
100 105 110	
Ser Phe Ile Arg Cys Val Glu Ser Asp Thr Lys Gly Trp Glu Ser Cys	
115 120 125	
Val Lys Asn Ser Gly Arg Glu Lys Asp Ala Ser Glu Glu Asp	

130 135 140

(2) INFORMATION FOR SEQ ID NO:1553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 605 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..605

(D) OTHER INFORMATION: / Ceres Seq. ID 1500633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553:

gcaccctttt	tattgtagcg	acgcaagaag	aagcagctat	agcgtacgat	atcgcagcta	60
tcgagtaccg	tggaactaac	gcggttacta	acttcgacat	cagccggtat	ctgaaactcc	120
cggtgcggga	gaaccctatc	gataccgcga	ataatctcct	cgagagtcgg	cattctgata	180
ttagcccat	tataaaacct	aaccacgagt	ctgacttata	acagagtcaa	tcttcgtcag	240
aggacaacga	tgatcggaaa	acaaagctct	tgaagtcgtc	acctttagtg	gcagaggagg	300
taatcggacc	atcgacgcga	cctgagattg	ctccgcctcg	tcggagcttc	ccggaagata	360
tccagacgta	tttcgggtgt	caaaactccg	gcaagttaac	ggcggaggaa	gatgatgta	420
tcttcggtga	tttagattct	ttccttacgc	ctgatttcta	cagcgagtta	aatgattgct	480
aaagtgtgtg	tcttctgata	agttttgttt	tttagttgtt	cagaatctcg	gttgtagaaa	540
tcaacattga	cacatcgatt	attctttctt	gtgacaatct	tatataataa	agtttgaatc	600
ttttt						

(2) INFORMATION FOR SEQ ID NO:1554:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1500634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1554:

Thr	Pro	Phe	Ile	Val	Ala	Thr	Gln	Glu	Glu	Ala	Ile	Ala	Tyr	Asp	
1															
				5						10				15	
Ile	Ala	Ala	Ile	Glu	Tyr	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn	Phe	Asp
				20				25					30		
Ile	Ser	Arg	Tyr	Leu	Lys	Leu	Pro	Val	Pro	Glu	Asn	Pro	Ile	Asp	Thr
				35				40					45		
Ala	Asn	Asn	Leu	Leu	Glu	Ser	Pro	His	Ser	Asp	Leu	Ser	Pro	Phe	Ile
				50				55					60		
Lys	Pro	Asn	His	Glu	Ser	Asp	Leu	Ser	Gln	Ser	Gln	Ser	Ser	Ser	Glu
				65				70					75		80
Asp	Asn	Asp	Asp	Arg	Lys	Thr	Lys	Leu	Leu	Lys	Ser	Ser	Pro	Leu	Val
				85				90					95		
Ala	Glu	Glu	Val	Ile	Gly	Pro	Ser	Thr	Pro	Pro	Glu	Ile	Ala	Pro	Pro
				100				105					110		
Arg	Arg	Ser	Phe	Pro	Glu	Asp	Ile	Gln	Thr	Tyr	Phe	Gly	Cys	Gln	Asn
				115				120					125		
Ser	Gly	Lys	Leu	Thr	Ala	Glu	Glu	Asp	Asp	Val	Ile	Phe	Gly	Asp	Leu
				130				135					140		
Asp	Ser	Phe	Leu	Thr	Pro	Asp	Phe	Tyr	Ser	Glu	Leu	Asn	Asp	Cys	
				145				150					155		

(2) INFORMATION FOR SEQ ID NO:1555:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1393 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1393
(D) OTHER INFORMATION: / Ceres Seq. ID 1500645
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1555:
aagccataga tattgacgaa atacactttt tgtctttttg ttgctgtgca acgtcataga 60
tctaactccg gaagaagaag aagatgagtg acgaaacgac gtcatctccg tccccagctc 120
cgggcagaag gaagcagaat ctgggatgga tggagtggat gaggggatgg agcagtggtt 180
ctggggagat tctcttccag aggatccacag ctctctattt ggagaatcct ctctctcttc 240
cttccgtcaa cgacctcaact tgcgttgtca ctggctccac cagcgcattt ggccgtgaaa 300
ccgcgaggca gcttgacgaa gctgggtgctc atgttgtgat ggccgtaagg aacacaaaagg 360
cggtccagga gctgatactg caatggcaga acgaaatggtc tggtaaaagg ctccccactg 420
aatattgagc aatggagatt gatctactct cactggattc tgtcgcgaga ttgtctgtag 480
ctttcaacgc tcggttagga cctttgcatg tcttgattaa caatgctggg atgttttgta 540
tgggagagcg gcaaaaattc tcagagggaag gatatgagca gcacatgcaa gtgaatcatt 600
tagctccagc gctgctttca gtaactcttt tgcgctctct gatccgaggc tctcctagcc 660
gaatcattaa tgtgaattcc gttatgcata gtgtcggttt tgttgaccgc gatgacatga 720
atgtttgttc tggtagacgt aagtaactcaa gccttatagg atactcaagc agcaagcttg 780
cccagattat gtttagtagc attctttttc aaaagcttcc tctggaacaa ggaatcagcg 840
tcgtatgtct atccccgtgt gttgtcctaa caaatgttgc cagggaatcta tccaggattc 900
ttcaagctct ttaacgagtg ataccttatt tcatattttc accccaagaa ggtttgtagaa 960
gttctctatt ctccggccaca gatcctcaga ttccagagta ctgggaacaa ctaaaaaaac 1020
atgattggcc tgtttggcca ttcactctctc aagattgcgc ccttgcaaat ccttccgaag 1080
aagcacacaa cacagaacct gcacagagag tgtggaaaaa gagcttagag ctgtgtgggtc 1140
ttcctctcga tgcagtttag aagctcatag aaggggaaaa tatccaatgc cggatgagg 1200
cacacacaga atagtctttc aaaattacca caggtttaagt gaccocattac agatcaaaag 1260
tgaggtaatt gagaaaaatg cttttttttt tgtttccttg tattaatcta cagcgtacag 1320
tggggaatgg atccccccag catgtagttt gcttgagaat gtttgattgt tggataaaag 1380
tcaagcttta gct
(2) INFORMATION FOR SEQ ID NO:1556:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 376 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..376
(D) OTHER INFORMATION: / Ceres Seq. ID 1500646
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1556:
Met Ser Asp Glu Thr Thr Ser Ser Pro Ser Pro Ala Pro Ala Lys Lys
1 5 10 15
Lys Gln Asn Leu Gly Trp Met Glu Trp Met Arg Gly Trp Ser Ser Val
20 25 30
Phe Gly Glu Ile Leu Phe Gln Arg Ile Thr Ala Ser His Leu Glu Asn
35 40 45
Pro Leu Pro Leu Pro Ser Val Asn Asp Leu Thr Cys Val Val Thr Gly
50 55 60
Ser Thr Ser Gly Ile Gly Arg Glu Thr Ala Arg Gln Leu Ala Glu Ala
65 70 75 80
Gly Ala His Val Val Met Ala Val Arg Asn Thr Lys Ala Ala Gln Glu
85 90 95
Leu Ile Leu Gln Trp Gln Asn Glu Trp Ser Gly Lys Gly Leu Pro Leu
100 105 110
Asn Ile Glu Ala Met Glu Ile Asp Leu Leu Ser Leu Asp Ser Val Ala
115 120 125
Arg Phe Ala Glu Ala Phe Asn Ala Arg Leu Gly Pro Leu His Val Leu
130 135 140

Ile Asn Asn Ala Gly Met Phe Ala Met Gly Glu Ala Gln Lys Phe Ser
145 150 155 160
Glu Glu Gly Tyr Glu Gln His Met Gln Val Asn His Leu Ala Pro Ala
165 170 175
Leu Leu Ser Val Leu Leu Leu Pro Ser Leu Ile Arg Gly Ser Pro Ser
180 185 190
Arg Ile Ile Asn Val Asn Ser Val Met His Ser Val Gly Phe Val Asp
195 200 205
Pro Asp Asp Met Asn Val Val Ser Gly Arg Arg Lys Tyr Ser Ser Leu
210 215 220
Ile Gly Tyr Ser Ser Ser Lys Leu Ala Gln Ile Met Phe Ser Ser Ile
225 230 235 240
Leu Phe Lys Lys Leu Pro Leu Glu Thr Gly Val Ser Val Val Cys Leu
245 250 255
Ser Pro Gly Val Val Leu Thr Asn Val Ala Arg Asp Leu Ser Arg Ile
260 265 270
Leu Gln Ala Leu Tyr Ala Val Ile Pro Tyr Phe Ile Phe Ser Pro Gln
275 280 285
Glu Gly Cys Arg Ser Ser Leu Phe Ser Ala Thr Asp Pro Gln Ile Pro
290 295 300
Glu Tyr Trp Glu Thr Leu Lys Asn Asp Asp Trp Pro Val Cys Pro Phe
305 310 315 320
Ile Ser Gln Asp Cys Arg Pro Ala Asn Pro Ser Glu Glu Ala His Asn
325 330 335
Thr Glu Thr Ala Gln Arg Val Trp Lys Lys Thr Leu Glu Leu Val Gly
340 345 350
Leu Pro Leu Asp Ala Val Glu Lys Leu Ile Glu Gly Glu Asn Ile Gln
355 360 365
Cys Arg Tyr Gly Ala Gln His Glu
370 375

(2) INFORMATION FOR SEQ ID NO:1557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..354
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1557:

Met Glu Trp Met Arg Gly Trp Ser Ser Val Phe Gly Glu Ile Leu Phe
1 5 10 15
Gln Arg Ile Thr Ala Ser His Leu Glu Asn Pro Leu Pro Leu Ser
20 25 30
Val Asn Asp Leu Thr Cys Val Val Thr Gly Ser Thr Ser Gly Ile Gly
35 40 45
Arg Glu Thr Ala Arg Gln Leu Ala Glu Ala Gly Ala His Val Val Met
50 55 60
Ala Val Arg Asn Thr Lys Ala Ala Gln Glu Leu Ile Leu Gln Trp Gln
65 70 75 80
Asn Glu Trp Ser Gly Lys Gly Leu Pro Leu Asn Ile Glu Ala Met Glu
85 90 95
Ile Asp Leu Leu Ser Leu Asp Ser Val Ala Arg Phe Ala Glu Ala Phe
100 105 110
Asn Ala Arg Leu Gly Pro Leu His Val Leu Ile Asn Asn Ala Gly Met
115 120 125
Phe Ala Met Gly Glu Ala Gln Lys Phe Ser Glu Glu Gly Tyr Glu Gln
130 135 140
His Met Gln Val Asn His Leu Ala Pro Ala Leu Leu Ser Val Leu Leu

145	150	155	160
Leu Pro Ser Leu Ile	Arg Gly Ser Pro Ser	Arg Ile Ile Asn Val Asn	
	165	170	175
Ser Val Met His Ser	Val Gly Phe Val Asp	Pro Asp Asp Met Asn Val	
	180	185	190
Val Ser Gly Arg Arg	Lys Tyr Ser Ser Leu Ile	Gly Tyr Ser Ser Ser	
	195	200	205
Lys Leu Ala Gln Ile	Met Phe Ser Ser Ile Leu	Phe Lys Lys Leu Pro	
	210	215	220
Leu Glu Thr Gly Val	Ser Val Val Cys Leu Ser	Pro Gly Val Val Leu	
	225	230	235
Thr Asn Val Ala Arg	Asp Leu Ser Arg Ile Leu	Gln Ala Leu Tyr Ala	
	245	250	255
Val Ile Pro Tyr Phe	Ile Phe Ser Pro Gln Glu	Gly Cys Arg Ser Ser	
	260	265	270
Leu Phe Ser Ala Thr	Asp Pro Gln Ile Pro Glu	Tyr Trp Glu Thr Leu	
	275	280	285
Lys Asn Asp Asp Trp	Pro Val Cys Pro Phe Ile	Ser Gln Asp Cys Arg	
	290	295	300
Pro Ala Asn Pro Ser	Glu Glu Ala His Asn Thr	Glu Thr Ala Gln Arg	
	305	310	315
Val Trp Lys Lys Thr	Leu Glu Leu Val Gly Leu	Pro Leu Asp Ala Val	
	325	330	335
Glu Lys Leu Ile Glu	Gly Glu Asn Ile Gln Cys	Arg Tyr Gly Ala Gln	
	340	345	350
His Glu			

(2) INFORMATION FOR SEQ ID NO:1558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..351
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1558:

Met Arg Gly Trp Ser Ser Val Phe Gly Glu Ile Leu Phe Gln Arg Ile	
1 5 10 15	
Thr Ala Ser His Leu Glu Asn Pro Leu Pro Leu Pro Ser Val Asn Asp	
20 25 30	
Leu Thr Cys Val Val Thr Gly Ser Thr Ser Gly Ile Gly Arg Glu Thr	
35 40 45	
Ala Arg Gln Leu Ala Glu Ala Gly Ala His Val Val Met Ala Val Arg	
50 55 60	
Asn Thr Lys Ala Ala Gln Glu Leu Ile Leu Gln Trp Gln Asn Glu Trp	
65 70 75 80	
Ser Gly Lys Gly Leu Pro Leu Asn Ile Glu Ala Met Glu Ile Asp Leu	
85 90 95	
Leu Ser Leu Asp Ser Val Ala Arg Phe Ala Glu Ala Phe Asn Ala Arg	
100 105 110	
Leu Gly Pro Leu His Val Leu Ile Asn Asn Ala Gly Met Phe Ala Met	
115 120 125	
Gly Glu Ala Gln Lys Phe Ser Glu Glu Gly Tyr Glu Gln His Met Gln	
130 135 140	
Val Asn His Leu Ala Pro Ala Leu Leu Ser Val Leu Leu Leu Pro Ser	
145 150 155 160	
Leu Ile Arg Gly Ser Pro Ser Arg Ile Ile Asn Val Asn Ser Val Met	
165 170 175	

His Ser Val Gly Phe Val Asp Pro Asp Asp Met Asn Val Val Ser Gly
180 185 190
Arg Arg Lys Tyr Ser Ser Leu Ile Gly Tyr Ser Ser Ser Lys Leu Ala
195 200 205
Gln Ile Met Phe Ser Ser Ile Leu Phe Lys Lys Leu Pro Leu Glu Thr
210 215 220
Gly Val Ser Val Val Cys Leu Ser Pro Gly Val Val Leu Thr Asn Val
225 230 235 240
Ala Arg Asp Leu Ser Arg Ile Leu Gln Ala Leu Tyr Ala Val Ile Pro
245 250 255
Tyr Phe Ile Phe Ser Pro Gln Glu Gly Cys Arg Ser Ser Leu Phe Ser
260 265 270
Ala Thr Asp Pro Gln Ile Pro Glu Tyr Trp Glu Thr Leu Lys Asn Asp
275 280 285
Asp Trp Pro Val Cys Pro Phe Ile Ser Gln Asp Cys Arg Pro Ala Asn
290 295 300
Pro Ser Glu Glu Ala His Asn Thr Glu Thr Ala Gln Arg Val Trp Lys
305 310 315 320
Lys Thr Leu Glu Leu Val Gly Leu Pro Leu Asp Ala Val Glu Lys Leu
325 330 335
Ile Glu Gly Glu Asn Ile Gln Cys Arg Tyr Gly Ala Gln His Glu
340 345 350

(2) INFORMATION FOR SEQ ID NO:1559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1272
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1559:

atagtaaacc	tattagccct	gtctttgtct	ttgaagcaac	ttctccagg	agggttggtt	60
jcaaaagctgc	tgctgggtgtg	tcagggtgact	tacctgagag	tactcctaag	gaacttagtc	120
agtatgagaa	gattattgag	cttttgacaa	ccctttttcc	actttgggtt	attttgggaa	180
cacttggttg	catcttcaag	coactccttg	ttacatggtt	ggaacacgat	ctcttttact	240
taggtctctg	atttcttatg	ctttccatgg	gtttgactct	tacgtttgaa	gatttcagaa	300
gatgtttacg	taatccatgg	acgggtgggtg	ttggtttttc	tgctcaatat	atgatcaacg	360
caattctagg	ttttctcatt	gcaatgactc	ttaagctttc	ggcacctctt	gcgactggcc	420
ttatcctagt	ctcatgctgc	cctggaggac	aggcgtaaaa	cgttgactact	tacatttcca	480
aggggaatgt	agcgctctct	gtactcatga	caacgtgttc	aaccattggg	gctattataa	540
tgactcctct	tctactaag	cttcttgctg	gtcagcttgt	tcccggtgac	ctgctgggac	600
ttgctcttag	taagttccaa	gtagtggttg	ttcctaccat	aattggagtt	ctggcaaatg	660
agttcttttc	taaaattacg	tctaagatca	taacagtgc	gcctctaato	ggagtcattc	720
tgactactct	gctctgtgct	agccctattg	gacaaagtgc	agatgttttg	aaaacccaag	780
gagctcaact	tactactccc	gtggcactcc	ttcatgctgc	agcctttgct	attggctatt	840
ggattttcaaa	gtttttcttc	ggcgagtcca	cttcgcgtac	cattttctata	gaatgtggaa	900
tgcaaaagtgc	agcgctcggg	ttcttgcttg	cacaaaagca	tttcacaaac	cctctagtgt	960
ctgttctctc	tcagtcagtt	gtttgtctgt	tggcgcttgg	cgggagcggc	ctggccgtgt	1020
tctggagaaa	cctacacgatt	ccggcagatg	acaaggatga	cttcaaaagag	taaatgaagt	1080
aggaagagct	gtttgcatct	tctccaaacg	atgtgattgt	ttgtttgttaa	gtttagtaaa	1140
cattacaaaa	tttgtgttga	aaaacatgaa	acaaaatgtg	tttaagagac	atagaacaaa	1200
gggcgtgcac	gatgacaact	tttgtgtcaa	cccttttttt	atttctcaat	taatggacaa	1260
atcttttttg	gc					

(2) INFORMATION FOR SEQ ID NO:1560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..356
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500650
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560:

Ser	Lys	Pro	Ile	Ser	Pro	Val	Phe	Ala	Leu	Glu	Ala	Thr	Ser	Ser	Arg
1				5						10				15	
Arg	Val	Val	Cys	Lys	Ala	Ala	Ala	Gly	Val	Ser	Gly	Asp	Leu	Pro	Glu
			20					25					30		
Ser	Thr	Pro	Lys	Glu	Leu	Ser	Gln	Tyr	Glu	Lys	Ile	Ile	Glu	Leu	Leu
		35					40					45			
Thr	Thr	Leu	Phe	Pro	Leu	Trp	Val	Ile	Leu	Gly	Thr	Leu	Val	Gly	Ile
		50				55					60				
Phe	Lys	Pro	Ser	Leu	Val	Thr	Trp	Leu	Glu	Thr	Asp	Leu	Phe	Thr	Leu
65				70						75					80
Gly	Leu	Gly	Phe	Leu	Met	Leu	Ser	Met	Gly	Leu	Thr	Leu	Thr	Phe	Glu
			85						90				95		
Asp	Phe	Arg	Arg	Cys	Leu	Arg	Asn	Pro	Trp	Thr	Val	Gly	Val	Gly	Phe
		100						105					110		
Leu	Ala	Gln	Tyr	Met	Ile	Lys	Pro	Ile	Leu	Gly	Phe	Leu	Ile	Ala	Met
		115					120					125			
Thr	Leu	Lys	Leu	Ser	Ala	Pro	Leu	Ala	Thr	Gly	Leu	Ile	Leu	Val	Ser
		130				135					140				
Cys	Cys	Pro	Gly	Gly	Gln	Ala	Ser	Asn	Val	Ala	Thr	Tyr	Ile	Ser	Lys
145				150						155				160	
Gly	Asn	Val	Ala	Leu	Ser	Val	Leu	Met	Thr	Thr	Cys	Ser	Thr	Ile	Gly
			165					170					175		
Ala	Ile	Ile	Met	Thr	Pro	Leu	Leu	Thr	Lys	Leu	Leu	Ala	Gly	Gln	Leu
			180					185					190		
Val	Pro	Val	Asp	Ala	Ala	Gly	Leu	Ala	Leu	Ser	Thr	Phe	Gln	Val	Val
		195					200					205			
Leu	Val	Pro	Thr	Ile	Ile	Gly	Val	Leu	Ala	Asn	Glu	Phe	Phe	Pro	Lys
		210				215					220				
Phe	Thr	Ser	Lys	Ile	Ile	Thr	Val	Thr	Pro	Leu	Ile	Gly	Val	Ile	Leu
225				230						235				240	
Thr	Thr	Leu	Leu	Cys	Ala	Ser	Pro	Ile	Gly	Gln	Val	Ala	Asp	Val	Leu
			245						250				255		
Lys	Thr	Gln	Gly	Ala	Gln	Leu	Ile	Leu	Pro	Val	Ala	Leu	Leu	His	Ala
		260						265					270		
Ala	Ala	Phe	Ala	Ile	Gly	Tyr	Trp	Ile	Ser	Lys	Phe	Ser	Phe	Gly	Glu
		275					280					285			
Ser	Thr	Ser	Arg	Thr	Ile	Ser	Ile	Glu	Cys	Gly	Met	Gln	Ser	Ser	Ala
		290				295					300				
Leu	Gly	Phe	Leu	Leu	Ala	Gln	Lys	His	Phe	Thr	Asn	Pro	Leu	Val	Ala
305				310						315				320	
Val	Pro	Ser	Ala	Val	Ser	Val	Val	Cys	Met	Ala	Leu	Gly	Gly	Ser	Gly
			325						330				335		
Leu	Ala	Val	Phe	Trp	Arg	Asn	Leu	Pro	Ile	Pro	Ala	Asp	Asp	Lys	Asp
			340				345					350			
Asp	Phe	Lys	Glu												
			355												

(2) INFORMATION FOR SEQ ID NO:1561:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 271 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1500651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561:

Met	Leu	Ser	Met	Gly	Leu	Thr	Leu	Thr	Phe	Glu	Asp	Phe	Arg	Arg	Cys	
1			5					10					15			
Leu	Arg	Asn	Pro	Trp	Thr	Val	Gly	Val	Gly	Phe	Leu	Ala	Gln	Tyr	Met	
			20					25					30			
Ile	Lys	Pro	Ile	Leu	Gly	Phe	Leu	Ile	Ala	Met	Thr	Leu	Lys	Leu	Ser	
		35				40					45					
Ala	Pro	Leu	Ala	Thr	Gly	Leu	Ile	Leu	Val	Ser	Cys	Cys	Pro	Gly	Gly	
		50				55					60					
Gln	Ala	Ser	Asn	Val	Ala	Thr	Tyr	Ile	Ser	Lys	Gly	Asn	Val	Ala	Leu	
65						70				75				80		
Ser	Val	Leu	Met	Thr	Thr	Cys	Ser	Thr	Ile	Gly	Ala	Ile	Ile	Met	Thr	
				85					90					95		
Pro	Leu	Leu	Thr	Lys	Leu	Leu	Ala	Gly	Gln	Leu	Val	Pro	Val	Asp	Ala	
			100					105					110			
Ala	Gly	Leu	Ala	Leu	Ser	Thr	Phe	Gln	Val	Val	Leu	Val	Pro	Thr	Ile	
		115					120					125				
Ile	Gly	Val	Leu	Ala	Asn	Glu	Phe	Phe	Pro	Lys	Phe	Thr	Ser	Lys	Ile	
		130				135					140					
Ile	Thr	Val	Thr	Pro	Leu	Ile	Gly	Val	Ile	Leu	Thr	Thr	Leu	Leu	Cys	
145					150					155				160		
Ala	Ser	Pro	Ile	Gly	Gln	Val	Ala	Asp	Val	Leu	Lys	Thr	Gln	Gly	Ala	
				165				170						175		
Gln	Leu	Ile	Leu	Pro	Val	Ala	Leu	Leu	His	Ala	Ala	Ala	Phe	Ala	Ile	
			180					185					190			
Gly	Tyr	Trp	Ile	Ser	Lys	Phe	Ser	Phe	Gly	Glu	Ser	Thr	Ser	Arg	Thr	
		195					200					205				
Ile	Ser	Ile	Glu	Cys	Gly	Met	Gln	Ser	Ser	Ala	Leu	Gly	Phe	Leu	Leu	
		210				215					220					
Ala	Gln	Lys	His	Phe	Thr	Asn	Pro	Leu	Val	Ala	Val	Pro	Ser	Ala	Val	
					230						235				240	
Ser	Val	Val	Cys	Met	Ala	Leu	Gly	Gly	Ser	Gly	Leu	Ala	Val	Phe	Trp	
				245					250					255		
Arg	Asn	Leu	Pro	Ile	Pro	Ala	Asp	Asp	Lys	Asp	Asp	Phe	Lys	Glu		
			260					265					270			

(2) INFORMATION FOR SEQ ID NO:1562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..268

(D) OTHER INFORMATION: / Ceres Seq. ID 1500652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562:

Met	Gly	Leu	Thr	Leu	Thr	Phe	Glu	Asp	Phe	Arg	Arg	Cys	Leu	Arg	Asn	
1			5					10					15			
Pro	Trp	Thr	Val	Gly	Val	Gly	Phe	Leu	Ala	Gln	Tyr	Met	Ile	Lys	Pro	
			20				25						30			
Ile	Leu	Gly	Phe	Leu	Ile	Ala	Met	Thr	Leu	Lys	Leu	Ser	Ala	Pro	Leu	
		35				40					45					
Ala	Thr	Gly	Leu	Ile	Leu	Val	Ser	Cys	Cys	Pro	Gly	Gly	Gln	Ala	Ser	
		50				55					60					
Asn	Val	Ala	Thr	Tyr	Ile	Ser	Lys	Gly	Asn	Val	Ala	Leu	Ser	Val	Leu	
65					70				75				80			
Met	Thr	Thr	Cys	Ser	Thr	Ile	Gly	Ala	Ile	Ile	Met	Thr	Pro	Leu	Leu	

	85		90		95
Thr Lys Leu	Leu Ala Gly	Gln Leu Val	Pro Val Asp	Ala Ala Gly	Leu
	100		105		110
Ala Leu Ser	Thr Phe Gln	Val Val Leu	Val Pro Thr	Ile Ile Gly	Val
	115		120		125
Leu Ala Asn	Glu Phe Phe	Pro Lys Phe	Thr Ser Lys	Ile Ile Thr	Val
	130		135		140
Thr Pro Leu	Ile Gly Val	Ile Leu Thr	Thr Leu Leu	Cys Ala Ser	Pro
	145		150		155
Ile Gly Gln	Val Ala Asp	Val Leu Lys	Thr Gln Gly	Ala Gln Leu	Ile
	165		170		175
Leu Pro Val	Ala Leu Leu	His Ala Ala	Phe Ala Ile	Gly Tyr Trp	
	180		185		190
Ile Ser Lys	Phe Ser Phe	Gly Glu Ser	Thr Ser Arg	Thr Ile Ser	Ile
	195		200		205
Glu Cys Gly	Met Gln Ser	Ser Ala Leu	Gly Phe Leu	Leu Ala Gln	Lys
	210		215		220
His Phe Thr	Asn Pro Leu	Val Ala Val	Pro Ser Ala	Val Ser Val	Val
	225		230		235
Cys Met Ala	Leu Gly Gly	Ser Gly Leu	Ala Val Phe	Trp Arg Asn	Leu
	245		250		255
Pro Ile Pro	Ala Asp Asp	Lys Asp Asp	Phe Lys Glu		
	260		265		

(2) INFORMATION FOR SEQ ID NO:1563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1563:

gagactgaag	atattttaac	tttttgattt	tggaagcaca	gagtgcctgat	gatcgggtgaa	60
gcctaaggaa	ggatttttaga	aagcaactga	gaacaaacct	tatccgttac	agtggcaatg	120
gaggacaaat	cgcgcagctt	accgatttct	gaagatttat	cccggaaaaa	aattctctctt	180
gccccgggtg	aagctcatac	gatacgtctg	accggcgatg	gatgtgtgta	ctcatgggga	240
agaggaatgt	ttgggcgtct	tggtacgggt	aaggaatcgg	acgagcttgt	tccagttcga	300
gtcgagttcg	agttcccaaa	tcaagcggaa	ggagaacgga	ttcgaatcat	tggtgttgct	360
gctggtgctt	atcacagtct	cgctgtctca	gatgatggct	cggtttgggt	ttgggggttat	420
aacatttatg	gtcaacttgg	ttttgatggg	gaaaactcct	ttgcaccatg	tttgggtcaaa	480
aatttggttg	aacaagaagc	atctagtctt	tctct			

(2) INFORMATION FOR SEQ ID NO:1564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1564:

Met Glu Asp	Lys Ser Pro	Thr Leu Pro	Ile Ser Glu	Asp Leu Ser	Arg
1	5	10	15		
Lys Ile Ile	Ser Leu Ala	Ala Gly Glu	Ala His Thr	Ile Ala Leu	Thr
	20	25	30		
Gly Asp Gly	Cys Val Tyr	Ser Trp Gly	Arg Gly Met	Phe Gly Arg	Leu

35	40	45
Gly Thr Gly Lys Glu Ser Asp Glu Leu Val Pro Val Arg Val Glu Phe		
50	55	60
Glu Phe Pro Asn Gln Ala Glu Gly Glu Arg Ile Arg Ile Ile Gly Val		
65	70	75
Ala Ala Gly Ala Tyr His Ser Leu Ala Val Ser Asp Asp Gly Ser Val		
85	90	95
Trp Cys Trp Gly Tyr Asn Ile Tyr Gly Gln Leu Gly Phe Asp Gly Glu		
100	105	110
Asn Ser Leu Ala Pro Cys Leu Val Lys Asn Leu Phe Glu Gln Glu Ala		
115	120	125
Ser Ser Ser Ser		
130		

(2) INFORMATION FOR SEQ ID NO:1565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..99

- (D) OTHER INFORMATION: / Ceres Seq. ID 1500655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565:

Met Asp Val Cys Thr His Gly Glu Glu Glu Cys Leu Gly Val Leu Val		
1	5	10
Arg Val Arg Asn Arg Thr Ser Leu Phe Gln Phe Glu Ser Ser Ser Ser		
20	25	30
Ser Gln Ile Lys Arg Lys Glu Asn Gly Phe Glu Ser Leu Val Leu Leu		
35	40	45
Leu Val Leu Ile Thr Val Ser Leu Ser Gln Met Met Ala Arg Phe Gly		
50	55	60
Val Gly Val Ile Thr Phe Met Val Asn Leu Val Leu Met Gly Lys Thr		
65	70	75
Pro Trp His His Val Trp Ser Lys Ile Cys Leu Asn Lys Lys His Leu		
85	90	95
Val Leu Leu		

(2) INFORMATION FOR SEQ ID NO:1566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..89

- (D) OTHER INFORMATION: / Ceres Seq. ID 1500656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566:

Met Phe Gly Arg Leu Gly Thr Gly Lys Glu Ser Asp Glu Leu Val Pro		
1	5	10
Val Arg Val Glu Phe Glu Phe Pro Asn Gln Ala Glu Gly Glu Arg Ile		
20	25	30
Arg Ile Ile Gly Val Ala Ala Gly Ala Tyr His Ser Leu Ala Val Ser		
35	40	45
Asp Asp Gly Ser Val Trp Cys Trp Gly Tyr Asn Ile Tyr Gly Gln Leu		
50	55	60
Gly Phe Asp Gly Glu Asn Ser Leu Ala Pro Cys Leu Val Lys Asn Leu		
65	70	75
		80

(2) INFORMATION FOR SEO ID NO:1567:

(2) INFORMATION FOR SEO ID NO:1567:

(A) LENGTH: 1326 base pa

- (A) LENGTH: 1326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1326
(D) OTHER INFORMATION: / Ceres Seq. ID 1500661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567:

aaaaaccctca	gaaaaccctt	ggagctgatg	agatagatgca	ggattccagt	caagtcocata	150
ggatctccaca	atcgaaagat	gtcgatggag	ttagatggct	tcacaaagct	tctgctttga	160
atcgtctctga	cgcacaacgc	tccatgaagc	cggaattgtga	tcttccatca	atcgacgatcc	180
aatcgctctga	cccaaacctc	agagggaatc	caacacacgaa	cccgcttaatc	ggctcgttat	240
cttcgatggac	ttcaacctct	cgagctttcgt	ctctagaagt	cgcgggaaac	ggcggtgtgt	300
cgggttccatt	caaaacccaat	gtttccacagc	ctacgctctc	tggttcttga	caagcttctga	360
tgaattgatt	gggtgaaagg	gtcgcgatgt	aagaagcttta	cgctcgccgaa	gggggaagag	420
ttctcatrtg	ggacgcgttg	aaggtgttga	tgtgaagag	ggaggaagaat	gtgttactgt	480
tgtgaagat	ggggagatga	attgagttaa	tgattgtaat	gtgaaaggtt	taagttatag	540
aaaggtctttt	gatgggaatg	gattgtggtc	tatatagaag	tgtaaatggg	cttctccgac	600
tgaagttctt	actggaggat	attggttttt	tttgcaagt	gtggactaga	ggaagtctgg	660
tgaagctgtt	tcacaactca	aagggaatgt	gtttcagaag	aaaaactctg	caattgtcca	720
ctccattcat	attcatccat	ctcggaagca	cacttgcatc	cgcggaagtt	cttcaggtag	780
tgtatttctg	ttgggatctc	gtgtgccaca	caaccccat	gtttcttctg	ggggtggagc	840
aagtagaagt	ataaacaatc	ctctgtctga	aagtaggta	tgggaagtct	agtagtaac	900
tcaacacaaa	tccaacgtct	caatcccaag	gattctccct	gttatagct	gctctgaaga	960
tggaaatct	ggtatcatag	acaacaggga	agaaacaaat	gaagctcttg	ctgaaccttg	1020
tgccattcaat	agttttgaca	tcgcacggca	aaatccacag	gatgttgat	tatgctttga	1080
gtgggaatac	atagcagttt	ttccaaggct	ttagtataat	atggaacagt	gcacggtatg	1140
ctagcttttc	ttctgcgacg	tcaacaagag	aaattgagga	aggttagtat	agatgatgag	1200
acaaagtttt	aaggaaagag	gtgtggaagt	ttgtttaa	ttccattata	acaagatctt	1260
aaataacatt	ctgcacaaac	agagttttgt	attcatctta	aagttagtgt	gatcttgaag	1320
attatgc						

(2) INFORMATION FOR SEQ ID NO:1568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide
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(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..157
(D) OTHER INFORMATION: / Ceres Seq. ID 1500662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568:

Met	Glu	Met	Met	Gln	Asp	Ser	Phe	Gln	Val	His	Arg	Ile	Pro	Gln	Ser
1				5				10					15		
Lys	Tyr	Val	Asp	Gly	Val	Arg	Trp	Leu	Pro	Gln	Ala	Ser	Ala	Leu	Asn
			20					25					30		
Arg	Phe	Phe	Ala	Thr	Ala	Ser	Tyr	Asp	Ala	Asp	Cys	Asp	Ser	Ser	Ser
		35					40					45			
Ile	Glu	Ile	Gln	Ser	Leu	Asp	Pro	Asn	Pro	Arg	Gly	Asn	His	Asn	Thr
	50					55					60				
Asn	Pro	Leu	Ile	Glu	Ser	Leu	Ser	Ser	Trp	Thr	Ser	Pro	Ser	Arg	Val
65					70					75				80	
Ser	Ser	Leu	Glu	Val	Ala	Gly	Asn	Gly	Gly	Gly	Gly	Ser	Phe	Lys	
				85				90					95		

Pro Met Val Ser Ala Ala Thr Ser Ser Gly Ser Leu His Val Leu Met
100 105 110
Ile Asp Leu Val Glu Gly Ala Ala Ile Glu Glu Val Trp Ala Ala Glu
115 120 125
Gly Gly Glu Val Ser Xaa Trp Asp Ala Trp Lys Val Trp Ile Gly Glu
130 135 140
Arg Glu Glu Asn Val Leu Leu Leu Val Lys Met Gly Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:1569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1569:

Met Met Gln Asp Ser Phe Gln Val His Arg Ile Pro Gln Ser Lys Tyr
1 5 10 15
Val Asp Gly Val Arg Trp Leu Pro Gln Ala Ser Ala Leu Asn Arg Phe
20 25 30
Phe Ala Thr Ala Ser Tyr Asp Ala Asp Cys Asp Ser Ser Ile Glu
35 40 45
Ile Gln Ser Leu Asp Pro Asn Pro Arg Gly Asn His Asn Thr Asn Pro
50 55 60
Leu Ile Glu Ser Leu Ser Ser Trp Thr Ser Pro Ser Arg Val Ser Ser
65 70 75 80
Leu Glu Val Ala Gly Asn Gly Gly Gly Gly Ser Phe Lys Pro Met
85 90 95
Val Ser Ala Ala Thr Ser Ser Gly Ser Leu His Val Leu Met Ile Asp
100 105 110
Leu Val Glu Gly Ala Ala Ile Glu Glu Val Tyr Ala Ala Glu Gly Gly
115 120 125
Glu Val Ser Xaa Trp Asp Ala Trp Lys Val Trp Ile Gly Glu Arg Glu
130 135 140
Glu Asn Val Leu Leu Leu Val Lys Met Gly Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:1570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570:

Met Gln Asp Ser Phe Gln Val His Arg Ile Pro Gln Ser Lys Tyr Val
1 5 10 15
Asp Gly Val Arg Trp Leu Pro Gln Ala Ser Ala Leu Asn Arg Phe Phe
20 25 30
Ala Thr Ala Ser Tyr Asp Ala Asp Cys Asp Ser Ser Ile Glu Ile
35 40 45
Gln Ser Leu Asp Pro Asn Pro Arg Gly Asn His Asn Thr Asn Pro Leu
50 55 60
Ile Glu Ser Leu Ser Ser Trp Thr Ser Pro Ser Arg Val Ser Ser Leu

65					70						75						80
Glu	Val	Ala	Gly	Asn	Gly	Gly	Gly	Gly	Gly	Ser	Phe	Lys	Pro	Met	Val		
				85					90					95			
Ser	Ala	Ala	Thr	Ser	Ser	Gly	Ser	Leu	His	Val	Leu	Met	Ile	Asp	Leu		
				100					105					110			
Val	Glu	Gly	Ala	Ala	Ile	Glu	Glu	Val	Tyr	Ala	Ala	Glu	Gly	Gly	Glu		
				115					120					125			
Val	Ser	Xaa	Trp	Asp	Ala	Trp	Lys	Val	Trp	Ile	Gly	Glu	Arg	Glu	Glu		
				130					135					140			
Asn	Val	Leu	Leu	Leu	Val	Lys	Met	Gly	Glu								
145					150												

(2) INFORMATION FOR SEQ ID NO:1571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..542
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1571:

acataagttct	ctctctttaca	ttttgaaacc	ctaattttctc	aaaataaatg	tctgaagttg	60
agtaccgggtg	ctttgtgggc	ggcctttgcct	gggccaacaa	tgatgaagat	cttcaaaagga	120
cgttctcaaca	gttcggcgac	gttatcgatt	ctaagatcat	taacgaccgc	gagagtggaa	180
gatcaagggg	attcggattc	gtcaccttca	aggacgagaa	agccatgagg	gatgcgattg	240
aagagatgaa	cggtaaaagag	ctcgaatggac	gtgtcatcac	cgtgaacgag	gctcagtcga	300
gaggtacggc	cggatgatgt	gaaagtacg	gaggcggtgg	tgccgctgg	taatacaaga	360
tagagttgtt	tgctgtctgc	tgctctgttt	ttggtttaga	tttggtattg	tgtaaccact	420
tctgtttgtg	ttatcgttgc	tttggtttac	ttttttgatg	aaacagtttc	gttttaagtct	480
tctttgtctg	gatcgaaatg	ttaattcgcg	tgttgtttac	taaatattata	acgttttcctt	540
tt						

(2) INFORMATION FOR SEQ ID NO:1572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1572:

Met	Ser	Glu	Val	Glu	Tyr	Arg	Cys	Phe	Val	Gly	Gly	Leu	Ala	Trp	Ala	
1				5					10					15		
Thr	Asn	Asp	Glu	Asp	Leu	Gln	Arg	Thr	Phe	Ser	Gln	Phe	Gly	Asp	Val	
				20				25						30		
Ile	Asp	Ser	Lys	Ile	Ile	Asn	Asp	Arg	Glu	Ser	Gly	Arg	Ser	Arg	Gly	
				35				40						45		
Phe	Gly	Phe	Val	Thr	Phe	Lys	Asp	Glu	Lys	Ala	Met	Arg	Asp	Ala	Ile	
				50				55						60		
Glu	Gly	Met	Asn	Gly	Lys	Glu	Leu	Asp	Gly	Arg	Val	Ile	Thr	Val	Asn	
				65				70						75		
Glu	Ala	Gln	Ser	Arg	Gly	Ser	Gly	Gly	Asp	Gly	Glu	Ser	Tyr	Gly	Gly	
				85				90						95		
Gly	Gly	Gly	Gly	Trp												
				100												

(2) INFORMATION FOR SEQ ID NO:1573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 931 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..931
(D) OTHER INFORMATION: / Ceres Seq. ID 1500667
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1573:
aagatgggga cgaattgag ctggatatag aagctgtcga caatgagact ctatggggagc 60
ttgatcgttt tgtgacgaac tacaagaaga tggcttagcaa aatcaagcgc caaggggttta 120
tcagggaacgt gtcaactcca cttaggaaca tggcttcgggt agcagaaaatg ggtagtgcggg 180
agaagagaaac aaggagagga gatgcagggg aagaggatgt tgacattgga gaggaacatac 240
caatcgaaga ttatccatct stagagatcg aaagagatgg gtactgcagt tgcagctgct 300
gctagttagtg gttctagttc ttcaggcagt tccagttcta gtggtggtag ttctcgtct 360
agtgattcag ggtcagggtg gagtctcatca ggtagtgtatt ctgatgcaga tagtgttcaa 420
tcgccatttg tggaaagaaa agaagcccaa tgttaaaato atttgggaat ttaaccgttg 480
attctgtcct gaagtactag gaacgttttag ctgagggtgt aaagggaggga atgaagggga 540
aaactgaagg aaaggatttg tttttcttt cgatgataaa ctttaggaagc agatgtagtt 600
agaaagaaaa aatgtaaatg gtatagatgaa agagaatgct agtttaagca agaagaagag 660
ttcgttattt aatacctttt acatttagga gttgtttagt gtatttgtga gatcgtgaac 720
agagggtagg agtgagtggg taggtactgt aggagaagaa gaagaagaaa agagtctttt 780
taggttctat gactttattt attttcttt gttagtatgt ttaaagagtc tggttggtgt 840
aggaaaaatg gtgtagaaga agaagaaga aatcaatgca atgtatcaga tgtaaatggt 900
tggcatatta aaaaagaaaa gttgattttc c
(2) INFORMATION FOR SEQ ID NO:1574:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..100
(D) OTHER INFORMATION: / Ceres Seq. ID 1500668
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1574:
Asp Gly Asp Glu Ile Glu Leu Asp Ile Glu Ala Val Asp Asn Glu Thr
1 5 10 15
Leu Trp Glu Leu Asp Arg Phe Val Thr Asn Tyr Lys Lys Met Ala Ser
20 25 30
Lys Ile Lys Arg Gln Gly Phe Ile Arg Asn Val Ser Thr Pro Leu Arg
35 40 45
Asn Met Ala Ser Val Ala Glu Met Gly Ser Ala Glu Lys Arg Thr Arg
50 55 60
Arg Gly Asp Ala Gly Glu Glu Asp Val Asp Ile Gly Glu Asp Ile Pro
65 70 75 80
Ile Glu Asp Tyr Pro Ser Xaa Glu Ile Glu Arg Asp Gly Tyr Cys Ser
85 90 95
Cys Ser Cys Cys
100
(2) INFORMATION FOR SEQ ID NO:1575:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1500669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1575:

Met	Ala	Ser	Lys	Ile	Lys	Arg	Gln	Gly	Phe	Ile	Arg	Asn	Val	Ser	Thr	
1			5					10					15			
Pro	Leu	Arg	Asn	Met	Ala	Ser	Val	Ala	Glu	Met	Gly	Ser	Ala	Glu	Lys	
			20					25					30			
Arg	Thr	Arg	Arg	Gly	Asp	Ala	Gly	Glu	Asp	Val	Asp	Ile	Gly	Glu		
			35				40				45					
Asp	Ile	Pro	Ile	Glu	Asp	Tyr	Pro	Ser	Xaa	Glu	Ile	Glu	Arg	Asp	Gly	
	50				55					60						
Thr	Cys	Ser	Cys	Ser	Cys											
65				70												

(2) INFORMATION FOR SEQ ID NO:1576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1500670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1576:

Met	Gly	Thr	Ala	Val	Ala	Ala	Ala	Ala	Ser	Ser	Gly	Ser	Ser	Ser		
1			5					10					15			
Gly	Ser	Ser	Ser	Ser	Ser	Gly	Gly	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Gly	
			20					25					30			
Ser	Gly	Gly	Ser	Ser	Ser	Gly	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Val	Gln	
			35			40					45					
Ser	Pro	Phe	Val	Glu	Ala	Lys	Glu	Ala	Gln	Cys						
	50				55											

(2) INFORMATION FOR SEQ ID NO:1577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1506 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1506

(D) OTHER INFORMATION: / Ceres Seq. ID 1500675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577:

accgagaaat	gggactgtca	gcgaatacac	aaaccaacgg	caacgcaccg	ccaccgtcgt	60
cgaatcaaaa	gcctccggct	acgaacggcg	ttgatgggtc	tcactctcct	ctctctcctt	120
taactctcta	tcaagctatt	atagagtcgg	atccgctcga	gaagaggaaa	atgggggatgc	180
ttctctaga	agtgggtact	cgtgtgatgt	gtcgggtggg	agacggggaa	caccatccgg	240
tgaagaatatt	tgagcgccgg	cggataycat	aacggcggtc	aaaatgatta	cgagtattac	300
gttcattaca	ctgagtttaa	taggaggctg	gatgaatgga	ctcagctgga	ccaactggac	360
cttgatttgc	tagagtgcgc	tgtatagtga	aaattggaag	acaaggtaac	aagcttgaag	420
gatgacacgt	caccagaaga	ggaagatcga	tgaggacaca	tatagagggt	catgaagagc	480
tggatgcagc	aagtttgcgt	gaacatgaag	agttcacgaa	agtgagaac	atatcaacaa	540
ttgagcttgg	aaaatgatag	attgagacct	ggctactctc	cccttttccg	ccagaataca	600
atgactgtgt	gaagctcttt	ttttgtgagt	tttgcttgaa	cttcattgaa	cgcaaaagagc	660
agcttcaaag	gcataatgag	aagttgtgac	tgaagcacc	acctgtgtgat	gaattttacc	720
gaagtgatgc	cttgtcaatg	tttgaggtag	atggcaaaaa	gaacaaggtt	tatgcacaga	780
atctctgcta	cctgcgcaag	ttatttcttg	accacaaaac	tctttactac	gatgttgatt	840
gtttttctatt	ctacgttctt	tgcgaaatgt	atgaccgagg	atgccacatg	gttgggtact	900
tttcaaaagga	gaagcattcg	gaagaagcat	acaacttagc	ttgcattcta	accctgcctt	960

catatcaaaag	aaaaggctat	gaaaagtctt	taatagccct	ttcctatgaa	ctgtcaaaaga	1020
aagagggaag	agttgggaca	ccggraaaga	cccttgctcg	atctaggctt	actaagctac	1080
agaggttatt	ggactcgtgt	tctattagaa	atcttgaaaa	aacataaggg	aaacatttct	1140
atcaaggagc	tgagcgacgt	gacagcaatc	aaagcggaag	atatattaa	cacacttcaag	1200
agcctagaac	tgatacagta	caggaaagga	cagcatgtga	tctgtgcgga	tccaaaggtt	1260
ctggaccgac	atctgaaagc	tcagggccga	ggtggtcttg	atgtagatgc	tagcaaaactg	1320
atttgacac	cttacaagga	ccagagttaa	gagtaagtac	actcctcttg	tgccattgga	1380
tttgatttga	gtgtgtaagt	aaggggctgt	cttattctcc	tgaatgtaa	gtgtacttta	1440
cttgtaaatg	ttgaaatgt	acttggaatg	gtgtttgttt	acaactnctt	ataatgagga	1500
aatttg						

(2) INFORMATION FOR SEQ ID NO:1578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..225

(D) OTHER INFORMATION: / Ceres Seq. ID 1500676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578:

Met	Arg	Thr	His	Ile	Glu	Gly	His	Glu	Leu	Asp	Ala	Ala	Ser	Leu
1			5					10					15	
Arg	Glu	His	Glu	Glu	Phe	Thr	Lys	Val	Lys	Asn	Ile	Ser	Thr	Ile
			20					25				30		
Leu	Gly	Lys	Tyr	Glu	Ile	Glu	Thr	Trp	Tyr	Phe	Ser	Pro	Phe	Pro
			35				40				45			
Glu	Tyr	Asn	Asp	Cys	Val	Lys	Leu	Phe	Phe	Cys	Glu	Phe	Cys	Leu
			50			55					60			
Phe	Met	Lys	Arg	Lys	Glu	Gln	Leu	Gln	Arg	His	Met	Xaa	Lys	Cys
65					70				75					80
Leu	Lys	His	Pro	Pro	Gly	Asp	Glu	Ile	Tyr	Arg	Ser	Gly	Thr	Leu
			85						90				95	
Met	Phe	Glu	Val	Asp	Gly	Lys	Lys	Asn	Lys	Val	Tyr	Ala	Gln	Asn
			100					105					110	
Cys	Tyr	Leu	Ala	Lys	Leu	Phe	Leu	Asp	His	Lys	Thr	Leu	Tyr	Asp
			115				120					125		
Val	Asp	Leu	Phe	Leu	Phe	Tyr	Val	Leu	Cys	Glu	Cys	Asp	Asp	Arg
			130			135					140			
Cys	His	Met	Val	Gly	Tyr	Phe	Ser	Lys	Glu	Lys	His	Ser	Glu	Glu
145					150				155					160
Tyr	Asn	Leu	Ala	Cys	Ile	Leu	Thr	Leu	Pro	Ser	Tyr	Gln	Arg	Lys
			165						170				175	
Tyr	Gly	Lys	Phe	Leu	Ile	Ala	Phe	Ser	Tyr	Glu	Leu	Ser	Lys	Glu
			180					185					190	
Gly	Lys	Val	Gly	Thr	Pro	Xaa	Lys	Thr	Leu	Val	Gly	Ser	Arg	Leu
			195				200					205		
Lys	Leu	Gln	Arg	Leu	Leu	Asp	Ser	Cys	Ser	Ile	Arg	Asn	Leu	Glu
			210				215				220			

Thr
225

(2) INFORMATION FOR SEQ ID NO:1579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1500677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1579:

Met	Lys	Arg	Lys	Glu	Gln	Leu	Gln	Arg	His	Met	Xaa	Lys	Cys	Asp	Leu
1				5					10					15	
Lys	His	Pro	Pro	Gly	Asp	Glu	Ile	Tyr	Arg	Ser	Gly	Thr	Leu	Ser	Met
			20					25					30		
Phe	Glu	Val	Asp	Gly	Lys	Lys	Asn	Lys	Val	Tyr	Ala	Gln	Asn	Leu	Cys
		35					40				45				
Tyr	Leu	Ala	Lys	Leu	Phe	Leu	Asp	His	Lys	Thr	Leu	Tyr	Tyr	Asp	Val
		50				55				60					
Asp	Leu	Phe	Leu	Phe	Tyr	Val	Leu	Cys	Glu	Cys	Asp	Asp	Arg	Gly	Cys
65					70				75					80	
His	Met	Val	Gly	Tyr	Phe	Ser	Lys	Glu	Lys	His	Ser	Glu	Glu	Ala	Tyr
			85					90						95	
Asn	Leu	Ala	Cys	Ile	Leu	Thr	Leu	Pro	Ser	Tyr	Gln	Arg	Lys	Gly	Tyr
			100					105					110		
Gly	Lys	Phe	Leu	Ile	Ala	Phe	Ser	Tyr	Glu	Leu	Ser	Lys	Lys	Glu	Gly
		115					120					125			
Lys	Val	Gly	Thr	Pro	Xaa	Lys	Thr	Leu	Val	Gly	Ser	Arg	Leu	Thr	Lys
		130				135					140				
Leu	Gln	Arg	Leu	Leu	Asp	Ser	Cys	Ser	Ile	Arg	Asn	Leu	Glu	Lys	Thr
145					150					155					160

(2) INFORMATION FOR SEQ ID NO:1580:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1500678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580:

Met	Xaa	Lys	Cys	Asp	Leu	Lys	His	Pro	Pro	Gly	Asp	Glu	Ile	Tyr	Arg
1				5					10					15	
Ser	Gly	Thr	Leu	Ser	Met	Phe	Glu	Val	Asp	Gly	Lys	Lys	Asn	Lys	Val
			20					25					30		
Tyr	Ala	Gln	Asn	Leu	Cys	Tyr	Leu	Ala	Lys	Leu	Phe	Leu	Asp	His	Lys
		35					40				45				
Thr	Leu	Tyr	Tyr	Asp	Val	Asp	Leu	Phe	Leu	Phe	Tyr	Val	Leu	Cys	Glu
		50				55				60					
Cys	Asp	Asp	Arg	Gly	Cys	His	Met	Val	Gly	Tyr	Phe	Ser	Lys	Glu	Lys
65					70				75					80	
His	Ser	Glu	Glu	Ala	Tyr	Asn	Leu	Ala	Cys	Ile	Leu	Thr	Leu	Pro	Ser
			85					90						95	
Tyr	Gln	Arg	Lys	Gly	Tyr	Gly	Lys	Phe	Leu	Ile	Ala	Phe	Ser	Tyr	Glu
			100				105					110			
Leu	Ser	Lys	Lys	Glu	Gly	Lys	Val	Gly	Thr	Pro	Xaa	Lys	Thr	Leu	Val
		115				120						125			
Gly	Ser	Arg	Leu	Thr	Lys	Leu	Gln	Arg	Leu	Leu	Asp	Ser	Cys	Ser	Ile
		130				135					140				
Arg	Asn	Leu	Glu	Lys	Thr										
145					150										

(2) INFORMATION FOR SEQ ID NO:1581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 889 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..889
(D) OTHER INFORMATION: / Ceres Seq. ID 1500679
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1581:
aaaacgaact agagacagtt tgattcgaaa atcttgctcg aaaatggagg atatcgtcga 60
ccaagaatta agcaattact gggaacctag ctccctgctc caaaacgaat acttcgaata 120
cgacagcttg cctttggaag aagccatttc tgggtcgatg gattcgagtt cgccggatgg 180
agctgcttgc tcgccggctt ctaagaatat tgtgtcggag agaacacagaa gacagaaact 240
taaccagaga ctcttcgctc ttgatcagtt tgttcccaat atcactaaga tggataaagc 300
ctcaataatc aaagatgcta ttagttacat agaaggatta caatatgaag aaaagaagct 360
cgaagctgag atcagagaaac ttgaatctac accaaagagt agccttagtt tcagcaaaag 420
attttgatcg tgatttaactt gttcctgtca catccaagaa gatgaagcag cttgattctg 480
gttcttcac ttctctcatc gaagttctcg aattgaaggt aacattcatg ggagagagga 540
caatgtgtgt gagtgttaaca tgtaataaga ggacagatac aatggtgaaa ctgtgtgaa 600
tctttgagtc attgaatctc aaaaatctca cttccaatct cactcttttc tctggcatga 660
tcttcacac tgcttttatt gaggcgatg aagaagaaca agagggtgtt cggttaaaaa 720
tagaacaagg aataggagct tataatgaaa ctcaagcccc tactttgagc atcgactctc 780
tttactaata atactttttt tcttctttt ttggttcatt ttggtctctc tctttacaat 840
aatgtatgtc tctcttttca tttttatgat ctctacgctt tgtttgtcc

(2) INFORMATION FOR SEQ ID NO:1582:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..141
(D) OTHER INFORMATION: / Ceres Seq. ID 1500680
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582:
Lys Arg Thr Arg Asp Ser Leu Ile Arg Lys Ser Cys Arg Lys Met Glu
1 5 10 15
Asp Ile Val Asp Gln Glu Leu Ser Asn Tyr Trp Glu Pro Ser Ser Leu
20 25 30
Leu Gln Asn Glu Tyr Phe Glu Tyr Asp Ser Trp Pro Leu Glu Glu Ala
35 40 45
Ile Ser Gly Ser Tyr Asp Ser Ser Ser Pro Asp Gly Ala Ala Ser Ser
50 55 60
Pro Ala Ser Lys Asn Ile Val Ser Glu Arg Asn Arg Arg Gln Lys Leu
65 70 75 80
Asn Gln Arg Leu Phe Ala Leu Arg Ser Val Val Pro Asn Ile Thr Lys
85 90 95
Met Asp Lys Ala Ser Ile Ile Lys Asp Ala Ile Ser Tyr Ile Glu Gly
100 105 110
Leu Gln Tyr Glu Glu Lys Lys Leu Glu Ala Glu Ile Arg Glu Leu Glu
115 120 125
Ser Thr Pro Lys Ser Ser Leu Ser Phe Ser Lys Gly Phe
130 135 140

(2) INFORMATION FOR SEQ ID NO:1583:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..127
(D) OTHER INFORMATION: / Ceres Seq. ID 1500681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1583:

Met	Glu	Asp	Ile	Val	Asp	Gln	Glu	Leu	Ser	Asn	Tyr	Trp	Glu	Pro	Ser
1			5				10				15				
Ser	Leu	Leu	Gln	Asn	Glu	Tyr	Phe	Glu	Tyr	Asp	Ser	Trp	Pro	Leu	Glu
			20				25				30				
Glu	Ala	Ile	Ser	Gly	Ser	Tyr	Asp	Ser	Ser	Ser	Pro	Asp	Gly	Ala	Ala
			35				40				45				
Ser	Ser	Pro	Ala	Ser	Lys	Asn	Ile	Val	Ser	Glu	Arg	Asn	Arg	Arg	Gln
			50				55				60				
Lys	Leu	Asn	Gln	Arg	Leu	Phe	Ala	Leu	Arg	Ser	Val	Val	Pro	Asn	Ile
65			70				75				80				
Thr	Lys	Met	Asp	Lys	Ala	Ser	Ile	Ile	Lys	Asp	Ala	Ile	Ser	Tyr	Ile
			85				90				95				
Glu	Gly	Leu	Gln	Tyr	Glu	Glu	Lys	Lys	Leu	Glu	Ala	Glu	Ile	Arg	Glu
			100				105				110				
Leu	Glu	Ser	Thr	Pro	Lys	Ser	Ser	Leu	Ser	Phe	Ser	Lys	Gly	Phe	
			115				120				125				

(2) INFORMATION FOR SEQ ID NO:1584:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..147
(D) OTHER INFORMATION: / Ceres Seq. ID 1500682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584:

Met	Lys	Lys	Arg	Ser	Ser	Lys	Leu	Arg	Ser	Glu	Asn	Leu	Asn	Leu	His
1			5				10				15				
Gln	Arg	Val	Ala	Leu	Val	Ser	Ala	Lys	Asp	Phe	Asp	Arg	Asp	Leu	Leu
			20				25				30				
Val	Pro	Val	Thr	Ser	Lys	Lys	Met	Lys	Gln	Leu	Asp	Ser	Gly	Ser	Ser
			35				40				45				
Thr	Ser	Leu	Ile	Glu	Val	Leu	Glu	Leu	Lys	Val	Thr	Phe	Met	Gly	Glu
			50				55				60				
Arg	Thr	Met	Val	Val	Ser	Val	Thr	Cys	Asn	Lys	Arg	Thr	Asp	Thr	Met
65			70				75				80				
Val	Lys	Leu	Cys	Glu	Val	Phe	Glu	Ser	Leu	Asn	Leu	Lys	Ile	Leu	Thr
			85				90				95				
Ser	Asn	Leu	Thr	Ser	Phe	Ser	Gly	Met	Ile	Phe	His	Thr	Val	Phe	Ile
			100				105				110				
Glu	Ala	Asp	Glu	Glu	Glu	Gln	Glu	Val	Leu	Arg	Leu	Lys	Ile	Glu	Thr
			115				120				125				
Gly	Ile	Gly	Ala	Tyr	Asn	Glu	Thr	Gln	Ser	Pro	Thr	Leu	Ser	Ile	Asp
130			135				140								

Ser Leu Tyr
145

(2) INFORMATION FOR SEQ ID NO:1585:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 672 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587:

Met Asn Phe Ile Ser Asp Gln Val Lys Lys Leu Ser Ser Ser Thr Pro
1 5 10 15
Glu Glu Pro Asp His Asn Lys Pro Val Glu Gly Thr Glu Thr Ala Thr
20 25 30
Arg Pro Ala Thr Asn Ala Glu Leu Met Ala Ser Ala Lys Val Val Ala
35 40 45
Glu Ala Ala Gln Ala Ala Arg Asn Glu Ser Asp Lys Leu Asp Lys
50 55 60
Gly Lys Val Ala Gly Ala Ser Ala Asp Ile Leu Asp Ala Ala Glu Lys
65 70 75 80
Tyr Gly Lys Phe Asp Glu Lys Ser Ser Thr Gly Gln Tyr Leu Asp Lys
85 90 95
Ala Glu Lys Tyr Leu Asn Asp Tyr Glu Ser Ser His Ser Thr Gly Ala
100 105 110
Gly Gly Pro Pro Pro Pro Thr Ser Gln Ala Glu Pro Ala Ser Gln Pro
115 120 125
Glu Pro Ala Ala Lys Lys Asp Asp Glu Glu Ser Gly Gly Leu Gly
130 135 140
Gly Tyr Ala Lys Met Ala Gln Gly Phe Leu Lys
145 150 155

(2) INFORMATION FOR SEQ ID NO:1588:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1500686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588:

Met Ala Ser Ala Lys Val Val Ala Glu Ala Ala Gln Ala Ala Ala Arg
1 5 10 15
Asn Glu Ser Asp Lys Leu Asp Lys Gly Lys Val Ala Gly Ala Ser Ala
20 25 30
Asp Ile Leu Asp Ala Ala Glu Lys Tyr Gly Lys Phe Asp Glu Lys Ser
35 40 45
Ser Thr Gly Gln Tyr Leu Asp Lys Ala Glu Lys Tyr Leu Asn Asp Tyr
50 55 60
Glu Ser Ser His Ser Thr Gly Ala Gly Gly Pro Pro Pro Thr Ser
65 70 75 80
Gln Ala Glu Pro Ala Ser Gln Pro Glu Pro Ala Ala Lys Lys Asp Asp
85 90 95
Glu Glu Ser Gly Gly Gly Leu Gly Gly Tyr Ala Lys Met Ala Gln Gly
100 105 110
Phe Leu Lys
115

(2) INFORMATION FOR SEQ ID NO:1589:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1057 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1057

(D) OTHER INFORMATION: / Ceres Seq. ID 1500687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1589:

aagctttctt cttgttccta cataccatc ttccctcacc tacatcaaac ctagggtttc

[illegible]

(2) INFORMATION FOR SEQ ID NO:1591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..248

(D) OTHER INFORMATION: / Ceres Seq. ID 1500689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1591:

Met Cys Ser Arg Gly His Trp Arg Pro Ala Glu Asp Glu Lys Leu Arg
1 5 10 15
Glu Leu Val Glu Gln Phe Gly Pro His Asn Trp Asn Ala Ile Ala Gln
20 25 30
Lys Leu Ser Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Phe Asn
35 40 45
Gln Leu Asp Pro Arg Ile Asn Arg Asn Pro Phe Thr Glu Glu Glu
50 55 60
Glu Arg Leu Leu Ala Ser His Arg Ile His Gly Asn Arg Trp Ser Val
65 70 75 80
Ile Ala Arg Phe Phe Pro Gly Arg Thr Asp Asn Ala Val Lys Asn His
85 90 95
Trp His Val Ile Met Ala Arg Arg Gly Arg Glu Arg Ser Lys Leu Arg
100 105 110
Pro Arg Gly Leu Gly His Asp Gly Thr Val Ala Ala Thr Gly Met Ile
115 120 125
Gly Asn Tyr Lys Asp Cys Asp Lys Glu Arg Arg Leu Ala Thr Thr Thr
130 135 140
Ala Ile Asn Phe Pro Tyr Gln Phe Ser His Ile Asn His Phe Gln Val
145 150 155 160
Leu Lys Glu Phe Leu Thr Val Lys Ile Gly Phe Arg Asn Ser Thr Thr
165 170 175
Pro Ile Gln Glu Gly Ala Ile Asp Gln Thr Lys Arg Pro Met Glu Phe
180 185 190
Tyr Asn Phe Leu Gln Val Asn Thr Asp Ser Lys Ile His Glu Leu Ile
195 200 205
Asp Asn Ser Arg Lys Asp Glu Glu Glu Asp Val Asp Gln Asn Asn Arg
210 215 220
Ile Pro Asn Glu Asn Cys Val Pro Phe Phe Asp Phe Leu Ser Val Gly
225 230 235 240
Asn Ser Ala Ser Gln Gly Leu Cys
245

(2) INFORMATION FOR SEQ ID NO:1592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1592:

Met Ala Arg Arg Gly Arg Glu Arg Ser Lys Leu Arg Pro Arg Gly Leu
1 5 10 15
Gly His Asp Gly Thr Val Ala Ala Thr Gly Met Ile Gly Asn Tyr Lys
20 25 30
Asp Cys Asp Lys Glu Arg Arg Leu Ala Thr Thr Thr Ala Ile Asn Phe

35 40 45
Pro Tyr Gln Phe Ser His Ile Asn His Phe Gln Val Leu Lys Glu Phe
50 55 60
Leu Thr Val Lys Ile Gly Phe Arg Asn Ser Thr Thr Pro Ile Gln Glu
65 70 75 80
Gly Ala Ile Asp Gln Thr Lys Arg Pro Met Glu Phe Tyr Asn Phe Leu
85 90 95
Gln Val Asn Thr Asp Ser Lys Ile His Glu Leu Ile Asp Asn Ser Arg
100 105 110
Lys Asp Glu Glu Glu Asp Val Asp Gln Asn Asn Arg Ile Pro Asn Glu
115 120 125
Asn Cys Val Pro Phe Phe Asp Phe Leu Ser Val Gly Asn Ser Ala Ser
130 135 140
Gln Gly Leu Cys
145

(2) INFORMATION FOR SEQ ID NO:1593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..546
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1593:

agtaattttc agtcggcgctc cttcttttgt ctgaaccacc ggaggagctc gatccattga 60
ttagaagatg acaactccac aagtgaagac cggtttgttc gttgggttga acaagggaca 120
tgttgttac agacgtgaat tagctcctcg tcctcgttct cgcaaggaa aaacgagcaa 180
gaggacaact tttatcagaa acttgataaa ggaagtgtct ggtcaagctc cctatgagaa 240
gagaatcact gagcttttga aggttgctaa gaggaagttg ggaacccaca agagagccaa 300
gcgaagagaga gaggagatgt ccaagtgttct ccgcaagatg aggtctggcg gttgggtgtc 360
aactgagaag aagaagtga cgtcatotta agtttgtgaa tcgctcgtaa agagttatgg 420
tttcttggtt caaaatcgtt attatgattc ctaagcttct cgtattatgt tttgttagaa 480
tatcggaact aaagagagtt ttgtctgaga ccagtgaact tgcctttaa ctatttgctt 540
cttttg

(2) INFORMATION FOR SEQ ID NO:1594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1594:

Met Thr Thr Pro Gln Val Lys Thr Gly Leu Phe Val Gly Leu Asn Lys
1 5 10 15
Gly His Val Val Thr Arg Arg Glu Leu Ala Pro Arg Pro Arg Ser Arg
20 25 30
Lys Gly Lys Thr Ser Lys Arg Thr Ile Phe Ile Arg Asn Leu Ile Lys
35 40 45
Glu Val Ala Gly Gln Ala Pro Tyr Glu Lys Arg Ile Thr Glu Leu Leu
50 55 60
Lys Val Ala Lys Arg Lys Leu Gly Thr His Lys Arg Ala Lys Arg Lys
65 70 75 80
Arg Glu Glu Met Ser Ser Val Leu Arg Lys Met Arg Ser Gly Gly Gly
85 90 95

Gly Ala Thr Glu Lys Lys Lys
100

(2) INFORMATION FOR SEQ ID NO:1595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..702
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1595:

tcttttgcgt	gactgtc	aaa	tctcattctt	ctctttcttc	tctctctcca	agagaaagaa	60
aatctgagtt	tccgagaaaa	taaaatctca	agagttaaaa	agaaagaaac	ttttgtcgaa		120
gagattccaa	tcggtgatct	ttgtctttct	ttctctaga	aaatctctgt	tgctctatat		180
atatccatat	agatgctcta	agactatagt	tgttgttgca	gataataatg	gagggagaca		240
caatactctag	gatgatggga	agtgaggttc	aaatggatgg	gaagattctt	caaacgtttg		300
agaaaagttt	tgttcaagtg	caaaacatat	tgaccacaa	cagatgtgct	ataaacgaga		360
taaacacaaa	ccatgagttc	aaaatcccg	acaacctcgg	acgaaacgtc	ggtttgatcc		420
gagaattgaa	caataacgtg	agaaggggtg	ctcatcttta	tgtcgatctt	tccaacaact		480
tctccaaatc	catggaagct	tctctgaag	gagactcatc	agaaggacga	ggtaacagaa		540
gaatcaggcc	tgcttaatta	agaatcaggg	ttgtttcttc	aaaattagct	tcgaaattag		600
cttttaattg	gggctaactc	cttttctcaa	gtgattggcg	ataaatgttt	taagcagaa		660
atgggtgattg	taattgaaaa	atatgttcaa	tactattatt	tg			

(2) INFORMATION FOR SEQ ID NO:1596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596:

Met	Glu	Gly	Asp	Thr	Ile	Ser	Arg	Met	Met	Gly	Ser	Gly	Val	Gln	Met	
1				5				10					15			
Asp	Gly	Lys	Ile	Leu	Gln	Thr	Phe	Glu	Lys	Ser	Phe	Val	Gln	Val	Gln	
			20					25					30			
Asn	Ile	Leu	Asp	His	Asn	Arg	Leu	Ile	Asn	Glu	Ile	Asn	Gln	Asn		
			35				40					45				
His	Glu	Ser	Lys	Ile	Pro	Asp	Asn	Leu	Gly	Arg	Asn	Val	Gly	Leu	Ile	
			50				55					60				
Arg	Glu	Leu	Asn	Asn	Asn	Val	Arg	Arg	Val	Ala	His	Leu	Tyr	Val	Asp	
			65			70				75				80		
Leu	Ser	Asn	Asn	Phe	Ser	Lys	Ser	Met	Glu	Ala	Ser	Ser	Glu	Gly	Asp	
			85					90						95		
Ser	Ser	Glu	Gly	Arg	Gly	Asn	Arg	Arg	Ile	Arg	Pro	Ala				
			100					105								

(2) INFORMATION FOR SEQ ID NO:1597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1500697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597:

Met Met Gly Ser Gly Val Gln Met Asp Gly Lys Ile Leu Gln Thr Phe
1 5 10 15
Glu Lys Ser Phe Val Gln Val Gln Asn Ile Leu Asp His Asn Arg Leu
20 25 30
Leu Ile Asn Glu Ile Asn Gln Asn His Glu Ser Lys Ile Pro Asp Asn
35 40 45
Leu Gly Arg Asn Val Gly Leu Ile Arg Glu Leu Asn Asn Asn Val Arg
50 55 60
Arg Val Ala His Leu Tyr Val Asp Leu Ser Asn Asn Phe Ser Lys Ser
65 70 75 80
Met Glu Ala Ser Ser Glu Gly Asp Ser Ser Glu Gly Arg Gly Asn Arg
85 90 95
Arg Ile Arg Pro Ala
100

(2) INFORMATION FOR SEQ ID NO:1598:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1500698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598:

Met Gly Ser Gly Val Gln Met Asp Gly Lys Ile Leu Gln Thr Phe Glu
1 5 10 15
Lys Ser Phe Val Gln Val Gln Asn Ile Leu Asp His Asn Arg Leu Leu
20 25 30
Ile Asn Glu Ile Asn Gln Asn His Glu Ser Lys Ile Pro Asp Asn Leu
35 40 45
Gly Arg Asn Val Gly Leu Ile Arg Glu Leu Asn Asn Asn Val Arg Arg
50 55 60
Val Ala His Leu Tyr Val Asp Leu Ser Asn Asn Phe Ser Lys Ser Met
65 70 75 80
Glu Ala Ser Ser Glu Gly Asp Ser Ser Glu Gly Arg Gly Asn Arg Arg
85 90 95
Ile Arg Pro Ala
100

(2) INFORMATION FOR SEQ ID NO:1599:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1422 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1422

(D) OTHER INFORMATION: / Ceres Seq. ID 1500703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599:

ammaacaagaag tctctctccc tctcctattc aactttttca gttactttac tccggttcac 60
ttttattttt cttttctgctg atttccatca atactacaaa aatatatact tctatatact 120
gtgcagaggt tacatgcatt gtrcaatttt gttgtscbga gaaacaagcg gatcagagac 180
aaaatcagag tcggttttccct gctttttgat tctcttttat taatcagcaa agatcgattc 240
cacttctcct cttctctcct cttctctcct gttctttaat tttagagaaa aaaataagca 300
ttcttctctc tcgtgttttcg agcgggaaat tctgagatg gctatacaag cgcagttgaa 360

ttacaacgct	cogaatgcga	atcaaatcgg	tttgggtggg	tcagagtttt	ctttgatcaa	420
caacaattggc	gttattggaa	tcggtaacga	tcagtcctat	cttgtcaata	atctccagtt	480
gcagaagaat	ttcaaccaac	atgctctgtt	tcacatcatg	catcatcaac	aacaacagtc	540
tcctttctcaa	agcttttttag	ctgctcagat	ggagaaacag	aagcaagaga	tcgatcagtt	600
catcaaaaata	cagaacgaga	gggttgagata	tggtttgcaa	gaacagagga	agcgagaaat	660
ggagatgatt	ttaaggaaaa	tgagagagtaa	agcttttgctt	ttgatgagtc	agaaggaaga	720
agaaatgtcg	aaagcattga	acaagaacat	ggaactcgaa	gatctgttga	gaaaaatgga	780
aatggagaat	cagacgtggc	agagaatggc	tcgtgagac	gaagcaattg	tgcaaacgct	840
aaacacaaacg	ctcgaacagg	ttcgcgagag	agccggccacg	tgttacgacg	ctgggtgaggc	900
agaggtggag	gacgaagggt	cggttttgcg	cgkagaagga	gacgggaata	gtttgccggc	960
gaagaagatt	aagatgagta	gtttgtgtcg	caattgtggg	tctaaccgag	taacagagrt	1020
ctgtgttcys	ccgttttaggc	atctctgttg	ctgcattgat	tscgagraag	ggctttmctt	1080
ttgtccgac	tgtaataccc	ccaagaaaag	cagaatcgag	gcctcatatt	tbtatgggaaa	1140
atcctttctt	ttctctcmcc	ggaaaaatgc	ttgcctttgt	gttccggtga	acgraragtt	1200
tttactccgg	gtaratgacg	ggcagggga	atttggtaaa	aaatagggag	gaaagggaaa	1260
tgagattagg	gaaaggttag	aaatagtaaa	aggttatctc	aaaraagtaa	ttctgtattag	1320
gggtttcaatt	ttcccttttt	gttttttgg	tccttttcca	ttcaatggag	gaaaaaaaaga	1380
aaaccagctg	gatttgatga	acataattca	tattttcctt	ct		

(2) INFORMATION FOR SEQ ID NO:1600:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..265

(D) OTHER INFORMATION: / Ceres Seq. ID 1500704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600:

Met Ala Ile Gln Ala Gln Leu Asn Tyr Asn Ala Pro Asn Ala Asn Gln
1 5 10 15
Ile Gly Phe Gly Gly Ser Glu Phe Ser Leu Ile Asn Asn Asn Gly Val
20 25 30
Ile Gly Ile Gly Asn Asp Gln Ser Tyr Leu Val Asn Asn Leu Gln Leu
35 40 45
Gln Lys Asp Phe Asn Gln His Ala Leu Phe His His Gln His His Gln
50 55 60
Gln Gln Gln Ser Pro Ser Gln Ser Phe Leu Ala Ala Gln Met Glu Lys
65 70 75 80
Gln Lys Gln Glu Ile Asp Gln Phe Ile Lys Ile Gln Asn Glu Arg Leu
85 90 95
Arg Tyr Val Leu Gln Glu Gln Arg Lys Arg Glu Met Glu Met Ile Leu
100 105 110
Arg Lys Met Glu Ser Lys Ala Leu Leu Met Ser Gln Lys Glu Glu
115 120 125
Glu Met Ser Lys Ala Leu Asn Lys Asn Met Glu Leu Glu Asp Leu Leu
130 135 140
Arg Lys Met Glu Met Glu Asn Gln Thr Trp Gln Arg Met Ala Arg Glu
145 150 155 160
Asn Glu Ala Ile Val Gln Thr Leu Asn Thr Thr Leu Glu Gln Val Arg
165 170 175
Glu Arg Ala Ala Thr Cys Tyr Asp Ala Gly Glu Ala Glu Val Glu Asp
180 185 190
Glu Gly Ser Phe Cys Gly Xaa Glu Gly Asp Gly Asn Ser Leu Pro Ala
195 200 205
Lys Lys Met Lys Met Ser Ser Cys Cys Asn Cys Gly Ser Asn Gly
210 215 220
Val Thr Xaa Val Leu Phe Xaa Pro Phe Arg His Leu Cys Cys Cys Met
225 230 235 240
Asp Xaa Glu Xaa Gly Leu Xaa Leu Cys Pro Ile Cys Asn Thr Pro Lys

245 250 255
Lys Ser Arg Ile Glu Ala Leu Ile Xaa
260 265
(2) INFORMATION FOR SEQ ID NO:1601:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..188
(D) OTHER INFORMATION: / Ceres Seq. ID 1500705
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1601:
Met Glu Lys Gln Lys Gln Glu Ile Asp Gln Phe Ile Lys Ile Gln Asn
1 5 10 15
Glu Arg Leu Arg Tyr Val Leu Gln Glu Gln Arg Lys Arg Glu Met Glu
20 25 30
Met Ile Leu Arg Lys Met Glu Ser Lys Ala Leu Leu Leu Met Ser Gln
35 40 45
Lys Glu Glu Glu Met Ser Lys Ala Leu Asn Lys Asn Met Glu Leu Glu
50 55 60
Asp Leu Leu Arg Lys Met Glu Met Glu Asn Gln Thr Trp Gln Arg Met
65 70 75 80
Ala Arg Glu Asn Glu Ala Ile Val Gln Thr Leu Asn Thr Thr Leu Glu
85 90 95
Gln Val Arg Glu Arg Ala Ala Thr Cys Tyr Asp Ala Gly Glu Ala Glu
100 105 110
Val Glu Asp Glu Gly Ser Phe Cys Gly Xaa Glu Gly Asp Gly Asn Ser
115 120 125
Leu Pro Ala Lys Lys Met Lys Met Ser Ser Cys Cys Cys Asn Cys Gly
130 135 140
Ser Asn Gly Val Thr Xaa Val Leu Phe Xaa Pro Phe Arg His Leu Cys
145 150 155 160
Cys Cys Met Asp Xaa Glu Xaa Gly Leu Xaa Leu Cys Pro Ile Cys Asn
165 170 175
Thr Pro Lys Lys Ser Arg Ile Glu Ala Leu Ile Xaa
180 185
(2) INFORMATION FOR SEQ ID NO:1602:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..158
(D) OTHER INFORMATION: / Ceres Seq. ID 1500706
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1602:
Met Glu Met Ile Leu Arg Lys Met Glu Ser Lys Ala Leu Leu Leu Met
1 5 10 15
Ser Gln Lys Glu Glu Glu Met Ser Lys Ala Leu Asn Lys Asn Met Glu
20 25 30
Leu Glu Asp Leu Leu Arg Lys Met Glu Met Glu Asn Gln Thr Trp Gln
35 40 45
Arg Met Ala Arg Glu Asn Glu Ala Ile Val Gln Thr Leu Asn Thr Thr
50 55 60
Leu Glu Gln Val Arg Glu Arg Ala Ala Thr Cys Tyr Asp Ala Gly Glu
65 70 75 80

Ala Glu Val Glu Asp Glu Gly Ser Phe Cys Gly Xaa Glu Gly Asp Gly
85 90 95
Asn Ser Leu Pro Ala Lys Lys Met Lys Met Ser Ser Cys Cys Cys Asn
100 105 110
Cys Gly Ser Asn Gly Val Thr Xaa Val Leu Phe Xaa Pro Phe Arg His
115 120 125
Leu Cys Cys Cys Met Asp Xaa Glu Xaa Gly Leu Xaa Leu Cys Pro Ile
130 135 140
Cys Asn Thr Pro Lys Lys Ser Arg Ile Glu Ala Leu Ile Xaa
145 150 155

(2) INFORMATION FOR SEQ ID NO:1603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1188

(D) OTHER INFORMATION: / Ceres Seq. ID 1500707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1603:

atcattctcg	gtttaactga	aacacataat	aaaacaaaga	gaaagagata	taatatgggt	60
gggtggcgaa	tcgcagtaga	cggtggtgcc	ggtatcgacc	ctaattcttc	ggcagagaga	120
caagaagagg	cgaaacagct	ttaactctgt	tgtctcaacc	tcggcataat	agctttcgct	180
tcacaatgtt	cgccattga	cgtcgttgag	ctcgtcatta	gagaattgga	gacggatcct	240
ctgtttaatt	caggccgttg	atcttctttg	acggagaaaag	gaacgggtga	gatggaagct	300
agcattatgg	acggtagcaa	gagacgatgc	ggtgcggttt	cggggataac	caccgtgaac	360
aatcctatat	ctcttgcctg	tctcgtcatg	gacaaaatct	cccatcttta	ctttgctttc	420
tcaggtgcag	aggatttcgc	ccgcaaacag	ggagttgaaa	ttgtggacaa	cgagtacttt	480
gtcacggacg	acaaacgtag	aatgctcaag	ttggccaagg	aagctaaact	catcttgttt	540
gattaccgga	tccgcgcgat	gggatgtgcc	ggcgagctgc	cgaccgacag	tccaatccaa	600
atgaacggtc	ttccgatcag	catttacgca	ccgggagaca	gtcgggtgcg	ttgtggttga	660
cgggaaaagga	cattgtgccg	ccggggacatc	cacgggttgt	taattgaaca	agatgatggg	720
aaggtattgt	gactcgccgc	tgataggagc	cgggacgat	gcgtcgaggt	ttgtgtgtgt	780
gtcgtgtacc	ggagaaggag	aagccattat	aagagcaacc	ctagtctcgt	atgtgtcagc	840
tgttatggag	tataaaggac	ttaacctcca	agaagcggtt	gattacgtca	tcaagcatcg	900
acttgacgaa	gggttcgctg	gactcattgc	tgtctcgaat	aaaggagagg	tgggtttgtg	960
ttttaactct	aatgggatgt	tcagggggatg	tgcaactgag	gatggattca	tgagcgttgc	1020
tatttgaggag	tgagaatat	tttagattaa	gaaaatgtct	tactagtatt	taatcagttca	1080
tcgctctatt	aatttggtta	ttcattatca	taaaagctgga	gtagtaattt	tagttctgtc	1140
gttatcacc	gtcctatatt	gatttgtgtt	taatgcggtt	tcaaatgtg		

(2) INFORMATION FOR SEQ ID NO:1604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1500708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1604:

Ile Ile Leu Gly Leu Thr Glu Thr His Asn Lys Thr Lys Arg Lys Arg
1 5 10 15
Tyr Asn Met Gly Gly Trp Ala Ile Ala Val His Gly Gly Ala Gly Ile
20 25 30
Asp Pro Asn Leu Pro Ala Glu Arg Gln Glu Glu Ala Lys Gln Leu Leu
35 40 45
Thr Arg Cys Leu Asn Leu Gly Ile Ile Ala Leu Arg Ser Asn Val Ser

50	55	60
Ala Ile Asp Val Val Glu Leu Val Ile Arg Glu Leu Glu Thr Asp Pro		
65	70	75
Leu Phe Asn Ser Gly Arg Gly Ser Ser Leu Thr Glu Lys Gly Thr Val		80
	85	90
Glu Met Glu Ala Ser Ile Met Asp Gly Thr Lys Arg Arg Cys Gly Ala		95
	100	105
Val Ser Gly Ile Thr Thr Val Lys Asn Pro Ile Ser Leu Ala Arg Leu		110
	115	120
Val Met Asp Lys Ser Pro His Ser Tyr Leu Ala Phe Ser Gly Ala Glu		125
	130	135
Asp Phe Ala Arg Lys Gln Gly Val Glu Ile Val Asp Asn Glu Tyr Phe		140
	145	150
Val Thr Asp Asp Asn Val Gly Met Leu Lys Leu Ala Lys Glu Ala Asn		155
	165	170
Ser Ile Leu Phe Asp Tyr Arg Ile Pro Pro Met Gly Cys Ala Gly Ala		175
	180	185
Ala Ala Thr Asp Ser Pro Ile Gln Met Asn Gly Leu Pro Ile Ser Ile		190
	195	200
Tyr Ala Pro Gly Asp Ser Arg Val Arg Cys Gly		205
210	215	

(2) INFORMATION FOR SEQ ID NO:1605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..201

(D) OTHER INFORMATION: / Ceres Seq. ID 1500709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1605:

Met Gly Gly Trp Ala Ile Ala Val His Gly Gly Ala Gly Ile Asp Pro		
1	5	10
Asn Leu Pro Ala Glu Arg Gln Glu Glu Ala Lys Gln Leu Leu Thr Arg		15
	20	25
Cys Leu Asn Leu Gly Ile Ile Ala Leu Arg Ser Asn Val Ser Ala Ile		30
	35	40
Asp Val Val Glu Leu Val Ile Arg Glu Leu Glu Thr Asp Pro Leu Phe		45
	50	55
Asn Ser Gly Arg Gly Ser Ser Leu Thr Glu Lys Gly Thr Val Glu Met		60
	65	70
Glu Ala Ser Ile Met Asp Gly Thr Lys Arg Arg Cys Gly Ala Val Ser		75
	85	90
Gly Ile Thr Thr Val Lys Asn Pro Ile Ser Leu Ala Arg Leu Val Met		95
	100	105
Asp Lys Ser Pro His Ser Tyr Leu Ala Phe Ser Gly Ala Glu Asp Phe		110
	115	120
Ala Arg Lys Gln Gly Val Glu Ile Val Asp Asn Glu Tyr Phe Val Thr		125
	130	135
Asp Asp Asn Val Gly Met Leu Lys Leu Ala Lys Glu Ala Asn Ser Ile		140
	145	150
Leu Phe Asp Tyr Arg Ile Pro Pro Met Gly Cys Ala Gly Ala Ala Ala		155
	165	170
Thr Asp Ser Pro Ile Gln Met Asn Gly Leu Pro Ile Ser Ile Tyr Ala		175
	180	185
Pro Gly Asp Ser Arg Val Arg Cys Gly		190
	195	200

(2) INFORMATION FOR SEQ ID NO:1606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..122
(D) OTHER INFORMATION: / Ceres Seq. ID 1500710
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1606:
Met Glu Ala Ser Ile Met Asp Gly Thr Lys Arg Arg Cys Gly Ala Val
1 5 10 15
Ser Gly Ile Thr Thr Val Lys Asn Pro Ile Ser Leu Ala Arg Leu Val
20 25 30
Met Asp Lys Ser Pro His Ser Tyr Leu Ala Phe Ser Gly Ala Glu Asp
35 40 45
Phe Ala Arg Lys Gln Gly Val Glu Ile Val Asp Asn Glu Tyr Phe Val
50 55 60
Thr Asp Asp Asn Val Gly Met Leu Lys Leu Ala Lys Glu Ala Asn Ser
65 70 75 80
Ile Leu Phe Asp Tyr Arg Ile Pro Pro Met Gly Cys Ala Gly Ala Ala
85 90 95
Ala Thr Asp Ser Pro Ile Gln Met Asn Gly Leu Pro Ile Ser Ile Tyr
100 105 110
Ala Pro Gly Asp Ser Arg Val Arg Cys Gly
115 120

(2) INFORMATION FOR SEQ ID NO:1607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..868
(D) OTHER INFORMATION: / Ceres Seq. ID 1500719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607:

aatcacttgt taattctaa gcttctctct ttccaaaaat ggcgtcatca tcggttttag 60
ctctcaggag acttctctct tcttccaccg tcgcccgtccc tcgcgcctta agagccgttc 120
gtccggtgtc tgcttctctc cgctcttcca ataccaacgc cgccagaaaac tatgaagacg 180
gtgtcgtatg gaaccatcac tcaaacccgac atgtttctcg ccacggcggc gatttctctt 240
cagataatac cgaaccgttt actccaacga gaagcttgag ccagatgctg aatttcatgg 300
accagtgta gcaaatccct ttggtatcag ctactcgtgg aatgggagct tctggagtta 360
gacgtggttg gaacgtgaaa gagaagaagc acgcgttgca tctaaggata gatagccgg 420
gactaagcag agaggatgtg aaattggcct tggaaacagaa cacattgggtg attagaggag 480
aaggggaaac agaggaggga gaagatgttt ctggagatgg acggaggttt acgagtagga 540
ttgagttacc ggagaaaagta tacaagactg atgagattaa ggcggaaaatg aagaatgggtg 600
tgttgaagt ggtgattcca aagattaaaagg aggatgagcg taacaaatatt cgctcacataa 660
acgttgacta gagtgtttta ttttggattg tttgagatgg aatggaagta agtgagttaa 720
tttgtgaact ttaaggtgtc ctttgggtgaa tcaaggagaa tgacatttcc cacggtccta 780
tgtgtccggg attttgactt ttttcgttac atcaatgatc tatgtacgtt tgactacttt 840
catatcatag gtccggattt tgtttccc

(2) INFORMATION FOR SEQ ID NO:1608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..222
(D) OTHER INFORMATION: / Ceres Seq. ID 1500720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1608:

Ser Leu Val Asn Ser Lys Leu Leu Leu Phe Pro Lys Met Ala Ser Ser
1 5 10 15
Ser Ala Leu Ala Leu Arg Arg Leu Leu Ser Ser Ser Thr Val Ala Val
20 25 30
Pro Arg Ala Leu Arg Ala Val Arg Pro Val Ser Ala Ser Ser Arg Leu
35 40 45
Phe Asn Thr Asn Ala Ala Arg Asn Tyr Glu Asp Gly Val Asp Arg Asn
50 55 60
His His Ser Asn Arg His Val Ser Arg His Gly Gly Asp Phe Phe Ser
65 70 75 80
Asp Ile Leu Asp Pro Phe Thr Pro Thr Arg Ser Leu Ser Gln Met Leu
85 90 95
Asn Phe Met Asp Gln Val Ser Glu Ile Pro Leu Val Ser Ala Thr Arg
100 105 110
Gly Met Gly Ala Ser Gly Val Arg Arg Gly Trp Asn Val Lys Glu Lys
115 120 125
Asp Asp Ala Leu His Leu Arg Ile Asp Met Pro Gly Leu Ser Arg Glu
130 135 140
Asp Val Lys Leu Ala Leu Glu Gln Asn Thr Leu Val Ile Arg Gly Glu
145 150 155 160
Gly Glu Thr Glu Glu Gly Glu Asp Val Ser Gly Asp Gly Arg Arg Phe
165 170 175
Thr Ser Arg Ile Glu Leu Pro Glu Lys Val Tyr Lys Thr Asp Glu Ile
180 185 190
Lys Ala Glu Met Lys Asn Gly Val Leu Lys Val Val Ile Pro Lys Ile
195 200 205
Lys Glu Asp Glu Arg Asn Asn Ile Arg His Ile Asn Val Asp
210 215 220

(2) INFORMATION FOR SEQ ID NO:1609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..210
(D) OTHER INFORMATION: / Ceres Seq. ID 1500721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1609:

Met Ala Ser Ser Ser Ala Leu Ala Leu Arg Arg Leu Leu Ser Ser Ser
1 5 10 15
Thr Val Ala Val Pro Arg Ala Leu Arg Ala Val Arg Pro Val Ser Ala
20 25 30
Ser Ser Arg Leu Phe Asn Thr Asn Ala Ala Arg Asn Tyr Glu Asp Gly
35 40 45
Val Asp Arg Asn His His Ser Asn Arg His Val Ser Arg His Gly Gly
50 55 60
Asp Phe Phe Ser Asp Ile Leu Asp Pro Phe Thr Pro Thr Arg Ser Leu
65 70 75 80
Ser Gln Met Leu Asn Phe Met Asp Gln Val Ser Glu Ile Pro Leu Val
85 90 95
Ser Ala Thr Arg Gly Met Gly Ala Ser Gly Val Arg Arg Gly Trp Asn
100 105 110
Val Lys Glu Lys Asp Asp Ala Leu His Leu Arg Ile Asp Met Pro Gly
115 120 125
Leu Ser Arg Glu Asp Val Lys Leu Ala Leu Glu Gln Asn Thr Leu Val

130					135					140									
Ile	Arg	Gly	Glu	Gly	Glu	Thr	Glu	Glu	Gly	Glu	Asp	Val	Ser	Gly	Asp				
145					150					155					160				
Gly	Arg	Arg	Phe	Thr	Ser	Arg	Ile	Glu	Leu	Pro	Glu	Lys	Val	Tyr	Lys				
					165					170				175					
Thr	Asp	Glu	Ile	Lys	Ala	Glu	Met	Lys	Asn	Gly	Val	Leu	Lys	Val	Val				
					180				185				190						
Ile	Pro	Lys	Ile	Lys	Glu	Asp	Glu	Arg	Asn	Asn	Ile	Arg	His	Ile	Asn				
					195			200				205							
Val	Asp																		
210																			

(2) INFORMATION FOR SEQ ID NO:1610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1610:

Met	Leu	Asn	Phe	Met	Asp	Gln	Val	Ser	Glu	Ile	Pro	Leu	Val	Ser	Ala
1				5					10					15	
Thr	Arg	Gly	Met	Gly	Ala	Ser	Gly	Val	Arg	Arg	Gly	Trp	Asn	Val	Lys
			20					25					30		
Glu	Lys	Asp	Asp	Ala	Leu	His	Leu	Arg	Ile	Asp	Met	Pro	Gly	Leu	Ser
			35				40					45			
Arg	Glu	Asp	Val	Lys	Leu	Ala	Leu	Glu	Gln	Asn	Thr	Leu	Val	Ile	Arg
			50			55				60					
Gly	Glu	Gly	Glu	Thr	Glu	Gly	Glu	Asp	Val	Ser	Gly	Asp	Gly	Arg	
			65			70			75					80	
Arg	Phe	Thr	Ser	Arg	Ile	Glu	Leu	Pro	Glu	Lys	Val	Tyr	Lys	Thr	Asp
				85				90					95		
Glu	Ile	Lys	Ala	Glu	Met	Lys	Asn	Gly	Val	Leu	Lys	Val	Val	Ile	Pro
			100				105					110			
Lys	Ile	Lys	Glu	Asp	Glu	Arg	Asn	Asn	Ile	Arg	His	Ile	Asn	Val	Asp
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:1611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..763
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1611:

ctgttttttg	tctctcgcac	tcacaagtct	cacataatcg	aaagctcgca	gaagtcaaga	60
ggaagaagat	gagtggtaca	gtgacaatgc	acagtgctct	cgtctacggc	agtctcatgg	120
cggacgacgt	cgttcgtctc	ctcctcaacc	gtatccctca	aaccgcttcc	gcaacctctc	180
ctgaktkatt	cagcatcaaaa	ggctgtgttt	atccggcgat	tataccagct	aagctcttgat	240
aaagtctctg	gaaaggtgtt	atttgggaatc	acagatgatg	aacttaaatg	tttagatgag	300
tttgaggatg	ttgagtatga	aagagagaat	gttcaagttt	tgtaaacaga	tagttcacag	360
gagaaactgc	aaacaaaaac	ctacgttttg	gccaaagaa	atgatcctga	cctatacggg	420
acatgggatt	tcgaggaatg	gaagcaactt	cacatggaag	gtttcttgaa	gatgactaaa	480

gaatttgcgt aagagttgaa tttaccgaaa tccgagatat gactcgccgc tacattcggt 540
tcagtaaagt aaatcttggt tagtttcctc aatgaattgg tcaatatatt ctgtggtgtc 600
tctctaggaa ggggttagatt cttcttcatt aatacacata catgaggggg atttgggggt 660
ttgtggtatt acttaattca actgataagg aataagaaaa cagctacata tttctgtgcg 720
gtatgttatt atacaataca catatagaca tgtgtttagc ttc

(2) INFORMATION FOR SEQ ID NO:1612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612:

Val Phe Gly Leu Ser His Ser Gln Val Ser His Asn Arg Lys Leu Ala
1 5 10 15
Glu Val Lys Arg Lys Lys Met Ser Gly Thr Val Thr Met His Ser Val
20 25 30
Phe Val Tyr Gly Ser Leu Met Ala Asp Asp Val Val Arg Leu Leu Leu
35 40 45
Asn Arg Ile Pro Gln Thr Ala Ser Ala Thr Leu Pro Xaa Xaa Phe Ser
50 55 60
Ile Lys Gly Arg Val Tyr Pro Ala Ile Ile Pro Ala Lys Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:1613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1613:

Met Ser Gly Thr Val Thr Met His Ser Val Phe Val Tyr Gly Ser Leu
1 5 10 15
Met Ala Asp Asp Val Val Arg Leu Leu Leu Asn Arg Ile Pro Gln Thr
20 25 30
Ala Ser Ala Thr Leu Pro Xaa Xaa Phe Ser Ile Lys Gly Arg Val Tyr
35 40 45
Pro Ala Ile Ile Pro Ala Lys Ser
50 55

(2) INFORMATION FOR SEQ ID NO:1614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1614:

Met His Ser Val Phe Val Tyr Gly Ser Leu Met Ala Asp Asp Val Val
1 5 10 15

Arg Leu Leu Leu Asn Arg Ile Pro Gln Thr Ala Ser Ala Thr Leu Pro
20 25 30
Xaa Xaa Phe Ser Ile Lys Gly Arg Val Tyr Pro Ala Ile Ile Pro Ala
35 40 45

Lys Ser
50

(2) INFORMATION FOR SEQ ID NO:1615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..846
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1615:

atcctgatcg	ggaaacccaa	aacgagtgg	cgaatagttt	ccgactgatt	cttccgaggg	60
ttgaagctca	atagctatgg	cttctctttc	agtctcttcc	tcttcaacca	tcacgatttc	120
aagagctcct	cttctcgac	tagcctccgc	ctccgcctct	tctccgtcgt	gcatttcaact	180
tcccacactt	ccgattcagt	ctcatacccg	tgccgcataa	gccactgctt	actgtcggaa	240
gattgtgagg	aacgttttga	cgagagctac	tactgaagtt	ggatgaagctc	ctgccactac	300
taccgaagct	gagactactg	agttaccctga	aatcgtaagt	actgtctaag	aagcttgagg	360
gaaagtggat	gacaagtacg	ctatttggtc	tcttgccctt	gctagtgtag	tggtctcttg	420
gggtctctgt	ggaatgawtt	csgcaatcga	taggcttcca	ttggttctcg	gtgtctctga	480
actttagtgc	atcggttaca	caggatgggt	cacttacaag	aacctgggtc	tcaaacccaga	540
caggagagct	ttggttgaga	aggtcaagag	cacatacaaa	gacatattag	ggagcagctg	600
aatcaaagg	ggaagaagaa	gaagaagagc	ctttttgagg	ccattcatga	attggaatga	660
aggatatcaa	aagaatctaa	cacaaaggcc	acgtctctcc	ttcaatcttt	ctcttctgtg	720
actaaataat	tttcatcctt	tctctctctc	tgctctctgt	cttttttagc	tcaagatc	780
atccatttat	gtcaaatgtt	tgtaaatctc	tcaagactat	atatgagatg	ttttgtttca	840
ttttcc						

(2) INFORMATION FOR SEQ ID NO:1616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1616:

Met Ala Ser Leu Ser Val Ser Ser Ser Thr Ile Ile Asp Ser Arg	
1 5 10 15	
Ala Pro Pro Ser Arg Leu Ala Ser Ala Ser Ala Ser Ser Pro Ser Cys	
20 25 30	
Ile Ser Leu Pro Thr Leu Pro Ile Gln Ser His Thr Arg Ala Ala Lys	
35 40 45	
Ala Thr Ala Tyr Cys Arg Lys Ile Val Arg Asn Val Val Thr Arg Ala	
50 55 60	
Thr Thr Glu Val Gly Glu Ala Pro Ala Thr Thr Thr Glu Ala Glu Thr	
65 70 75 80	
Thr Glu Leu Pro Glu Ile Val Lys Thr Ala Gln Glu Ala Trp Glu Lys	
85 90 95	
Val Asp Asp Lys Tyr Ala Ile Gly Ser Leu Ala Phe Ala Ser Val Val	
100 105 110	
Ala Leu Trp Gly Ser Ala Gly Met Xaa Xaa Ala Ile Asp Arg Leu Pro	
115 120 125	

Leu Val Pro Gly Val Leu Glu Leu Val Gly Ile Gly Tyr Thr Gly Trp
130 135 140
Phe Thr Tyr Lys Asn Leu Val Phe Lys Pro Asp Arg Glu Ala Leu Phe
145 150 155 160
Glu Lys Val Lys Ser Thr Tyr Lys Asp Ile Leu Gly Ser Ser
165 170

(2) INFORMATION FOR SEQ ID NO:1617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..621

(D) OTHER INFORMATION: / Ceres Seq. ID 1500748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1617:

aaatcaaaac	acaacattaa	aagctttggc	gattttttctc	tctgattcaa	tcttttcata	60
gttttctaagc	tctcagattc	ttgaagaagc	catggctcgt	acgaagcaaa	ccgcgagaaa	120
atcacacgga	ggaaaagctc	cgacgaagca	gctgcctacc	aagcgcgcaa	ggaaatctgc	180
accgactacc	ggaggagtca	agaaacctca	ccgtttccgt	cctggaacccg	tcgtctctgc	240
tgagattcgt	aaataccaaa	agagcacaga	gttggtgaac	cgtaaacttc	cattccaacg	300
tctttgttcgt	gaatctcgtc	aagatttcaa	gacggatctg	agattccaaa	gccatgcagt	360
gttagctctt	caagaagctg	cggaggcata	tttggttggt	ttgtttgaag	acacaaatct	420
ctgtgccaat	catgcaaaaga	gggttaccat	tatgcctaaa	gatgttcaat	tgccaagaag	480
gattcgtgca	gagcgtgctt	agaaattaga	attaatcaca	tcatatgaa	ctagtatttt	540
tttttttcta	ttaggggttt	cgattgtttt	tgctttgttg	ctttttaaca	aaaatacatt	600
atgtcacatt	ctctttgaga	g				

(2) INFORMATION FOR SEQ ID NO:1618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1500749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1618:

Met	Ala	Arg	Thr	Lys	Gln	Thr	Ala	Arg	Lys	Ser	His	Gly	Gly	Lys	Ala
1		5		10		15		20		25		30		35	
Pro	Thr	Lys	Gln	Leu	Ala	Thr	Lys	Ala	Ala	Arg	Lys	Ser	Ala	Pro	Thr
		20		25		30		35		40		45		50	
Thr	Gly	Gly	Val	Lys	Lys	Pro	His	Arg	Phe	Arg	Pro	Gly	Thr	Val	Ala
		35		40		45		50		55		60		65	
Leu	Arg	Glu	Ile	Arg	Lys	Tyr	Gln	Lys	Ser	Thr	Glu	Leu	Leu	Asn	Arg
		50		55		60		65		70		75		80	
Lys	Leu	Pro	Phe	Gln	Arg	Leu	Val	Arg	Glu	Ile	Ala	Gln	Asp	Phe	Lys
		65		70		75		80		85		90		95	
Thr	Asp	Leu	Arg	Phe	Gln	Ser	His	Ala	Val	Leu	Ala	Leu	Gln	Glu	Ala
		85		90		95		100		105		110		115	
Ala	Glu	Ala	Tyr	Leu	Val	Gly	Leu	Phe	Glu	Asp	Thr	Asn	Leu	Cys	Ala
		100		105		110		115		120		125		130	
Ile	His	Ala	Lys	Arg	Val	Thr	Ile	Met	Pro	Lys	Asp	Val	Gln	Leu	Ala
		115		120		125		130		135		140		145	
Arg	Arg	Ile	Arg	Ala	Glu	Arg	Ala								
		130		135		140		145		150		155		160	

(2) INFORMATION FOR SEQ ID NO:1619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1795 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1795
(D) OTHER INFORMATION: / Ceres Seq. ID 1500758
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1619:

agagatcaag	agagagatat	ggagagaaact	ttgcttcaat	ggagactatt	gcctcttctc	60
gcactcatcg	ttgctctttt	ctccttcttc	ttcgtcttct	ctcgtctctt	acaggggaaat	120
aataagtgtg	gtcttcttcc	tcatgatcat	tactggatct	caagtaaacg	catcgtcaca	180
cctaagtgtc	tcatctctgg	ttctgtggag	gtgaagggag	gaattattgt	gtcgttggtg	240
aagggaattg	attggcataa	gagtcaaaag	agtcgagtga	aagtgattga	ttagggagaa	300
gctgtcctca	tgccctgtct	cattgatgtg	catgttcttc	ttagtatgcc	tggagaagaat	360
gaatggggaag	gttttctctc	tggaaactaa	gctgctgctg	ctgggggaat	aactacattg	420
gttgacatgc	ccttaaacag	tttcccttca	actgtatctc	ctgaaacttt	gaaactcaag	480
attgaagctg	cgaaaacacg	aatacatggt	gatgttgggt	tctggggagg	tctggtaacct	540
gacaatgcac	tcaactcaag	tgctcttgag	tctctcttag	atgctggagt	tcttggtctc	600
aagtccttta	ttgtgccttc	aggaatcaac	gattttccaa	tgacaaacat	cactcatata	660
aaggaaggac	tatctgtatt	agctaataac	aaacgacctt	tgctgttaca	cgcagagatc	720
gagagagact	tagagattga	agatggtagt	gaaaatgato	ctcgttctta	tctgacttat	780
ttaaaaacca	ggcctacttc	atgggaggag	ggagcaatca	gaaacctatt	atcggttact	840
gaaaacacaa	gaattggtgg	ttctgcagaa	ggagctctac	tctcatattg	acatttatct	900
gatgcagttt	cttctcttga	tttgataaag	gaagcaaaaag	gcaaaaggga	caggtgttact	960
gttgaacaat	gtccacattt	cctagctttc	tcagccgaag	agattccaga	aggtgatact	1020
cgtttcaaat	gctcccctcc	tatactgtat	gcggcaaat	gagaaaaatt	gtgggaagct	1080
ttgatggaa	gagacattga	tatgctgagc	tctgatcatt	cacctacaaa	gcctgaactc	1140
aaacttatga	gtgatggcaa	cttcttgaaa	gcttgggggt	ggatatcttc	ttcacagttt	1200
gtctcttcta	tcacatgttc	ttatggaaaa	aagatggag	taacgctcga	gcaggttaact	1260
tcttggtgga	gtgataggcc	ttccaaactc	gctcgactac	actctaagg	agcggttaacg	1320
gttggaaaac	acgcagatct	tgttgtgtgg	gaacctgaag	ccgaatttga	tgtatagtaa	1380
gatcatccaa	ttcacttcaa	acacctagtt	atctcagctt	atttgggaag	aagatatatca	1440
ggcaaaagtgg	tttcgacatt	tgtgagagg	aacttggttt	ttggagaagg	caagcatgct	1500
tctgatgctt	gcgggtctct	gcaacttgca	actacttaac	ttaaaaagg	atttaaaaga	1560
tcttgatctg	caccattttt	acaaatgtaa	atatgcgatt	aagagttgct	ctcatgttgc	1620
aagatggttg	atgtaagtga	ttagtctttt	ttgccaattg	taagttttaag	actctctaaa	1680
tcttggttgt	ggctttaagg	ttagtggact	catstata	ttgtsatgc	aaataattta	1740
tatgcgttaa	gtaaatgatg	tatatattgt	tgatgcaaat	aatttaaaag	tatac	

(2) INFORMATION FOR SEQ ID NO:1620:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 512 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..512
(D) OTHER INFORMATION: / Ceres Seq. ID 1500759
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1620:

Arg	Asp	Gln	Glu	Arg	Asp	Met	Glu	Arg	Thr	Leu	Leu	Gln	Trp	Arg	Leu
1				5					10					15	
Leu	Pro	Leu	Leu	Ala	Leu	Ile	Val	Ala	Leu	Phe	Ser	Phe	Phe	Phe	Ala
				20				25						30	
Ser	Pro	Arg	Ser	Leu	Gln	Gly	Asn	Asn	Lys	Cys	Ser	Leu	Leu	Pro	His
				35			40					45			
Asp	His	Thr	Trp	Ile	Ser	Ser	Lys	Arg	Ile	Val	Thr	Pro	Asn	Gly	Leu
				50			55				60				
Ile	Ser	Gly	Ser	Val	Glu	Val	Lys	Gly	Gly	Ile	Ile	Val	Ser	Val	Val

65					70					75					80
Lys	Glu	Val	Asp	Trp	His	Lys	Ser	Gln	Arg	Ser	Arg	Val	Lys	Val	Ile
					85					90				95	
Asp	Tyr	Gly	Glu	Ala	Val	Leu	Met	Pro	Gly	Leu	Ile	Asp	Val	His	Val
			100					105					110		
His	Leu	Asp	Asp	Pro	Gly	Arg	Ser	Glu	Trp	Glu	Gly	Phe	Pro	Ser	Gly
			115				120					125			
Thr	Lys	Ala	Ala	Ala	Ala	Gly	Gly	Ile	Thr	Thr	Leu	Val	Asp	Met	Pro
			130			135					140				
Leu	Asn	Ser	Phe	Pro	Ser	Thr	Val	Ser	Pro	Glu	Thr	Leu	Lys	Leu	Lys
					150				155					160	
Ile	Glu	Ala	Ala	Lys	Asn	Arg	Ile	His	Val	Asp	Val	Gly	Phe	Trp	Gly
				165				170						175	
Gly	Leu	Val	Pro	Asp	Asn	Ala	Leu	Asn	Ser	Ser	Ala	Leu	Glu	Ser	Leu
			180				185						190		
Leu	Asp	Ala	Gly	Val	Leu	Gly	Leu	Lys	Ser	Phe	Met	Cys	Pro	Ser	Gly
			195				200					205			
Ile	Asn	Asp	Phe	Pro	Met	Thr	Asn	Ile	Thr	His	Ile	Lys	Glu	Gly	Leu
			210			215					220				
Ser	Val	Leu	Ala	Lys	Tyr	Lys	Arg	Pro	Leu	Leu	Val	His	Ala	Glu	Ile
					230						235				240
Glu	Arg	Asp	Leu	Glu	Ile	Glu	Asp	Gly	Ser	Glu	Asn	Asp	Pro	Arg	Ser
				245					250					255	
Tyr	Leu	Thr	Tyr	Leu	Lys	Thr	Arg	Pro	Thr	Ser	Trp	Glu	Glu	Gly	Ala
				260				265					270		
Ile	Arg	Asn	Leu	Leu	Ser	Val	Thr	Glu	Asn	Thr	Arg	Ile	Gly	Gly	Ser
				275			280					285			
Ala	Glu	Gly	Ala	His	Leu	His	Ile	Val	His	Leu	Ser	Asp	Ala	Ser	Ser
				290		295					300				
Ser	Leu	Asp	Leu	Ile	Lys	Glu	Ala	Lys	Gly	Lys	Gly	Asp	Ser	Val	Thr
					310				315					320	
Val	Glu	Thr	Cys	Pro	His	Tyr	Leu	Ala	Phe	Ser	Ala	Glu	Glu	Ile	Pro
				325					330					335	
Glu	Gly	Asp	Thr	Arg	Phe	Lys	Cys	Ser	Pro	Pro	Ile	Arg	Asp	Ala	Ala
				340				345					350		
Asn	Arg	Glu	Lys	Leu	Trp	Glu	Ala	Leu	Met	Glu	Gly	Asp	Ile	Asp	Met
				355			360					365			
Leu	Ser	Ser	Asp	His	Ser	Pro	Thr	Lys	Pro	Glu	Leu	Lys	Leu	Met	Ser
						375						380			
Asp	Gly	Asn	Phe	Leu	Lys	Ala	Trp	Gly	Gly	Ile	Ser	Ser	Leu	Gln	Phe
					390					395				400	
Val	Leu	Pro	Ile	Thr	Trp	Ser	Tyr	Gly	Lys	Lys	Tyr	Gly	Val	Thr	Leu
				405					410					415	
Glu	Gln	Val	Thr	Ser	Trp	Trp	Ser	Asp	Arg	Pro	Ser	Lys	Leu	Ala	Arg
				420				425						430	
Leu	His	Ser	Lys	Gly	Ala	Val	Thr	Val	Gly	Lys	His	Ala	Asp	Leu	Val
				435			440					445			
Val	Trp	Glu	Pro	Glu	Ala	Glu	Phe	Asp	Val	Asp	Glu	Asp	His	Pro	Ile
				450		455				460					
His	Phe	Lys	His	Pro	Ser	Ile	Ser	Ala	Tyr	Leu	Gly	Arg	Arg	Leu	Ser
					470				475					480	
Gly	Lys	Val	Val	Ser	Thr	Phe	Val	Arg	Gly	Asn	Leu	Val	Phe	Gly	Glu
					485				490					495	
Gly	Lys	His	Ala	Ser	Asp	Ala	Cys	Gly	Ser	Leu	Gln	Leu	Ala	Thr	Thr
				500				505						510	

(2) INFORMATION FOR SEQ ID NO:1621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 506 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..506
(D) OTHER INFORMATION: / Ceres Seq. ID 1500760
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621:

Met	Glu	Arg	Thr	Leu	Leu	Gln	Trp	Arg	Leu	Leu	Pro	Leu	Leu	Ala	Leu
1			5					10						15	
Ile	Val	Ala	Leu	Phe	Ser	Phe	Phe	Ala	Ser	Pro	Arg	Ser	Leu	Gln	
			20				25					30			
Gly	Asn	Asn	Lys	Cys	Ser	Leu	Leu	Pro	His	Asp	His	Tyr	Trp	Ile	Ser
			35				40				45				
Ser	Lys	Arg	Ile	Val	Thr	Pro	Asn	Gly	Leu	Ile	Ser	Gly	Ser	Val	Glu
			50				55				60				
Val	Lys	Gly	Gly	Ile	Ile	Val	Ser	Val	Val	Lys	Glu	Val	Asp	Trp	His
							70				75				80
Lys	Ser	Gln	Arg	Ser	Arg	Val	Lys	Val	Ile	Asp	Tyr	Gly	Glu	Ala	Val
							85			90				95	
Leu	Met	Pro	Gly	Leu	Ile	Asp	Val	His	Val	His	Leu	Asp	Asp	Pro	Gly
			100					105					110		
Arg	Ser	Glu	Trp	Glu	Gly	Phe	Pro	Ser	Gly	Thr	Lys	Ala	Ala	Ala	
			115					120				125			
Gly	Gly	Ile	Thr	Thr	Leu	Val	Asp	Met	Pro	Leu	Asn	Ser	Phe	Pro	Ser
			130				135					140			
Thr	Val	Ser	Pro	Glu	Thr	Leu	Lys	Leu	Lys	Ile	Glu	Ala	Ala	Lys	Asn
							150				155				160
Arg	Ile	His	Val	Asp	Val	Gly	Phe	Trp	Gly	Gly	Leu	Val	Pro	Asp	Asn
							165				170				175
Ala	Leu	Asn	Ser	Ser	Ala	Leu	Glu	Ser	Leu	Leu	Asp	Ala	Gly	Val	Leu
							180				185			190	
Gly	Leu	Lys	Ser	Phe	Met	Cys	Pro	Ser	Gly	Ile	Asn	Asp	Phe	Pro	Met
			195				200					205			
Thr	Asn	Ile	Thr	His	Ile	Lys	Glu	Gly	Leu	Ser	Val	Leu	Ala	Lys	Tyr
			210				215				220				
Lys	Arg	Pro	Leu	Leu	Val	His	Ala	Glu	Ile	Glu	Arg	Asp	Leu	Glu	Ile
							230				235				240
Glu	Asp	Gly	Ser	Glu	Asn	Asp	Pro	Arg	Ser	Tyr	Leu	Thr	Tyr	Leu	Lys
							245				250			255	
Thr	Arg	Pro	Thr	Ser	Trp	Glu	Glu	Gly	Ala	Ile	Arg	Asn	Leu	Leu	Ser
							260			265				270	
Val	Thr	Glu	Asn	Thr	Arg	Ile	Gly	Gly	Ser	Ala	Glu	Gly	Ala	His	Leu
			275				280					285			
His	Ile	Val	His	Leu	Ser	Asp	Ala	Ser	Ser	Ser	Leu	Asp	Leu	Ile	Lys
			290				295					300			
Glu	Ala	Lys	Gly	Lys	Gly	Asp	Ser	Val	Thr	Val	Glu	Thr	Cys	Pro	His
							310				315				320
Tyr	Leu	Ala	Phe	Ser	Ala	Glu	Glu	Ile	Pro	Glu	Gly	Asp	Thr	Arg	Phe
							325				330				335
Lys	Cys	Ser	Pro	Pro	Ile	Arg	Asp	Ala	Ala	Asn	Arg	Glu	Lys	Leu	Trp
							340				345			350	
Glu	Ala	Leu	Met	Glu	Gly	Asp	Ile	Asp	Met	Leu	Ser	Ser	Asp	His	Ser
							355				360			365	
Pro	Thr	Lys	Pro	Glu	Leu	Lys	Leu	Met	Ser	Asp	Gly	Asn	Phe	Leu	Lys
							370				375			380	
Ala	Trp	Gly	Gly	Ile	Ser	Ser	Leu	Gln	Phe	Val	Leu	Pro	Ile	Thr	Trp
							385				390				400
Ser	Tyr	Gly	Lys	Lys	Tyr	Gly	Val	Thr	Leu	Glu	Gln	Val	Thr	Ser	Trp
							405				410				415
Trp	Ser	Asp	Arg	Pro	Ser	Lys	Leu	Ala	Arg	Leu	His	Ser	Lys	Gly	Ala

Val Thr Val Gly Lys His Ala Asp Leu Val Val Trp Glu Pro Glu Ala	420	425	430
435	440	445	
Glu Phe Asp Val Asp Glu Asp His Pro Ile His Phe Lys His Pro Ser	450	455	460
465	470	475	480
Ile Ser Ala Tyr Leu Gly Arg Arg Leu Ser Gly Lys Val Val Ser Thr			
Phe Val Arg Gly Asn Leu Val Phe Gly Glu Gly Lys His Ala Ser Asp	485	490	495
Ala Cys Gly Ser Leu Gln Leu Ala Thr Thr	500	505	

(2) INFORMATION FOR SEQ ID NO:1622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..409
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1622:

```

Met Pro Gly Leu Ile Asp Val His Val His Leu Asp Asp Pro Gly Arg
1          5          10          15
Ser Glu Trp Glu Gly Phe Pro Ser Gly Thr Lys Ala Ala Ala Gly
20          25          30
Gly Ile Thr Thr Leu Val Asp Met Pro Leu Asn Ser Phe Pro Ser Thr
35          40          45
Val Ser Pro Glu Thr Leu Lys Leu Lys Ile Glu Ala Ala Lys Asn Arg
50          55          60
Ile His Val Asp Val Gly Phe Trp Gly Gly Leu Val Pro Asp Asn Ala
65          70          75          80
Leu Asn Ser Ser Ala Leu Glu Ser Leu Leu Asp Ala Gly Val Leu Gly
85          90          95
Leu Lys Ser Phe Met Cys Pro Ser Gly Ile Asn Asp Phe Pro Met Thr
100         105         110
Asn Ile Thr His Ile Lys Glu Gly Leu Ser Val Leu Ala Lys Tyr Lys
115         120         125
Arg Pro Leu Leu Val His Ala Glu Ile Glu Arg Asp Leu Glu Ile Glu
130         135         140
Asp Gly Ser Glu Asn Asp Pro Arg Ser Tyr Leu Thr Tyr Leu Lys Thr
145         150         155         160
Arg Pro Thr Ser Trp Glu Glu Gly Ala Ile Arg Asn Leu Leu Ser Val
165         170         175
Thr Glu Asn Thr Arg Ile Gly Gly Ser Ala Glu Gly Ala His Leu His
180         185         190
Ile Val His Leu Ser Asp Ala Ser Ser Ser Leu Asp Leu Ile Lys Glu
195         200         205
Ala Lys Gly Lys Gly Asp Ser Val Thr Val Glu Thr Cys Pro His Tyr
210         215         220
Leu Ala Phe Ser Ala Glu Glu Ile Pro Glu Gly Asp Thr Arg Phe Lys
225         230         235         240
Cys Ser Pro Pro Ile Arg Asp Ala Ala Asn Arg Glu Lys Leu Trp Glu
245         250         255
Ala Leu Met Glu Gly Asp Ile Asp Met Leu Ser Ser Asp His Ser Pro
260         265         270
Thr Lys Pro Glu Leu Lys Leu Met Ser Asp Gly Asn Phe Leu Lys Ala
275         280         285
Trp Gly Gly Ile Ser Ser Leu Gln Phe Val Leu Pro Ile Thr Trp Ser
290         295         300

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Tyr Gly Lys Lys Tyr Gly Val Thr Leu Glu Gln Val Thr Ser Trp Trp
305 310 315 320
Ser Asp Arg Pro Ser Lys Leu Ala Arg Leu His Ser Lys Gly Ala Val
325 330 335
Thr Val Gly Lys His Ala Asp Leu Val Val Trp Glu Pro Glu Ala Glu
340 345 350
Phe Asp Val Asp Glu Asp His Pro Ile His Phe Lys His Pro Ser Ile
355 360 365
Ser Ala Tyr Leu Gly Arg Arg Leu Ser Gly Lys Val Val Ser Thr Phe
370 375 380
Val Arg Gly Asn Leu Val Phe Gly Glu Gly Lys His Ala Ser Asp Ala
385 390 395 400
Cys Gly Ser Leu Gln Leu Ala Thr Thr
405

(2) INFORMATION FOR SEQ ID NO:1623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1623:

atacaaatca	taactcaaa	aaaaaca	acc	cctcaac	cggt	cgatgtgtga	tcccattaga	60
gaagatgct	ctaacaaa	agggcgc	ggtg	agtaagg	aaaa	aaaggccgta	tattcataga	120
gaatggtcgt	gggcccga	tata	aatacag	cg	g	ttaccggtta	tcaaatgtga	180
ctcttggcac	catttaacta	caaatggg	aa	gcattac	gggt	tcggtttcgt	gctctacgcg	240
ttgactcac	tcagcatcac	attctcatac		catagga	aact	tgggctcacc	ggagctttaa	300
gcttcgcaaa	tgggttgaa	atcctttagc		ttattttg	ct	gtttttgctc	ttcagggtga	360
tcogttggat	tgggtgagca	tacataggg	t	tcacaccca		gttcacagat	tctgaccgtg	420
accacatag	cccatcgaa	ggattttg	gt	tcagtcagt		gtgggtggata	tgtgacactc	480
gttatatcaa	atataagt	gt	ggaggacg	ta	acaacgt	gat	ggacttgaag	540
tctattggtt	tctacgaat	acaattggt	t	tcacgctct		aatgttttgg	actgtcctct	600
atctctatgg	tggtttac	ct	tacottac	at	g	ggggcgggg	cggtggaggt	660
accacgtgac	atggctcgtg	aactcggc	at	gccatatt	tt	gggttcgaga	tcatggga	720
ctaaagacac	atctcgta	aac	gtttggtg	gc		taagcttatt	tacaatggga	780
acaataatca	ccacgccttt	gagtcac	gg	cgaggca	agg	attggagttg	tggcagatag	840
acataactgt	gtatcttatt	cgactatt	g	aggttct	cg	gttagccact	gacgtgaaat	900
tgccctcgga	attccagaaa	cagaaa	actg	ctctgact	cg	ttgatcatct	gcattgagaga	960
tttatcagaa	tttttatatt	ttagaaaa	att	atcaaa	ggtta	ctataaaa	gagataatata	1020
gatgagagtt	tatgattgtt	atagcttat	t	tgatatttt	c	actataaat	tgtgttttc	1080
tgtcttgga	gtaggattta	aatggcgcaa	aaaaagg	t	at	tttttttt	ttttaataaa	1140

aggcttaagt tg

(2) INFORMATION FOR SEQ ID NO:1624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1624:

Met	Asp	Leu	Lys	Gln	Gln	Trp	Phe	Tyr	Trp	Phe	Leu	Arg	Met	Thr	Ile
1			5					10					15		
Gly	Phe	His	Val	Leu	Met	Phe	Trp	Thr	Val	Leu	Tyr	Leu	Tyr	Gly	Gly

(2) INFORMATION FOR SEQ ID NO:1625:

(xi) SEQUENCE DESCRIPTION: SEQ ID: NO: 102:

Met	Phe	Trp	Thr	Val	Leu	Tyr	Leu	Tyr	Gly	Gly	Leu	Pro	Tyr	Leu	Thr
1			5						10					15	
Cys	Gly	Gly	Gly	Val	Gly	Gly	Val	Ile	Gly	Tyr	His	Val	Thr	Trp	Leu
			20					25					30		

Val Asn Ser Ala Cys His Ile Trp Gly Ser Arg Ser Trp Lys Thr Lys
35 40 45
Asp Thr Ser Arg Asn Val Trp Trp Leu Ser Leu Phe Thr Met Gly Glu
50 55 60
Ser Trp His Asn Asn His His Ala Phe Glu Ser Ser Ala Arg Gln Gly
65 70 75 80
Leu Glu Trp Trp Gln Ile Asp Ile Thr Trp Tyr Leu Ile Arg Leu Phe
85 90 95
Glu Val Leu Gly Leu Ala Thr Asp Val Lys Leu Pro Ser Glu Phe Gln
100 105 110
Lys Gln Lys Leu Ala Leu Thr Arg
115 120

(2) INFORMATION FOR SEQ ID NO:1627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1178

(D) OTHER INFORMATION: / Ceres Seq. ID 1500778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1627:

acaagtcaca	acccaccat	gcattgcata	tctctttcgt	tatctccaat	attctttttc	60
ctcttctcca	catcaaccat	ttgattttct	ccggtacaac	ccacaacctc	taagcctccg	120
gcaccacggc	cccacagaga	gctctccgcc	gattactact	ccaagaaatg	tcctcagctt	180
gaaactctcg	tcggttcctg	cactttctca	cggtttcaaa	aagtccecat	ctcagctcca	240
gccaccattc	gcctcttctt	tcacgactgc	ttcggttgagg	gtgtgtgatg	gtcgatattg	300
atagaaacaa	agaaaggaag	caagaaatta	gcagagagag	aagcatatga	gaataagaga	360
ttgagagagg	aaggatttga	tagtatcatc	aaggcgaaag	ccttggttga	gtctcatctg	420
ccttctctcg	tctcttctct	tgatattctc	gctattgcgc	ctcgagattt	catctcatctg	480
gcaggtgggc	cttactatca	agtgaaaaaa	ggaaggtggg	acggaaaaaa	atcaacggca	540
aagaacgtcc	ctccaaacat	acctcgatca	aactccaccg	ttgatcaact	catcaagctc	600
ttcgcgctca	aaggactaac	cgtagaggaa	ctcgtcgtcc	ttctcgttcc	ccacaccatc	660
ggttcgcccc	ttgtaaaaaa	ttccttggtc	gtctctacga	ctacaaagtc	acaaaacgac	720
ccgaccggag	tcttgaccaa	agattactaa	aagagctccg	gatgtctttg	ccctttttccg	780
gcggaagctc	tgaggtcgtc	cttcgcgtcg	acgctacaac	tcctgtttgtg	tttgataatg	840
gatatttcac	aggtctagga	accaacatgg	gccttctcgc	gtcggaccac	gctttgtttc	900
ttgacccgag	gacgaagccc	attgcacttg	agatggcagg	agataagcag	agatttttca	960
aggcggttgg	agacgctatg	gataaaatgg	gttccattgg	tgtaaaagaga	gggaagagac	1020
atggggaaat	acgtacggat	tgctgagctc	ttttatagat	tttctttatt	gtctgtgtctg	1080
atggtttttg	tcttgatctt	gagtgtttct	gtgtcatgtg	tcctttaatt	tattagcatt	1140
ttcgtgattg	ttttgttgat	agtataaggt	attttttt			

(2) INFORMATION FOR SEQ ID NO:1628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1500779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1628:

Thr Ser His Asn Pro Thr Met His Val	Ile Ser Leu Ser Leu Ser Ser	
1 5 10 15		
Ile Phe Phe Phe Leu Phe Leu Thr Ser Thr Ile Leu Ile Ser Pro Val		
20 25 30		
Gln Pro Thr Thr Ser Lys Pro Pro Ala Pro Arg Pro His Arg Glu Leu		

Met	His	Val	Ile	Ser	Leu	Ser	Leu	Ser	Ser	Ile	Phe	Phe	Phe	Leu	Phe
1				5					10					15	
Leu	Thr	Ser	Thr	Ile	Leu	Ile	Ser	Pro	Val	Gln	Pro	Thr	Thr	Ser	Lys
			20					25					30		
Pro	Pro	Ala	Pro	Arg	Pro	His	Arg	Glu	Leu	Ser	Ala	Asp	Tyr	Tyr	Ser
		35					40					45			
Lys	Lys	Cys	Pro	Gln	Leu	Glu	Thr	Leu	Val	Gly	Ser	Val	Thr	Ser	Gln
		50				55									
Arg	Phe	Lys	Glu	Val	Pro	Ile	Ser	Ala	Pro	Ala	Thr	Ile	Arg	Leu	Phe
65				70						75				80	
Phe	His	Asp	Cys	Phe	Val	Glu	Gly	Cys	Asp	Gly	Ser	Ile	Leu	Ile	Glu
				85					90					95	
Thr	Lys	Lys	Gly	Ser	Lys	Lys	Leu	Ala	Glu	Arg	Glu	Ala	Tyr	Glu	Asn
			100					105					110		
Lys	Glu	Leu	Arg	Glu	Glu	Gly	Phe	Asp	Ser	Ile	Ile	Lys	Ala	Lys	Ala
		115					120					125			
Leu	Val	Glu	Ser	His	Cys	Pro	Ser	Leu	Val	Ser	Xaa	Ser	Asp	Ile	Leu
		130				135					140				
Ala	Ile	Ala	Ala	Arg	Asp	Phe	Ile	His	Leu	Ala	Gly	Gly	Pro	Tyr	Tyr
145					150					155				160	
Gln	Val	Lys	Lys	Gly	Arg	Trp	Asp	Gly	Lys	Arg	Ser	Thr	Ala	Lys	Asn
				165					170					175	

(2) INFORMATION FOR SEQ ID NO:1630:

(A) LENGTH: 1123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ix) FEATURE:
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(B) LOCATION: 1..1123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1630:

aaaaacacaa	acgtaaacag	gattcagagct	ctctctgagct	gatgcaagcg	aaaatacaatt	60
ctttctcttca	gcocctoctct	ttctctctcta	ttctgtgactc	agtaacacaca	gacacagacg	120
atrgtstttaa	ctgtcttgga	gaacaatcgg	aacgcocatcg	ctaacacacta	ccagctgcga	180
ctctgcgatta	ccgaagaaga	tgaagtgcct	aaaggatgca	tcgaaaaagc	gctgaagaaa	240
ggatctcttct	ctctgactaa	aaataacacaa	aaaggagcga	attatcacaa	attccacata	300
gagttggggcc	aatctgattt	ttctctcaga	caatgcgcag	aaaagtggagc	taagtatgct	360
ctctggagatg	aattatgata	gaagaacact	caaaagtttct	acaaggacta	tatgtatgga	420
ctctctcttta	agggtgtgca	aaacgagaaa	gcgtttacat	cacctttgtt	ctcaagaaga	480
cgcatctgtta	tggtatcaga	aaatgatcttc	ctctgcacaa	gaacaacaggt	gcaagaggtt	540
tggaataatga	tggaggttga	ggtgggtgag	gattggattc	ttctaccaaa	ttgtaagttt	600
tatctattcca	tatctctcca	ggaggtactct	ggatgctctag	ttgtcgaaac	aattaaaggaa	660
tgcttttaagc	tcattgatctc	ttctgatgat	gaagaacagct	tacaaaaaag	gagctcatcc	720
gcgccttcaa	ctctcattca	gttttgaaac	atttgtctcat	aaaggagaggt	atcgaaaaga	780
ctctgaaacat	cagatgatag	atagataaac	ggagctcact	tatgtgaaag	agaagctaaa	840
ccagctgtgtt	gtgggattag	agcgatttgg	gtctcacctt	ctaatgaaga	aaaaggcata	900
gcacacatggt	tactcattatc	caacgagggaa	agctttcgca	acaattgggtg	catgtcggag	960
aaatctcagt	tagcattttc	acaaccaacc	tcocataggaa	tccttttggg	attctaatat	1020
tttggaaact	gttctattct	acttttcaaa	gctcagctaa	tgtgactcta	cttttcttaa	1080
acggcataga	gttctatcaca	tcacaacctc	ttctctcaact	gtc		

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(ix) FEATURE:
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(B) LOCATION: 1..222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1631:

1	Met	Tyr	Gly	Leu	Pro	Phe	Lys	Gly	Trp	Gln	Asn	Glu	Lys	Ala	Phe	Thr
				5						10					15	
1	Ser	Pro	Leu	Phe	Ile	Lys	Asn	Arg	Ile	Val	Met	Val	Ser	Glu	Asn	Asp
			20						25					30		
Ser	Pro	Ala	His	Arg	Asn	Lys	Val	Gln	Glu	Val	Val	Lys	Met	Met	Glu	
		35					40						45			
Val	Glu	Leu	Gly	Glu	Asp	Trp	Ile	Leu	His	Gln	His	Cys	Lys	Val	Tyr	
	50					55						60				

Leu Phe Ile Ser Ser Gln Arg Ile Ser Gly Cys Leu Val Ala Glu Pro
65 70 75 80
Ile Lys Glu Ala Phe Lys Leu Ile Ala Ser Pro Asp Asp Glu Arg Gln
85 90 95
Leu Gln Lys Glu Ser Ser Ser Pro Ser Thr Ser Ile Gln Phe Gly
100 105 110
Asn Ile Val Leu Gln Arg Glu Val Ser Lys Arg Cys Arg Thr Ser Asp
115 120 125
Asp Arg Leu Asp Asn Gly Val Ile Val Cys Glu Glu Glu Ala Lys Pro
130 135 140
Ala Val Cys Gly Ile Arg Ala Ile Trp Val Ser Pro Ser Asn Arg Arg
145 150 155 160
Lys Gly Ile Ala Thr Trp Leu Leu Asp Thr Thr Arg Glu Ser Phe Arg
165 170 175
Asn Asn Gly Cys Met Leu Glu Lys Ser Gln Leu Ala Phe Ser Gln Pro
180 185 190
Thr Ser Ile Gly Arg Ser Phe Gly Ser Lys Tyr Phe Gly Thr Cys Ser
195 200 205
Phe Leu Leu Tyr Lys Ala Gln Leu Ile Asp Thr His Phe Ser
210 215 220

(2) INFORMATION FOR SEQ ID NO:1632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1632:

Met Val Ser Glu Asn Asp Ser Pro Ala His Arg Asn Lys Val Gln Glu
1 5 10 15
Val Val Lys Met Met Glu Val Glu Leu Gly Glu Asp Trp Ile Leu His
20 25 30
Gln His Cys Lys Val Tyr Leu Phe Ile Ser Ser Gln Arg Ile Ser Gly
35 40 45
Cys Leu Val Ala Glu Pro Ile Lys Glu Ala Phe Lys Leu Ile Ala Ser
50 55 60
Pro Asp Asp Glu Arg Gln Leu Gln Lys Glu Ser Ser Ser Pro Ser
65 70 75 80
Thr Ser Ile Gln Phe Gly Asn Ile Val Leu Gln Arg Glu Val Ser Lys
85 90 95
Arg Cys Arg Thr Ser Asp Asp Arg Leu Asp Asn Gly Val Ile Val Cys
100 105 110
Glu Glu Glu Ala Lys Pro Ala Val Cys Gly Ile Arg Ala Ile Trp Val
115 120 125
Ser Pro Ser Asn Arg Arg Lys Gly Ile Ala Thr Trp Leu Leu Asp Thr
130 135 140
Thr Arg Glu Ser Phe Arg Asn Asn Gly Cys Met Leu Glu Lys Ser Gln
145 150 155 160
Leu Ala Phe Ser Gln Pro Thr Ser Ile Gly Arg Ser Phe Gly Ser Lys
165 170 175
Tyr Phe Gly Thr Cys Ser Phe Leu Leu Tyr Lys Ala Gln Leu Ile Asp
180 185 190
Thr His Phe Ser
195

(2) INFORMATION FOR SEQ ID NO:1633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..177
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500788
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1633:
Met Met Glu Val Glu Leu Gly Glu Asp Trp Ile Leu His Gln His Cys
1 5 10 15
Lys Val Tyr Leu Phe Ile Ser Ser Gln Arg Ile Ser Gly Cys Leu Val
 20 25 30
Ala Glu Pro Ile Lys Glu Ala Phe Lys Leu Ile Ala Ser Pro Asp Asp
 35 40 45
Glu Arg Gln Leu Gln Lys Glu Ser Ser Ser Ser Pro Ser Thr Ser Ile
 50 55 60
Gln Phe Gly Asn Ile Val Leu Gln Arg Glu Val Ser Lys Arg Cys Arg
65 70 75 80
Thr Ser Asp Asp Arg Leu Asp Asn Gly Val Ile Val Cys Glu Glu Glu
 85 90 95
Ala Lys Pro Ala Val Cys Gly Ile Arg Ala Ile Trp Val Ser Pro Ser
 100 105 110
Asn Arg Arg Lys Gly Ile Ala Thr Trp Leu Leu Asp Thr Thr Arg Glu
 115 120 125
Ser Phe Arg Asn Asn Gly Cys Met Leu Glu Lys Ser Gln Leu Ala Phe
 130 135 140
Ser Gln Pro Thr Ser Ile Gly Arg Ser Phe Gly Ser Lys Tyr Phe Gly
145 150 155 160
Thr Cys Ser Phe Leu Leu Tyr Lys Ala Gln Leu Ile Asp Thr His Phe
 165 170 175
Ser

(2) INFORMATION FOR SEQ ID NO:1634:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1452 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1452

(D) OTHER INFORMATION: / Ceres Seq. ID 1500793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1634:

aagcattttg	cattcttgtt	tcttggtttt	gtgttttagt	tttgagagaa	aatgggacag	60
attccgaggt	tcttctcttg	gaggaatatg	tgggtcctct	cggtggccat	caacttcacg	120
ttgattctaa	agattttgaa	gggtgataga	gaacgaggag	attcatggga	cagaaacagcg	180
tatgttagca	tatggcccgt	ggatccacc	acgggttcag	aatcttcttc	gttggtcttca	240
gcattcttgc	actatagcaa	gattgaagaa	gacgatgata	gaattatcaa	tctcaaat	300
gggtgatacaa	cggtgtatga	gagatattgg	caggaataatg	gagaggtgac	aacaatgggtg	360
atacctggat	ggcaatctct	tagctatttt	tcagatgaaa	acaacctctg	ttggtttctt	420
gagccagagc	ttgccaaaga	gattgtgagg	gtgcataaag	ttgttgggaa	tgctgtaaacg	480
caagaacgct	tcattgttgt	tggcactggc	tcaacacaa	tgtatcagcg	tgtctcttat	540
gctctctccc	cacatgatga	ctccggtccc	attaatgtcg	gtgcagcccg	accctattat	600
agtacatacc	cggttgattac	agactgcctc	aaatcaggtt	tatatcgatg	gggtggagat	660
gcaaaagacgt	acaaagaaga	tggtccatac	attgaacttg	ttacatctcc	aaacaacctc	720
gatgggttct	tgagagaatc	agtagtgaac	agtactgaag	gtatatattg	catcatgtttg	780
gcttactatt	ggccacagta	tacacggata	acataaccag	ctgatcaaga	tgttatgctc	840
ttcactgctt	caaaagagac	tggccatgca	gggatacgga	ttggvtgggc	tttggtgaaa	900
gacagagaga	cggctagga	aatgatagag	tacattgaac	tcaacacgat	tggggtttca	960

aaggactcac	agcttagagt	agccaaggtt	cttaaggttg	tgtcagacag	ttgtgggaat	1020
gtaacgggca	aacttttctt	tgaccatagt	tatgatgcta	tgtatgagag	gtggaaacct	1080
ttgaaacaag	cagcaaaagg	tactaaacgt	ttcagtggtc	ctgatttcgt	ctctcaacgt	1140
tgcaatttct	ttggcagggt	ctttgagcca	caaccagcat	ttgcattggt	taagtgtgaa	1200
gaaggagtag	tggatttgtg	gaagtttctt	agagaggaga	agaagattct	aactaaaaat	1260
ggaaagtact	tcggagatga	gctaagtaat	gtgaggataa	gcatgttgga	tagagatact	1320
aactttaata	ttttccttca	caggattaca	tcttccttta	attcaacttt	gtaagtgcac	1380
atgcatgtga	ttatgatcga	ttgtcataac	ttgcaacaag	tgttttgtct	cataaatatt	1440
attggaaatt	tg					

(2) INFORMATION FOR SEQ ID NO:1635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1500794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1635:

Met	Gly	Gln	Ile	Pro	Arg	Phe	Leu	Ser	Trp	Arg	Asn	Met	Leu	Val	Leu	
1			5					10					15			
Ser	Leu	Ala	Ile	Asn	Phe	Ser	Leu	Ile	Leu	Lys	Ile	Leu	Lys	Gly	Asp	
			20					25					30			
Arg	Glu	Arg	Gly	Asp	Ser	Trp	Asp	Arg	Thr	Ala	Tyr	Val	Ser	Ile	Trp	
			35				40					45				
Pro	Val	Val	Ser	Thr	Thr	Ala	Ser	Glu	Ser	Ser	Ser	Leu	Ser	Ser	Ala	
			50			55					60					
Ser	Cys	Asn	Tyr	Ser	Lys	Ile	Glu	Glu	Asp	Asp	Asp	Arg	Ile	Ile	Asn	
65					70					75				80		
Leu	Lys	Phe	Gly	Asp	Pro	Thr	Val	Tyr	Glu	Arg	Tyr	Trp	Gln	Glu	Asn	
			85					90					95			
Gly	Glu	Val	Thr	Met	Val	Ile	Pro	Gly	Trp	Gln	Ser	Leu	Ser	Tyr		
			100				105					110				
Phe	Ser	Asp	Glu	Asn	Asn	Leu	Cys	Trp	Phe	Leu	Glu	Pro	Glu	Leu	Ala	
			115				120					125				
Lys	Glu	Ile	Val	Arg	Val	His	Lys	Val	Val	Gly	Asn	Ala	Val	Thr	Gln	
			130			135					140					
Asp	Arg	Phe	Ile	Val	Val	Gly	Thr	Gly	Ser	Thr	Gln	Leu	Tyr	Gln	Ala	
145					150					155					160	
Ala	Leu	Tyr	Ala	Leu	Ser	Pro	His	Asp	Asp	Ser	Gly	Pro	Ile	Asn	Val	
			165						170					175		
Val	Ser	Ala	Ala	Pro	Tyr	Tyr	Ser	Thr	Tyr	Pro	Leu	Ile	Thr	Asp	Cys	
			180				185						190			
Leu	Lys	Ser	Gly	Leu	Tyr	Arg	Trp	Gly	Gly	Asp	Ala	Lys	Thr	Tyr	Lys	
		195					200					205				
Glu	Asp	Gly	Pro	Tyr	Ile	Glu	Leu	Val	Thr	Ser	Pro	Asn	Asn	Pro	Asp	
		210				215					220					
Gly	Phe	Leu	Arg	Glu	Ser	Val	Val	Asn	Ser	Thr	Glu	Gly	Ile	Leu	Ile	
225					230					235					240	
His	Asp	Leu	Ala	Tyr	Tyr	Trp	Pro	Gln	Tyr	Thr	Pro	Ile	Thr			
			245						250							

(2) INFORMATION FOR SEQ ID NO:1636:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..242
(D) OTHER INFORMATION: / Ceres Seq. ID 1500795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1636:

Met	Leu	Val	Leu	Ser	Leu	Ala	Ile	Asn	Phe	Ser	Leu	Ile	Leu	Lys	Ile	
1			5					10						15		
Leu	Lys	Gly	Asp	Arg	Glu	Arg	Gly	Asp	Ser	Trp	Asp	Arg	Thr	Ala	Tyr	
		20					25						30			
Val	Ser	Ile	Trp	Pro	Val	Val	Ser	Thr	Thr	Ala	Ser	Glu	Ser	Ser	Ser	
		35					40					45				
Leu	Ser	Ser	Ala	Ser	Cys	Asn	Tyr	Ser	Lys	Ile	Glu	Glu	Asp	Asp	Asp	
	50					55					60					
Arg	Ile	Ile	Asn	Leu	Lys	Phe	Gly	Asp	Pro	Thr	Val	Tyr	Glu	Arg	Tyr	
	65			70					75					80		
Trp	Gln	Glu	Asn	Gly	Glu	Val	Thr	Thr	Met	Val	Ile	Pro	Gly	Trp	Gln	
			85						90				95			
Ser	Leu	Ser	Tyr	Phe	Ser	Asp	Glu	Asn	Asn	Leu	Cys	Trp	Phe	Leu	Glu	
			100					105					110			
Pro	Glu	Leu	Ala	Lys	Glu	Ile	Val	Arg	Val	His	Lys	Val	Val	Gly	Asn	
		115					120					125				
Ala	Val	Thr	Gln	Asp	Arg	Phe	Ile	Val	Val	Gly	Thr	Gly	Ser	Thr	Gln	
	130					135					140					
Leu	Tyr	Gln	Ala	Ala	Leu	Tyr	Ala	Leu	Ser	Pro	His	Asp	Asp	Ser	Gly	
	145			150						155					160	
Pro	Ile	Asn	Val	Val	Ser	Ala	Ala	Pro	Tyr	Ser	Thr	Tyr	Pro	Leu		
			165					170					175			
Ile	Thr	Asp	Cys	Leu	Lys	Ser	Gly	Leu	Tyr	Arg	Trp	Gly	Gly	Asp	Ala	
		180					185						190			
Lys	Thr	Tyr	Lys	Glu	Asp	Gly	Pro	Tyr	Ile	Glu	Leu	Val	Thr	Ser	Pro	
		195					200					205				
Asn	Asn	Pro	Asp	Gly	Phe	Leu	Arg	Glu	Ser	Val	Val	Asn	Ser	Thr	Glu	
	210					215					220					
Gly	Ile	Leu	Ile	His	Asp	Leu	Ala	Tyr	Tyr	Trp	Pro	Gln	Tyr	Thr	Pro	
	225				230					235					240	
Ile	Thr															

(2) INFORMATION FOR SEQ ID NO:1637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..179
(D) OTHER INFORMATION: / Ceres Seq. ID 1500796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1637:

Met	Leu	Phe	Thr	Ala	Ser	Lys	Ser	Thr	Gly	His	Ala	Gly	Ile	Arg	Ile	
1			5					10					15			
Xaa	Trp	Ala	Leu	Val	Lys	Asp	Arg	Glu	Thr	Ala	Arg	Lys	Met	Ile	Glu	
		20					25					30				
Tyr	Ile	Glu	Leu	Asn	Thr	Ile	Gly	Val	Ser	Lys	Asp	Ser	Gln	Leu	Arg	
		35				40					45					
Val	Ala	Lys	Val	Leu	Lys	Val	Val	Ser	Asp	Ser	Cys	Gly	Asn	Val	Thr	
	50					55					60					
Gly	Lys	Ser	Phe	Phe	Asp	His	Ser	Tyr	Asp	Ala	Met	Tyr	Glu	Arg	Trp	
	65			70					75					80		
Lys	Leu	Leu	Lys	Gln	Ala	Ala	Lys	Asp	Thr	Lys	Arg	Phe	Ser	Val	Pro	
			85					90				95				
Asp	Phe	Val	Ser	Gln	Arg	Cys	Asn	Phe	Gly	Arg	Val	Phe	Glu	Pro		

(2) INFORMATION FOR SEQ ID NO:1638:

(A) LENGTH: 1235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```
(ix) FEATURE:
```

- (A) NAME/KEY: -
(B) LOCATION: 1..1235
(D) OTHER INFORMATION: / Ceres Seq. ID 1500797

tactaataatca	gaagatattat	actaaacacaga	gtctttttttg	acttgccaaa	aacacactctg	60
tctctctctctc	tcttttcggga	tcttgaagatg	cgattctctgt	tctgatcttc	tccaaactca	120
atggtgagaag	aagagagagaag	acactgtctgt	aaatcgctag	agcttgcgaa	gagtggggagt	180
ttttcagct	ggtgaaacct	ggtatctcat	tggagctctct	aaaaaagctg	agaagaactga	240
ctgcagatgt	ctacaaaaca	gagagagaag	aagcattcaa	gaacttcta	cccgtagaagt	300
tgtcacaaga	atgtgttgca	agaataactg	gcgagaagct	agaaaacgtg	gaactggagta	360
atgtctctaac	tctcttggac	caataaccaa	acgaatggcc	atccaaaatt	aatgagagta	420
tgggagaata	cagagaagaaa	gtgagaagaag	tatgcagcaa	catgtgtgaa	gtgagtggatg	480
agaattttggg	tgtgcctaaa	gtgtacataa	agaaagcttt	gaatgaagga	atggaagagat	540
gagagaagac	agctcttctt	gggactaaa	tacgcacata	ccctcttgtt	ccctctactctg	600
acgtagtcaa	tggcctctga	ctgcataact	atgcaggagg	tctgtgtttg	cttttccaga	660
acgtggaata	tatgtggcctt	caggtcttga	aagacggcga	gtgtgactgt	gttcacgctc	720
tacctaatgc	cgatgtttatc	aacactgttga	atcagat tga	atgtcttagc	aaccggaagat	780
acaagaagtgc	gtgcccacag	gtggttgctg	gggaggaagg	acacagaaga	tctatagctt	840
ccctctacaa	tcctcgctac	aaggccgcga	taggggcagc	cacggtggcg	gaaggaggaag	900
gaagtggagaa	gaagtatcca	aagttttgtt	tgtggagata	catggatgtt	atgcacaaac	960
agaagttcat	gcctaaagag	ctcctgtttt	tactgtctaaa	gtctctctaa	tatgtactatt	1020
ttaatttattt	tacagtactt	atcactctct	tattctaacac	catatgtatg	ttctctcttaa	1080
gcataaataa	ccaaattata	tatgtaaata	tttggcatct	gcctctcagg	ctttatattt	1140
tttgtttttt	ttttgttttg	ccatgtgatg	taagaacttt	tctttgtgtg	octatgttct	1200
tattgtttttt	atataaattg	tctgtccttt	ttctt			

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..307
(D) OTHER INFORMATION: / Ceres Seq. ID 1500798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639:

Met	Ala	Ile	Pro	Val	Ile	Asp	Phe	Ser	Lys	Leu	Asn	Gly	Glu	Glu	Arg
1				5					10					15	
Glu	Lys	Thr	Leu	Ser	Glu	Ile	Ala	Arg	Ala	Cys	Glu	Glu	Trp	Gly	Phe
			20					25					30		
Phe	Gln	Leu	Val	Asn	His	Gly	Ile	Pro	Leu	Glu	Leu	Leu	Asn	Lys	Val


```

      35              40              45
Lys Lys Leu Ser Ser Asp Cys Tyr Lys Thr Glu Arg Glu Glu Ala Phe
 50              55              60
Lys Thr Ser Asn Pro Val Lys Leu Leu Asn Glu Leu Val Gln Lys Asn
 65              70              75
Ser Gly Glu Lys Leu Glu Asn Val Asp Trp Glu Asp Val Phe Thr Leu
      85              90              95
Leu Asp His Asn Gln Asn Glu Trp Pro Ser Lys Ile Lys Glu Thr Met
      100              105              110
Gly Glu Tyr Arg Glu Glu Val Arg Lys Leu Ala Ser Lys Met Met Glu
      115              120              125
Val Met Asp Glu Asn Leu Gly Leu Pro Lys Gly Tyr Ile Lys Lys Ala
      130              135              140
Phe Asn Glu Gly Met Glu Asp Gly Glu Glu Thr Ala Phe Phe Gly Thr
      145              150              155
Lys Val Ser His Tyr Pro Pro Cys Pro His Pro Glu Leu Val Asn Gly
      165              170              175
Leu Arg Ala His Thr Asp Ala Gly Gly Val Val Leu Leu Phe Gln Asp
      180              185              190
Asp Glu Tyr Asp Gly Leu Gln Val Leu Lys Asp Gly Glu Trp Ile Asp
      195              200              205
Val Gln Pro Leu Pro Asn Ala Ile Val Ile Asn Thr Gly Asp Gln Ile
      210              215              220
Glu Val Leu Ser Asn Gly Arg Tyr Lys Ser Ala Trp His Arg Val Val
      225              230              235
Ala Arg Glu Glu Gly Asn Arg Arg Ser Ile Ala Ser Phe Tyr Asn Pro
      245              250              255
Ser Tyr Lys Ala Ala Ile Gly Pro Ala Thr Val Ala Glu Glu Glu Gly
      260              265              270
Ser Glu Lys Lys Tyr Pro Lys Phe Val Phe Gly Asp Tyr Met Asp Val
      275              280              285
Tyr Ala Asn Gln Lys Phe Met Pro Lys Glu Pro Arg Phe Leu Ala Val
      290              295              300
Lys Ser Leu
305

```

(2) INFORMATION FOR SEQ ID NO:1640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1640:

```

Met Gly Glu Tyr Arg Glu Glu Val Arg Lys Leu Ala Ser Lys Met Met
 1              5              10              15
Glu Val Met Asp Glu Asn Leu Gly Leu Pro Lys Gly Tyr Ile Lys Lys
      20              25              30
Ala Phe Asn Glu Gly Met Glu Asp Gly Glu Thr Ala Phe Phe Gly
      35              40              45
Thr Lys Val Ser His Tyr Pro Pro Cys Pro His Pro Glu Leu Val Asn
      50              55              60
Gly Leu Arg Ala His Thr Asp Ala Gly Gly Val Val Leu Leu Phe Gln
      65              70              75
Asp Asp Glu Tyr Asp Gly Leu Gln Val Leu Lys Asp Gly Glu Trp Ile
      85              90              95
Asp Val Gln Pro Leu Pro Asn Ala Ile Val Ile Asn Thr Gly Asp Gln
      100              105              110

```

```

Ile Glu Val Leu Ser Asn Gly Arg Tyr Lys Ser Ala Trp His Arg Val
    115                120                125
Val Ala Arg Glu Glu Gly Asn Arg Arg Ser Ile Ala Ser Phe Tyr Asn
    130                135                140
Pro Ser Tyr Lys Ala Ala Ile Gly Pro Ala Thr Val Ala Glu Glu Glu
    145                150                155                160
Gly Ser Glu Lys Lys Tyr Pro Lys Phe Val Phe Gly Asp Tyr Met Asp
    165                170                175
Val Tyr Ala Asn Gln Lys Phe Met Pro Lys Glu Pro Arg Phe Leu Ala
    180                185                190
Val Lys Ser Leu
    195

```

(2) INFORMATION FOR SEQ ID NO:1641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1500800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641:

```

Met Met Glu Val Met Asp Glu Asn Leu Gly Leu Pro Lys Gly Tyr Ile
    1          5          10          15
Lys Lys Ala Phe Asn Glu Gly Met Glu Asp Gly Glu Glu Thr Ala Phe
    20          25          30
Phe Gly Thr Lys Val Ser His Tyr Pro Pro Cys Pro His Pro Glu Leu
    35          40          45
Val Asn Gly Leu Arg Ala His Thr Asp Ala Gly Gly Val Val Leu Leu
    50          55          60
Phe Gln Asp Asp Glu Tyr Asp Gly Leu Gln Val Leu Lys Asp Gly Glu
    65          70          75          80
Trp Ile Asp Val Gln Pro Leu Pro Asn Ala Ile Val Ile Asn Thr Gly
    85          90          95
Asp Gln Ile Glu Val Leu Ser Asn Gly Arg Tyr Lys Ser Ala Trp His
    100         105         110
Arg Val Val Ala Arg Glu Glu Gly Asn Arg Arg Ser Ile Ala Ser Phe
    115         120         125
Tyr Asn Pro Ser Tyr Lys Ala Ala Ile Gly Pro Ala Thr Val Ala Glu
    130         135         140
Glu Glu Gly Ser Glu Lys Lys Tyr Pro Lys Phe Val Phe Gly Asp Tyr
    145         150         155         160
Met Asp Val Tyr Ala Asn Gln Lys Phe Met Pro Lys Glu Pro Arg Phe
    165         170         175
Leu Ala Val Lys Ser Leu
    180

```

(2) INFORMATION FOR SEQ ID NO:1642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..619

(D) OTHER INFORMATION: / Ceres Seq. ID 1500801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642:

acaccggcgt ttggctgmsa tcatcgagat gatacacact gcaagcttga tacacgacga

tgtgttagac	gagagtgaca	tgcgaagagg	aaaggaaaac	gttcgatgac	ttttcggcac	120
aagagtagcg	gtgctagctg	gagatttcat	gtttgctcaa	gcgtcatggt	acttagcaaa	180
tctcgagaat	cttgaagtta	ttaagctcat	cagtcaggtg	atcaaagact	ttgcaagcgg	240
agagataaa	caggcgctca	gcttatttga	ctgcgacacc	aagctcgacg	agtacttact	300
caaaagtttc	tacaagacag	cctctttagt	ggctgcgagc	accaaaggag	ctgccatttt	360
cagcagagtt	gagcctgatg	tgacagaaca	aatgtacgag	tttgggaaga	atctcggtct	420
ctctttccag	atagtttgat	atattttgga	tttctactcag	tcgacagagc	agctcgggaa	480
gccagcaggg	agtgatttgg	ctaaaggtta	cttaacagca	cctgtgattt	tcgctctgga	540
gagggagcca	aggctaagag	agatcattga	gtcagagttt	tgtgaggcgg	gttctctgga	600
agaagcgatt	gaagcgggtg					

(2) INFORMATION FOR SEQ ID NO:1643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1500802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1643:

His	Arg	Arg	Leu	Ala	Xaa	Ile	Ile	Glu	Met	Ile	His	Thr	Ala	Ser	Leu
1				5				10						15	
Ile	His	Asp	Asp	Val	Leu	Asp	Glu	Ser	Asp	Met	Arg	Arg	Gly	Lys	Glu
			20					25					30		
Thr	Val	His	Glu	Leu	Phe	Gly	Thr	Arg	Val	Ala	Val	Leu	Ala	Gly	Asp
			35				40					45			
Phe	Met	Phe	Ala	Gln	Ala	Ser	Trp	Tyr	Leu	Ala	Asn	Leu	Glu	Asn	Leu
			50				55				60				
Glu	Val	Ile	Lys	Leu	Ile	Ser	Gln	Val	Ile	Lys	Asp	Phe	Ala	Ser	Gly
			65		70					75				80	
Glu	Ile	Lys	Gln	Ala	Ser	Ser	Leu	Phe	Asp	Cys	Asp	Thr	Lys	Leu	Asp
			85						90					95	
Glu	Tyr	Leu	Leu	Lys	Ser	Phe	Tyr	Lys	Thr	Ala	Ser	Leu	Val	Ala	Ala
			100					105					110		
Ser	Thr	Lys	Gly	Ala	Ala	Ile	Phe	Ser	Arg	Val	Glu	Pro	Asp	Val	Thr
			115				120					125			
Glu	Gln	Met	Tyr	Glu	Phe	Gly	Lys	Asn	Leu	Gly	Leu	Ser	Phe	Gln	Ile
			130				135				140				
Val	Asp	Asp	Ile	Leu	Asp	Phe	Thr	Gln	Ser	Thr	Glu	Gln	Leu	Gly	Lys
			145			150				155				160	
Pro	Ala	Gly	Ser	Asp	Leu	Ala	Lys	Gly	Asn	Leu	Thr	Ala	Pro	Val	Ile
			165					170					175		
Phe	Ala	Leu	Glu	Arg	Glu	Pro	Arg	Leu	Arg	Glu	Ile	Ile	Glu	Ser	Glu
			180					185					190		
Phe	Cys	Glu	Ala	Gly	Ser	Leu	Glu	Glu	Ala	Ile	Glu	Ala	Val		
			195				200					205			

(2) INFORMATION FOR SEQ ID NO:1644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1500803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1644:

Met Ile His Thr Ala Ser Leu Ile His Asp Asp Val Leu Asp Glu Ser

```

1           5           10           15
Asp Met Arg Arg Gly Lys Glu Thr Val His Glu Leu Phe Gly Thr Arg
                20           25           30
Val Ala Val Leu Ala Gly Asp Phe Met Phe Ala Gln Ala Ser Trp Tyr
                35           40           45
Leu Ala Asn Leu Glu Asn Leu Glu Val Ile Lys Leu Ile Ser Gln Val
                50           55           60
Ile Lys Asp Phe Ala Ser Gly Glu Ile Lys Gln Ala Ser Ser Leu Phe
                65           70           75           80
Asp Cys Asp Thr Lys Leu Asp Glu Tyr Leu Leu Lys Ser Phe Tyr Lys
                85           90           95
Thr Ala Ser Leu Val Ala Ala Ser Thr Lys Gly Ala Ala Ile Phe Ser
                100           105           110
Arg Val Glu Pro Asp Val Thr Glu Gln Met Tyr Glu Phe Gly Lys Asn
                115           120           125
Leu Gly Leu Ser Phe Gln Ile Val Asp Asp Ile Leu Asp Phe Thr Gln
                130           135           140
Ser Thr Glu Gln Leu Gly Lys Pro Ala Gly Ser Asp Leu Ala Lys Gly
                145           150           155           160
Asn Leu Thr Ala Pro Val Ile Phe Ala Leu Glu Arg Glu Pro Arg Leu
                165           170           175
Arg Glu Ile Ile Glu Ser Glu Phe Cys Glu Ala Gly Ser Leu Glu Glu
                180           185           190
Ala Ile Glu Ala Val
                195

```

(2) INFORMATION FOR SEQ ID NO:1645:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1500804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1645:

```

Met Arg Arg Gly Lys Glu Thr Val His Glu Leu Phe Gly Thr Arg Val
1           5           10           15
Ala Val Leu Ala Gly Asp Phe Met Phe Ala Gln Ala Ser Trp Tyr Leu
                20           25           30
Ala Asn Leu Glu Asn Leu Glu Val Ile Lys Leu Ile Ser Gln Val Ile
                35           40           45
Lys Asp Phe Ala Ser Gly Glu Ile Lys Gln Ala Ser Ser Leu Phe Asp
                50           55           60
Cys Asp Thr Lys Leu Asp Glu Tyr Leu Leu Lys Ser Phe Tyr Lys Thr
                65           70           75           80
Ala Ser Leu Val Ala Ala Ser Thr Lys Gly Ala Ala Ile Phe Ser Arg
                85           90           95
Val Glu Pro Asp Val Thr Glu Gln Met Tyr Glu Phe Gly Lys Asn Leu
                100           105           110
Gly Leu Ser Phe Gln Ile Val Asp Asp Ile Leu Asp Phe Thr Gln Ser
                115           120           125
Thr Glu Gln Leu Gly Lys Pro Ala Gly Ser Asp Leu Ala Lys Gly Asn
                130           135           140
Leu Thr Ala Pro Val Ile Phe Ala Leu Glu Arg Glu Pro Arg Leu Arg
                145           150           155           160
Glu Ile Ile Glu Ser Glu Phe Cys Glu Ala Gly Ser Leu Glu Ala
                165           170           175
Ile Glu Ala Val
                180

```

(2) INFORMATION FOR SEQ ID NO:1646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1776 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1776
(D) OTHER INFORMATION: / Ceres Seq. ID 1500805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1646:

```
gtctcatcac ttcccaattt cctctctgca tttgttgtct ctctctcctg aaaacccttg      60
aatttttgcta cagcatctct gaaacgtgtc ttttgtactg acttcaatct tctttatcac      120
ttaccgttttc tgggtttttt gaagcaactg agctaataaa aagcttcttc ttagactcgg      180
aagaagaataa aaacacagaat ctttatttgt taaagcttcc aaattcgaga agagaatttg      240
aaacgaccaa gtctcaggata tctgttttct cgtctacttt ggctctcttc tcttctcttt      300
cgaaaagggt ttattctgtc ttaaaagaaa ctttttgtag agggtaaaaa aagcttcaat      360
tttcagagaa acacaaaagg cagaaaacaga gaaaaacaaa tcatctaatt catgaaaacg      420
ggttcaatga atagatcgtg tctctgtagt gtcttaatca ccaactgctc gatttgtggg      480
gcttacttca ttgtcaatgc ttattcttgc aaagacttta aagagaagtt gctgaagtgg      540
gaaatcactg ataaagatga taacagtact gataagatgc agaagcaac aacaaccagt      600
acatgcaaga atttcaataa gccagtgggt actgaagcac taccgcaagg aattatcgag      660
aaaacatcga acctggaaac acaacatcta tggaactcac atgacacaaa aaagagaagg      720
cctaaccatt cgatgagttt gttagccatg gcggtcggta tcaaggcaaa ggagctagtt      780
aacaagaattt tccaaaagtt tctctctcga gatttcgagg tcatgttttt tcaattagat      840
gggtgtgtcg atgactggaa gcagtatoca tggaataatc atgcgatcca tgtttccgtg      900
atgaatcaaa caaaatgggt gttcgcgaag cgattcttgc atcccgatat agttgcagag      960
tacgagtata tatttctttg ggacgaagat cttgggtgtg gtcatttcaa tctctcaaga      1020
tatctatcta ttgtcaaaaga agaggggtcg gagatatcgc aacctgctct cagacttcca      1080
aaatcagaag tgcatcatcc tataaccgctc cgtcaaaaaa aatcaaaagt tcatagaaga      1140
attgtataat acaaaaggtag cgggcgatgt gatgaccata gcaccaatcc tctctgcatc      1200
gggtgggtgg aaatgatggc acctgttttc tctagagctg catggagatg ttcttgggat      1260
atgattcaga atgatttgat ceatgcttgg ggtctggata cgcagcttgg ttattgtgct      1320
caaggtgacc gaaagaaaaa tgtcgggtgt gttgatcggt agtacataat tcattatggt      1380
cttccaacac tcggtgtggt tgaaaaccgtc tcaagcgctt tgcggaatga gacagactcg      1440
aaatcaacgg aatcattaga gtctcgtgaa gtggataata gaccagaagt gaggatgaaa      1500
tcatttgtgg agatgaagag attcaaggaa cgttggaaga aagctgtgag ggatgataca      1560
tgttgggttg atccgtattg aaatccgagc ggtttaagta aaccgaatcg aaccggattc      1620
tttctcttgt tgagtgtgct ttgtgggtcca ttgtatacca ttatttttgt acatagattt      1680
tgttttactt cgagaaaata tagtgtattt atgtgtttta tggaccacag ttagatttta      1740
```

(2) INFORMATION FOR SEQ ID NO:1647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..389
(D) OTHER INFORMATION: / Ceres Seq. ID 1500806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1647:

```
Met Lys Gln Gly Ser Met Asn Arg Ser Cys Leu Cys Ser Val Leu Ile
1      5      10      15
Thr Thr Ala Leu Ile Cys Gly Ala Tyr Phe Ile Cys Asn Ala Tyr Leu
20      25      30
Ala Lys Asp Phe Lys Glu Lys Leu Leu Lys Trp Glu Ile Thr Asp Lys
35      40      45
Met His Asn Ser Thr Asp Lys Met Gln Asn Ala Thr Thr Ser Thr
```

50					55					60									
Cys	Lys	Asn	Phe	Asn	Lys	Pro	Val	Gly	Thr	Glu	Ala	Leu	Pro	Gln	Gly				
65					70					75					80				
Ile	Ile	Glu	Lys	Thr	Ser	Asn	Leu	Glu	Thr	Gln	His	Leu	Trp	Asn	Tyr				
				85						90				95					
Asp	Asp	Thr	Lys	Lys	Arg	Arg	Pro	Asn	His	Ser	Met	Ser	Leu	Leu	Ala				
				100					105					110					
Met	Ala	Val	Gly	Ile	Lys	Gln	Lys	Glu	Leu	Val	Asn	Lys	Val	Ile	Gln				
				115					120				125						
Lys	Phe	Pro	Pro	Arg	Asp	Phe	Ala	Val	Met	Leu	Phe	His	Tyr	Asp	Gly				
				130			135				140								
Val	Val	Asp	Asp	Trp	Lys	Gln	Tyr	Pro	Trp	Asn	Asn	His	Ala	Ile	His				
145					150					155					160				
Val	Ser	Val	Met	Asn	Gln	Thr	Lys	Trp	Trp	Phe	Ala	Lys	Arg	Phe	Leu				
				165					170					175					
His	Pro	Asp	Ile	Val	Ala	Glu	Tyr	Glu	Tyr	Ile	Phe	Leu	Trp	Asp	Glu				
				180					185					190					
Asp	Leu	Gly	Val	Gly	His	Phe	Asn	Pro	Gln	Arg	Tyr	Leu	Ser	Ile	Val				
				195			200				205								
Lys	Glu	Glu	Gly	Leu	Glu	Ile	Ser	Gln	Pro	Ala	Leu	Asp	Thr	Ser	Lys				
				210			215				220								
Ser	Glu	Val	His	His	Pro	Ile	Thr	Ala	Arg	Gln	Lys	Lys	Ser	Lys	Val				
225					230					235					240				
His	Arg	Arg	Met	Tyr	Lys	Tyr	Lys	Gly	Ser	Gly	Arg	Cys	Asp	Asp	His				
				245					250					255					
Ser	Thr	Asn	Pro	Pro	Cys	Ile	Gly	Trp	Val	Glu	Met	Met	Ala	Pro	Val				
				260				265					270						
Phe	Ser	Arg	Ala	Ala	Trp	Arg	Cys	Ser	Trp	Tyr	Met	Ile	Gln	Asn	Asp				
				275			280					285							
Leu	Ile	His	Ala	Trp	Gly	Leu	Asp	Thr	Gln	Leu	Gly	Tyr	Cys	Ala	Gln				
				290			295				300								
Gly	Asp	Arg	Lys	Lys	Asn	Val	Gly	Val	Val	Asp	Ala	Glu	Tyr	Ile	Ile				
305					310					315					320				
His	Tyr	Gly	Leu	Pro	Thr	Leu	Gly	Val	Val	Glu	Thr	Ala	Ser	Ser	Ala				
				325					330					335					
Leu	Arg	Asn	Glu	Thr	Asp	Ser	Lys	Ser	Thr	Glu	Ser	Leu	Glu	Ser	Arg				
				340			345						350						
Glu	Val	Asp	Asn	Arg	Pro	Glu	Val	Arg	Met	Lys	Ser	Phe	Val	Glu	Met				
				355			360					365							
Lys	Arg	Phe	Lys	Glu	Arg	Trp	Lys	Lys	Ala	Val	Arg	Asp	Asp	Thr	Cys				
				370			375				380								
Trp	Val	Asp	Pro	Tyr															
385																			

(2) INFORMATION FOR SEQ ID NO:1648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..384
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1648:

Met	Asn	Arg	Ser	Cys	Leu	Cys	Ser	Val	Leu	Ile	Thr	Thr	Ala	Leu	Ile
1				5				10					15		
Cys	Gly	Ala	Tyr	Phe	Ile	Cys	Asn	Ala	Tyr	Leu	Ala	Lys	Asp	Phe	Lys
				20			25					30			
Glu	Lys	Leu	Leu	Lys	Trp	Glu	Ile	Thr	Asp	Lys	Met	His	Asn	Ser	Thr
				35			40					45			

Asp	Lys	Met	Gln	Asn	Ala	Thr	Thr	Thr	Ser	Thr	Cys	Lys	Asn	Phe	Asn	
50					55						60					
Lys	Pro	Val	Gly	Thr	Glu	Ala	Leu	Pro	Gln	Gly	Ile	Ile	Glu	Lys	Thr	
65					70					75					80	
Ser	Asn	Leu	Glu	Thr	Gln	His	Leu	Trp	Asn	Tyr	Asp	Asp	Thr	Lys	Lys	
				85					90					95		
Arg	Arg	Pro	Asn	His	Ser	Met	Ser	Leu	Leu	Ala	Met	Ala	Val	Gly	Ile	
			100					105					110			
Lys	Gln	Lys	Glu	Leu	Val	Asn	Lys	Val	Ile	Gln	Lys	Phe	Pro	Pro	Arg	
			115				120					125				
Asp	Phe	Ala	Val	Met	Leu	Phe	His	Tyr	Asp	Gly	Val	Val	Asp	Asp	Trp	
130						135					140					
Lys	Gln	Tyr	Pro	Trp	Asn	Asn	His	Ala	Ile	His	Val	Ser	Val	Met	Asn	
145					150					155					160	
Gln	Thr	Lys	Trp	Trp	Phe	Ala	Lys	Arg	Phe	Leu	His	Pro	Asp	Ile	Val	
				165					170					175		
Ala	Glu	Tyr	Glu	Tyr	Ile	Phe	Leu	Trp	Asp	Glu	Asp	Leu	Gly	Val	Gly	
			180					185					190			
His	Phe	Asn	Pro	Gln	Arg	Tyr	Leu	Ser	Ile	Val	Lys	Glu	Glu	Gly	Leu	
			195				200					205				
Glu	Ile	Ser	Gln	Pro	Ala	Leu	Asp	Thr	Ser	Lys	Ser	Glu	Val	His	His	
					215						220					
Pro	Ile	Thr	Ala	Arg	Gln	Lys	Lys	Ser	Lys	Val	His	Arg	Arg	Met	Tyr	
225					230					235					240	
Lys	Tyr	Lys	Gly	Ser	Gly	Arg	Cys	Asp	Asp	His	Ser	Thr	Asn	Pro	Pro	
				245					250					255		
Cys	Ile	Gly	Trp	Val	Glu	Met	Met	Ala	Pro	Val	Phe	Ser	Arg	Ala	Ala	
			260					265					270			
Trp	Arg	Cys	Ser	Trp	Tyr	Met	Ile	Gln	Asn	Asp	Leu	Ile	His	Ala	Trp	
			275				280						285			
Gly	Leu	Asp	Thr	Gln	Leu	Gly	Tyr	Cys	Ala	Gln	Gly	Asp	Arg	Lys	Lys	
			290			295					300					
Asn	Val	Gly	Val	Val	Asp	Ala	Glu	Tyr	Ile	Ile	His	Tyr	Gly	Leu	Pro	
305					310					315					320	
Thr	Leu	Gly	Val	Val	Glu	Thr	Ala	Ser	Ser	Ala	Leu	Arg	Asn	Glu	Thr	
				325					330					335		
Asp	Ser	Lys	Ser	Thr	Glu	Ser	Leu	Glu	Ser	Arg	Glu	Val	Asp	Asn	Arg	
				340				345					350			
Pro	Glu	Val	Arg	Met	Lys	Ser	Phe	Val	Glu	Met	Lys	Arg	Phe	Lys	Glu	
			355				360					365				
Arg	Trp	Lys	Lys	Ala	Val	Arg	Asp	Asp	Thr	Cys	Trp	Val	Asp	Pro	Tyr	
370						375						380				

(2) INFORMATION FOR SEQ ID NO:1649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1500808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1649:

Met	His	Asn	Ser	Thr	Asp	Lys	Met	Gln	Asn	Ala	Thr	Thr	Thr	Ser	Thr	
1			5					10						15		
Cys	Lys	Asn	Phe	Asn	Lys	Pro	Val	Gly	Thr	Glu	Ala	Leu	Pro	Gln	Gly	
			20					25					30			
Ile	Ile	Glu	Lys	Thr	Ser	Asn	Leu	Glu	Thr	Gln	His	Leu	Trp	Asn	Tyr	

35	40	45
Asp Asp Thr Lys Lys Arg Arg Pro Asn His Ser Met Ser Leu Leu Ala		
50	55	60
Met Ala Val Gly Ile Lys Gln Lys Glu Leu Val Asn Lys Val Ile Gln		
65	70	75
Lys Phe Pro Pro Arg Asp Phe Ala Val Met Leu Phe His Tyr Asp Gly		
85	90	95
Val Val Asp Asp Trp Lys Gln Tyr Pro Trp Asn Asn His Ala Ile His		
100	105	110
Val Ser Val Met Asn Gln Thr Lys Trp Trp Phe Ala Lys Arg Phe Leu		
115	120	125
His Pro Asp Ile Val Ala Glu Tyr Glu Tyr Ile Phe Leu Trp Asp Glu		
130	135	140
Asp Leu Gly Val Gly His Phe Asn Pro Gln Arg Tyr Leu Ser Ile Val		
145	150	155
Lys Glu Glu Gly Leu Glu Ile Ser Gln Pro Ala Leu Asp Thr Ser Lys		
165	170	175
Ser Glu Val His His Pro Ile Thr Ala Arg Gln Lys Lys Ser Lys Val		
180	185	190
His Arg Arg Met Tyr Lys Tyr Lys Gly Ser Gly Arg Cys Asp Asp His		
195	200	205
Ser Thr Asn Pro Pro Cys Ile Gly Trp Val Glu Met Met Ala Pro Val		
210	215	220
Phe Ser Arg Ala Ala Trp Arg Cys Ser Trp Tyr Met Ile Gln Asn Asp		
225	230	235
Leu Ile His Ala Trp Gly Leu Asp Thr Gln Leu Gly Tyr Cys Ala Gln		
245	250	255
Gly Asp Arg Lys Lys Asn Val Gly Val Val Asp Ala Glu Tyr Ile Ile		
260	265	270
His Tyr Gly Leu Pro Thr Leu Gly Val Val Glu Thr Ala Ser Ser Ala		
275	280	285
Leu Arg Asn Glu Thr Asp Ser Lys Ser Thr Glu Ser Leu Glu Ser Arg		
290	295	300
Glu Val Asp Asn Arg Pro Glu Val Arg Met Lys Ser Phe Val Glu Met		
305	310	315
Lys Arg Phe Lys Glu Arg Trp Lys Lys Ala Val Arg Asp Asp Thr Cys		
325	330	335
Trp Val Asp Pro Tyr		
340		

(2) INFORMATION FOR SEQ ID NO:1650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..543

(D) OTHER INFORMATION: / Ceres Seq. ID 1500809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1650:

aacctccact	gttaataaac	tcaaacctct	gcaattgtct	tcttctcttc	aactccatca	60
tctccaccac	cgccattctc	gccggaatcc	aatggagctt	accagcttcc	atcgctcttc	120
tctcttattc	ctcatctcac	taacattgat	catctctccg	acgacaacaa	cttcaactcg	180
ggttaaacac	ggatcaaacg	gagacaacct	cccctcccca	accgacgtaa	tcccactaat	240
aaaatcaact	ggagcaacaa	aagtataaat	ctacgacgca	aatccacaaa	tcctcaaaag	300
tttctccaac	accggaatcg	aattcatcat	cggaactcgg	aacgaatacc	tctccaaaat	360
gaaagatcct	tcaaaagcct	taacatggat	caaacaaaac	gttactccat	ttttactcgc	420
gactaacatc	acatgcataa	ctatcggtaa	cgaatactct	gctctcaacg	actcttccat	480
cactaccaat	ctctctccag	cgatgcaagg	agtttactct	gctttaatca	ccgcgggtct	540
ctc						

(2) INFORMATION FOR SEQ ID NO:1651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1651:

```
Thr Ser Thr Val Asn Lys Leu Lys Pro Leu Gln Leu Ser Ser Ser Leu
1      5      10      15
Gln Leu His His Leu His His Arg His Ser Arg Arg Asn Pro Met Glu
20      25      30
Leu Thr Ser Phe His Arg Ser Ser Leu Leu Phe Leu Ile Ser Leu Thr
35      40      45
Leu Ile Ile Leu Pro Thr Thr Thr Thr Ser Ile Gly Val Asn Tyr Gly
50      55      60
Gln Ile Gly Asp Asn Leu Pro Ser Pro Thr Asp Val Ile Pro Leu Ile
65      70      75      80
Lys Ser Ile Gly Ala Thr Lys Val Lys Leu Tyr Asp Ala Asn Pro Gln
85      90      95
Ile Leu Lys Ala Phe Ser Asn Thr Gly Ile Glu Phe Ile Ile Gly Leu
100      105      110
Gly Asn Glu Tyr Leu Ser Lys Met Lys Asp Pro Ser Lys Ala Leu Thr
115      120      125
Trp Ile Lys Gln Asn Val Thr Pro Phe Leu Pro Ala Thr Asn Ile Thr
130      135      140
Cys Ile Thr Ile Gly Asn Glu Ile Leu Ala Leu Asn Asp Ser Ser Leu
145      150      155      160
Thr Thr Asn Leu Leu Pro Ala Met Gln Gly Val His Ser Ala Leu Ile
165      170      175
Thr Ala Gly Leu
180
```

(2) INFORMATION FOR SEQ ID NO:1652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1652:

```
Met Glu Leu Thr Ser Phe His Arg Ser Ser Leu Leu Phe Leu Ile Ser
1      5      10      15
Leu Thr Leu Ile Leu Pro Thr Thr Thr Thr Ser Ile Gly Val Asn
20      25      30
Tyr Gly Gln Ile Gly Asp Asn Leu Pro Ser Pro Thr Asp Val Ile Pro
35      40      45
Leu Ile Lys Ser Ile Gly Ala Thr Lys Val Lys Leu Tyr Asp Ala Asn
50      55      60
Pro Gln Ile Leu Lys Ala Phe Ser Asn Thr Gly Ile Glu Phe Ile Ile
65      70      75      80
Gly Leu Gly Asn Glu Tyr Leu Ser Lys Met Lys Asp Pro Ser Lys Ala
85      90      95
Leu Thr Trp Ile Lys Gln Asn Val Thr Pro Phe Leu Pro Ala Thr Asn
```

	100					105						110							
Ile	Thr	Cys	Ile	Thr	Ile	Gly	Asn	Glu	Ile	Leu	Ala	Leu	Asn	Asp	Ser				
	115						120						125						
Ser	Leu	Thr	Thr	Asn	Leu	Leu	Pro	Ala	Met	Gln	Gly	Val	His	Ser	Ala				
	130						135						140						
Leu	Ile	Thr	Ala	Gly	Leu														
	145						150												

(2) INFORMATION FOR SEQ ID NO:1653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..667
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1653:

caagtgtatca	aacaaaaaav	gaccaagtct	ttttggtwtt	tcagatcgag	aaaaaatgtg	60
gttgcaaggt	ttgaagtaat	cttgcaatgg	attctttgac	tggatttaga	atggaaccca	120
aatggcaaat	tgatcctcag	cttctctttg	ttggtccaaa	gattggtgaa	ggagctcatg	180
ctaaagtcta	tgaggggaaa	tacaagaatc	agacagttgc	tataaagata	gttcacagag	240
gagaaacacc	agaagagatt	gctaaaagag	attcaagatt	ccttagagaa	gtagaatgc	300
tctcactgtt	tcaacacaag	aatttggtca	agttcattgg	tgcttgcaag	gagcctgtaa	360
tgggtgatgt	tacagaactt	cttcaaggcg	gtacattggc	taaaatacta	ttaaacttga	420
gaccgcgatg	tttggagact	cggtgtgcta	tcggttttgc	gcttgatatt	gctcgttgta	480
tggaatgctt	gcattcccat	gggatcattc	accgtgatct	caaacccgag	aacttgcttt	540
taactgcaga	ccataaaaaca	gtaaaactag	cagattttgg	attagcaaga	gaagagtcat	600
tgactgagat	gatgacggct	gagacaggaa	catccgatg	gatggcacct	gagttgtaca	660
gcacgggt						

(2) INFORMATION FOR SEQ ID NO:1654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..193
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1654:

Met	Asp	Ser	Leu	Thr	Gly	Phe	Arg	Met	Glu	Pro	Lys	Trp	Gln	Ile	Asp				
1			5						10				15						
Pro	Gln	Leu	Leu	Phe	Val	Gly	Pro	Lys	Ile	Gly	Glu	Gly	Ala	His	Ala				
			20					25					30						
Lys	Val	Tyr	Glu	Gly	Lys	Tyr	Lys	Asn	Gln	Thr	Val	Ala	Ile	Lys	Ile				
			35				40					45							
Val	His	Arg	Gly	Glu	Thr	Pro	Glu	Glu	Ile	Ala	Lys	Arg	Asp	Ser	Arg				
			50			55				60									
Phe	Leu	Arg	Glu	Val	Glu	Met	Leu	Ser	Arg	Val	Gln	His	Lys	Asn	Leu				
			65			70			75					80					
Val	Lys	Phe	Ile	Gly	Ala	Cys	Lys	Glu	Pro	Val	Met	Val	Ile	Val	Thr				
			85					90					95						
Glu	Leu	Leu	Gln	Gly	Gly	Thr	Leu	Arg	Lys	Tyr	Leu	Leu	Asn	Leu	Arg				
			100				105						110						
Pro	Ala	Cys	Leu	Glu	Thr	Arg	Val	Ala	Ile	Gly	Phe	Ala	Leu	Asp	Ile				
			115				120						125						
Ala	Arg	Gly	Met	Glu	Cys	Leu	His	Ser	His	Gly	Ile	Ile	His	Arg	Asp				
			130				135					140							

Leu Lys Pro Glu Asn Leu Leu Leu Thr Ala Asp His Lys Thr Val Lys
145 150 155 160
Leu Ala Asp Phe Gly Leu Ala Arg Glu Glu Ser Leu Thr Glu Met Met
165 170 175
Thr Ala Glu Thr Gly Thr Tyr Arg Trp Met Ala Pro Glu Leu Tyr Ser
180 185 190
Thr

(2) INFORMATION FOR SEQ ID NO:1655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1500822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1655:

Met Glu Pro Lys Trp Gln Ile Asp Pro Gln Leu Leu Phe Val Gly Pro
1 5 10 15
Lys Ile Gly Glu Gly Ala His Ala Lys Val Tyr Glu Gly Lys Tyr Lys
20 25 30
Asn Gln Thr Val Ala Ile Lys Ile Val His Arg Gly Glu Thr Pro Glu
35 40 45
Glu Ile Ala Lys Arg Asp Ser Arg Phe Leu Arg Glu Val Glu Met Leu
50 55 60
Ser Arg Val Gln His Lys Asn Leu Val Lys Phe Ile Gly Ala Cys Lys
65 70 75 80
Glu Pro Val Met Val Ile Val Thr Glu Leu Leu Gln Gly Gly Thr Leu
85 90 95
Arg Lys Tyr Leu Leu Asn Leu Arg Pro Ala Cys Leu Glu Thr Arg Val
100 105 110
Ala Ile Gly Phe Ala Leu Asp Ile Ala Arg Gly Met Glu Cys Leu His
115 120 125
Ser His Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu
130 135 140
Thr Ala Asp His Lys Thr Val Lys Leu Ala Asp Phe Gly Leu Ala Arg
145 150 155 160
Glu Glu Ser Leu Thr Glu Met Met Thr Ala Glu Thr Gly Thr Tyr Arg
165 170 175
Trp Met Ala Pro Glu Leu Tyr Ser Thr
180 185

(2) INFORMATION FOR SEQ ID NO:1656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1500823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1656:

Met Leu Ser Arg Val Gln His Lys Asn Leu Val Lys Phe Ile Gly Ala
1 5 10 15
Cys Lys Glu Pro Val Met Val Ile Val Thr Glu Leu Leu Gln Gly Gly
20 25 30
Thr Leu Arg Lys Tyr Leu Leu Asn Leu Arg Pro Ala Cys Leu Glu Thr

35	40	45
Arg Val Ala Ile Gly Phe Ala Leu Asp Ile Ala Arg Gly Met Glu Cys		
50	55	60
Leu His Ser His Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Leu		
65	70	75
Leu Leu Thr Ala Asp His Lys Thr Val Lys Leu Ala Asp Phe Gly Leu		
85	90	95
Ala Arg Glu Glu Ser Leu Thr Glu Met Met Thr Ala Glu Thr Gly Thr		
100	105	110
Tyr Arg Trp Met Ala Pro Glu Leu Tyr Ser Thr		
115	120	

(2) INFORMATION FOR SEQ ID NO:1657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1887 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1887
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1657:

cacacattct	tgcagaaggt	tttagaatca	caaagcataa	ctcacctacc	cctaaaccac	60
ctcacaatttc	tctctctctc	tattaaatct	tcttcaatca	ctcttctttg	agtcttttgc	120
cttggaattcc	tgatctggc	gtcttctctc	acttccaaat	ccattctctg	gatgcaccaa	180
accgcgtctt	tcttcttttc	tatccgtcgg	agctccgtcg	tctctctctt	ccgcgccgttc	240
agatatctct	ccattcacaa	accaggaaga	acttccggca	gtcgtggggg	ttgaagaaga	300
gtgatctgat	gtctaatggt	tctgagattc	gtcctgtgaa	ggttatgggt	ctgttttcca	360
cgccggagaa	agcttccggag	attgtgcttc	aaccatttag	agaaatctgt	tgctctatta	420
agcttctcgg	ctccaagtct	ctctctaatc	gaattctgct	tctcgtctgt	ctatctgagg	480
gaaactactgt	agtggaaca	gtgtgaaaca	gtgatgacat	caattacatg	cttgatgcgt	540
tggaagatgt	gggaattaat	gtggaaactc	acagtgaaaa	caatctgtgt	gtagtgtga	600
gatgtggcgg	ggatattcca	gcttccattg	attccaagag	tgatatcgaa	ctttacctcg	660
gcaatgcagg	aacagcaatg	cgtccactta	ccgcgcgcagt	tactgtgtga	ggtggcgaac	720
caagtattgt	ccttgatggg	gtgcctcaga	tgagagagag	acctataggg	gatttggttg	780
ttggtcttaa	gcagcttggt	gctgatgttg	aatgtactct	tgggcaatac	tgccctcctg	840
ttcgtgtcaa	cgtcaatggt	ggccttctcg	gtggaaaggt	gaagctttct	ggatctatta	900
gtagtcatga	cttgaccgct	ctgctcatgg	cagctccctt	agctcttgga	gacgtcgaaa	960
ttgaaattgt	cgataaattg	atttctgttc	cgatgtttga	aatgacattg	aagttgatgg	1020
aacgtttttg	ggttaagtgt	gagcatagtg	aaagctggga	gtctttcttt	tgttaaggggtg	1080
ggcaaaaata	caagtcgccg	ggtaatgctt	acgtgaagag	tgatgtctct	agtgtctagt	1140
atttctggc	tggtgtcgcc	attaccgggt	aaactgtcac	tggtgaaggt	gttggaacga	1200
ccagtgttga	gggagatgtg	aaattgtccg	aggttcttga	gaaaatggga	tgtaaatgtg	1260
cctggacaga	gaacagtggt	actgtgacag	ggcgtgtctag	agatgctttt	ggatgtgagac	1320
acttgccggc	tattgatgtc	aacatgaaca	aaatgcttga	tgtagcaatg	actcttgccg	1380
tcgttgctct	cttctgccgat	ggtccaaacca	ccattagaga	tgtggctagc	tggaagagtaa	1440
aggagacgga	aggatgatgt	gccattttga	cagagccttag	gttcacttgg	gtcacagtgg	1500
aagaaggttc	agattattgt	gtgattactc	cgccgaaaaa	gggtgaaaccg	gcagagatgt	1560
atacatatga	tgtcatataga	atggcaatgg	cattctctct	tgacagctgt	gctgatgttc	1620
caatcaccat	caatgacccc	ggttgacacca	ggaaaacctt	ccccgactact	ttccaagtcc	1680
ttgaagaagt	cacaagaagt	taaacaaaaa	aactctaaaa	cttccactgt	tttttctctt	1740
gatccaagct	tatctgtttc	catttttctt	gtctctgtaa	cattattaga	aagcaagagt	1800
agtgtttgtt	ttgtgtgacc	tgaaactgag	gagattttgag	atgcaaatcat	tgaatcggct	1860
ttggtatata	tttactactc	gtttttcc				

(2) INFORMATION FOR SEQ ID NO:1658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..464

(D) OTHER INFORMATION: / Ceres Seq. ID 1500829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1658:

Met	Leu	Asn	Gly	Ser	Glu	Ile	Arg	Pro	Val	Lys	Val	Arg	Ala	Ser	Val	
1			5					10					15			
Ser	Thr	Ala	Glu	Lys	Ala	Ser	Glu	Ile	Val	Leu	Gln	Pro	Ile	Arg	Glu	
			20					25				30				
Ile	Ser	Gly	Leu	Ile	Lys	Leu	Pro	Gly	Ser	Lys	Ser	Leu	Ser	Asn	Arg	
			35				40				45					
Ile	Leu	Leu	Leu	Ala	Ala	Leu	Ser	Glu	Gly	Thr	Thr	Val	Val	Asp	Asn	
			50			55					60					
Leu	Leu	Asn	Ser	Asp	Asp	Ile	Asn	Tyr	Met	Leu	Asp	Ala	Leu	Lys	Ile	
65				70				75							80	
Leu	Gly	Leu	Asn	Val	Glu	Thr	His	Ser	Glu	Asn	Asn	Arg	Ala	Val	Val	
			85					90				95				
Glu	Gly	Cys	Gly	Gly	Val	Phe	Pro	Ala	Ser	Ile	Asp	Ser	Lys	Ser	Asp	
			100				105					110				
Ile	Glu	Leu	Tyr	Leu	Gly	Asn	Ala	Gly	Thr	Ala	Met	Arg	Pro	Leu	Thr	
			115				120				125					
Ala	Ala	Val	Thr	Ala	Ala	Gly	Gly	Asn	Ala	Ser	Tyr	Val	Leu	Asp	Gly	
			130			135					140					
Val	Pro	Gln	Met	Arg	Glu	Arg	Pro	Ile	Gly	Asp	Leu	Val	Val	Gly	Leu	
145					150				155						160	
Lys	Gln	Leu	Gly	Ala	Asp	Val	Glu	Cys	Thr	Leu	Gly	Thr	Asn	Cys	Pro	
			165					170					175			
Pro	Val	Arg	Val	Asn	Ala	Asn	Gly	Gly	Leu	Pro	Gly	Gly	Lys	Val	Lys	
			180				185					190				
Leu	Ser	Gly	Ser	Ile	Ser	Ser	Gln	Tyr	Leu	Thr	Ala	Leu	Leu	Met	Ala	
			195				200					205				
Ala	Pro	Leu	Ala	Leu	Gly	Asp	Val	Glu	Ile	Glu	Ile	Val	Asp	Lys	Leu	
			210			215					220					
Ile	Ser	Val	Pro	Tyr	Val	Glu	Met	Thr	Leu	Lys	Leu	Met	Glu	Arg	Phe	
225					230					235					240	
Gly	Val	Ser	Ala	Glu	His	Ser	Glu	Ser	Trp	Asp	Arg	Phe	Phe	Val	Lys	
			245						250					255		
Gly	Gly	Gln	Lys	Tyr	Lys	Ser	Pro	Gly	Asn	Ala	Tyr	Val	Glu	Gly	Asp	
			260					265				270				
Ala	Ser	Ser	Ala	Ser	Tyr	Phe	Leu	Ala	Gly	Ala	Ala	Ile	Thr	Gly	Glu	
			275			280					285					
Thr	Val	Thr	Val	Glu	Gly	Cys	Gly	Thr	Thr	Ser	Leu	Gln	Gly	Asp	Val	
			290			295					300					
Lys	Phe	Ala	Glu	Val	Leu	Glu	Lys	Met	Gly	Cys	Lys	Val	Ser	Trp	Thr	
305					310				315						320	
Glu	Asn	Ser	Val	Thr	Val	Thr	Gly	Pro	Ser	Arg	Asp	Ala	Phe	Gly	Met	
			325					330						335		
Arg	His	Leu	Arg	Ala	Ile	Asp	Val	Asn	Met	Asn	Lys	Met	Pro	Asp	Val	
			340				345					350				
Ala	Met	Thr	Leu	Ala	Val	Val	Ala	Leu	Phe	Ala	Asp	Gly	Pro	Thr	Thr	
			355				360				365					
Ile	Arg	Asp	Val	Ala	Ser	Trp	Arg	Val	Lys	Glu	Thr	Glu	Arg	Met	Ile	
			370			375					380					
Ala	Ile	Cys	Thr	Glu	Leu	Arg	Lys	Leu	Gly	Ala	Thr	Val	Glu	Glu	Gly	
385					390				395						400	
Ser	Asp	Tyr	Cys	Val	Ile	Thr	Pro	Pro	Lys	Lys	Val	Lys	Pro	Ala	Glu	
			405					410						415		
Ile	Asp	Thr	Tyr	Asp	Asp	His	Arg	Met	Ala	Met	Ala	Phe	Ser	Leu	Ala	
			420				425					430				
Ala	Cys	Ala	Asp	Val	Pro	Ile	Thr	Ile	Asn	Asp	Pro	Gly	Cys	Thr	Arg	

(2) INFORMATION FOR SEQ ID NO:1659:

(A) LENGTH: 391 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: / Ceres Seq. ID 1500830

Met	Leu	Asp	Ala	Leu	Lys	Ile	Leu	Gly	Leu	Asn	Val	Glu	Thr	His	Ser
1			5					10						15	
Glu	Asn	Asn	Arg	Ala	Val	Val	Glu	Gly	Cys	Gly	Gly	Val	Phe	Pro	Ala
		20						25					30		
Ser	Ile	Asp	Ser	Lys	Ser	Asp	Ile	Glu	Leu	Tyr	Leu	Gly	Asn	Ala	Gly
		35					40					45			
Thr	Ala	Met	Arg	Pro	Leu	Thr	Ala	Ala	Val	Thr	Ala	Ala	Gly	Gly	Asn
		50				55					60				
Ala	Ser	Tyr	Val	Leu	Asp	Gly	Val	Pro	Gln	Met	Arg	Glu	Arg	Pro	Ile
65				70					75						80
Gly	Asp	Leu	Val	Val	Gly	Leu	Lys	Gln	Leu	Gly	Ala	Asp	Val	Glu	Cys
			85					90					95		
Thr	Leu	Gly	Thr	Asn	Cys	Pro	Pro	Val	Arg	Val	Asn	Ala	Asn	Gly	Gly
		100						105					110		
Leu	Pro	Gly	Gly	Lys	Val	Lys	Leu	Ser	Gly	Ser	Ile	Ser	Ser	Gln	Tyr
		115					120					125			
Leu	Thr	Ala	Leu	Leu	Met	Ala	Ala	Pro	Leu	Ala	Leu	Gly	Asp	Val	Glu
	130					135					140				
Ile	Glu	Ile	Val	Asp	Lys	Lys	Ile	Ser	Val	Pro	Tyr	Val	Glu	Met	Thr
145				150					155						160
Leu	Lys	Leu	Met	Glu	Arg	Phe	Gly	Val	Ser	Ala	Glu	His	Ser	Glu	Ser
			165					170					175		
Trp	Asp	Arg	Phe	Phe	Val	Lys	Gly	Gly	Gln	Lys	Tyr	Lys	Ser	Pro	Gly
		180						185					190		
Asn	Ala	Tyr	Val	Glu	Gly	Asp	Ala	Ser	Ser	Ala	Ser	Tyr	Phe	Leu	Ala
		195					200					205			
Gly	Ala	Ala	Ile	Thr	Gly	Glu	Thr	Val	Thr	Val	Glu	Gly	Cys	Gly	Thr
	210					215					220				
Thr	Ser	Leu	Gln	Gly	Asp	Val	Lys	Phe	Ala	Glu	Val	Leu	Glu	Lys	Met
225				230					235						240
Gly	Cys	Lys	Val	Ser	Trp	Thr	Glu	Asn	Ser	Val	Thr	Val	Thr	Gly	Pro
			245					250					255		
Ser	Arg	Asp	Ala	Phe	Gly	Met	Arg	His	Leu	Arg	Ala	Ile	Asp	Val	Asn
		260						265					270		
Met	Asn	Lys	Met	Pro	Asp	Val	Ala	Met	Thr	Leu	Ala	Val	Val	Ala	Leu
		275					280					285			
Phe	Ala	Asp	Gly	Pro	Thr	Thr	Ile	Arg	Asp	Val	Ala	Ser	Trp	Arg	Val
	290					295					300				
Lys	Glu	Thr	Glu	Arg	Met	Ile	Ala	Ile	Cys	Thr	Glu	Leu	Arg	Lys	Leu
305				310					315						320
Gly	Ala	Thr	Val	Glu	Glu	Gly	Ser	Asp	Tyr	Cys	Val	Ile	Thr	Pro	Pro
			325					330					335		
Lys	Lys	Val	Lys	Pro	Ala	Glu	Ile	Asp	Thr	Tyr	Asp	Asp	His	Arg	Met
		340						345					350		

Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp Val Pro Ile Thr Ile
355 360 365
Asn Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro Asp Tyr Phe Gln Val
370 375 380
Leu Glu Arg Ile Thr Lys His
385 390

(2) INFORMATION FOR SEQ ID NO:1660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..341
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1660:

Met Arg Pro Leu Thr Ala Ala Val Thr Ala Ala Gly Ile Asn Ala Ser
1 5 10 15
Tyr Val Leu Asp Gly Val Pro Gln Met Arg Glu Arg Pro Ile Gly Asp
20 25 30
Leu Val Val Gly Leu Lys Gln Leu Gly Ala Asp Val Glu Cys Thr Leu
35 40 45
Gly Thr Asn Cys Pro Pro Val Arg Val Asn Ala Asn Gly Gly Leu Pro
50 55 60
Gly Gly Lys Val Lys Leu Ser Gly Ser Ile Ser Ser Gln Tyr Leu Thr
65 70 75 80
Ala Leu Leu Met Ala Ala Pro Leu Ala Leu Gly Asp Val Glu Ile Glu
85 90 95
Ile Val Asp Lys Lys Leu Ile Ser Val Pro Tyr Val Glu Met Thr Leu Lys
100 105 110
Leu Met Glu Arg Phe Gly Val Ser Ala Glu His Ser Glu Ser Trp Asp
115 120 125
Arg Phe Phe Val Lys Gly Gly Gln Lys Tyr Lys Ser Pro Gly Asn Ala
130 135 140
Tyr Val Glu Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Gly Ala
145 150 155 160
Ala Ile Thr Gly Glu Thr Val Thr Val Glu Gly Cys Gly Thr Thr Ser
165 170 175
Leu Gln Gly Asp Val Lys Phe Ala Glu Val Leu Glu Lys Met Gly Cys
180 185 190
Lys Val Ser Trp Thr Glu Asn Ser Val Thr Val Thr Gly Pro Ser Arg
195 200 205
Asp Ala Phe Gly Met Arg His Leu Arg Ala Ile Asp Val Asn Met Asn
210 215 220
Lys Met Pro Asp Val Ala Met Thr Leu Ala Val Val Ala Leu Phe Ala
225 230 235 240
Asp Gly Pro Thr Thr Ile Arg Asp Val Ala Ser Trp Arg Val Lys Glu
245 250 255
Thr Glu Arg Met Ile Ala Ile Cys Thr Glu Leu Arg Lys Leu Gly Ala
260 265 270
Thr Val Glu Glu Gly Ser Asp Tyr Cys Val Ile Thr Pro Pro Lys Lys
275 280 285
Val Lys Pro Ala Glu Ile Asp Thr Tyr Asp Asp His Arg Met Ala Met
290 295 300
Ala Phe Ser Leu Ala Ala Cys Ala Asp Val Pro Ile Thr Ile Asn Asp
305 310 315 320
Pro Gly Cys Thr Arg Lys Thr Phe Pro Asp Tyr Phe Gln Val Leu Glu
325 330 335
Arg Ile Thr Lys His

340

(2) INFORMATION FOR SEQ ID NO:1661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1673 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1673

(D) OTHER INFORMATION: / Ceres Seq. ID 1500832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1661:

aacgaggctg	tggagaaaaa	aaccaaaagg	gactgtgttt	agagatgagg	aatgcagagc	60
tcattcttc	cccaacacca	actgttggtc	atctgtgtcc	gtttcttgaa	tttgctaggg	120
gtctcattga	gcaggatgat	aaaatccgta	tcaccttctc	cttgatgaag	caacaaggctc	180
agtctcatct	ggattcctat	gttaagacaa	tttctcgtc	tctgccgttt	gttagattta	240
ttgagtgtcc	tgagttagag	gagaacacaa	cacttggtac	acagtctgtg	gaagcctatg	300
gtgtacgatt	tatttgaac	aaatgtccct	cttgtgcaaa	atataatcat	gggtatcccta	360
ctcttctctg	catttgatgg	agttacggtc	aagggaattc	tgtgtgattt	ttctgtcttc	420
ccgagtattg	atgttgcaaa	agatgcaagt	cttctttttt	atgtgttctt	gacttcaaat	480
tcgggattcc	tagctatgat	gcagtatctg	gcatatggac	ataaagaaga	tacctcagtt	540
tttgcaagaa	acctctgaag	aatgtttgca	atctctggat	ttgtaaacct	tgctccagcc	600
aaagtactcg	cgtcagctct	gtttattgag	gatggttatg	atgctgacgt	taaacctggct	660
atattgttta	caaaaggctaa	tgaatcccta	gtgaatacct	ccctttgat	tgagcctacc	720
tccttgaatc	attttcttga	agaagagaat	taccttctg	ttatgctgt	tgcccccata	780
tttaaccgga	aggcccatct	tcattccagat	caagacctcg	cctgtgttga	cgagctcgatg	840
aaatggcttg	atgtctcaacc	cgaggcatca	gttgtattcc	tttgttttgg	gagtatgggtg	900
agcttaagag	gtctcttagt	gaaggaaata	gcacatggac	tttagctatg	tcagtataga	960
ttctcttggt	cactccgcac	agaagaagtg	acaaatgatg	atcttttgcc	agadggattc	1020
atggaccctg	tcagtggacg	gggaatgata	tgccgttggt	ctctctcagt	ggaataactg	1080
gcccataaag	cagtgaggag	ttttgtttct	cattgtggat	ggaactcaat	agtagagagt	1140
ttatggtttg	gtgtgccaat	tgtgacatgg	cccaatgtat	gcagagcaac	agctcaatgc	1200
gtttcttgat	gtgaaggaa	tgaagctcgc	agtgaggctg	aaactcgatt	atagtgtaca	1260
tagtggtgag	attgtaagtg	caaacgagat	agagacagcg	atcttctgtg	taatgaacaa	1320
gataataaat	gttgtgagga	aacgagtgat	ggatatctcg	cagatgatcc	agagagctac	1380
gaagaatgtg	ggatcttcgt	ttgccgcaat	tgagaaattc	atacatgacg	tgataggaa	1440
caggacttag	ctttctctat	cggtattctc	ataaaactga	acctgattat	gcaacagttc	1500
tttgaatctg	ctttgtttct	aatatttttt	tctattcttt	tgtcatcagc	tttgccttta	1560
actttgtctg	tgttgattcc	tttatctacc	aagctgtgag	tttctttggt	agccaatgct	1620
gcattctctc	tggtatggat	tttgttcaaa	attgggtaca	tctcttattc	ttt	

(2) INFORMATION FOR SEQ ID NO:1662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..318

(D) OTHER INFORMATION: / Ceres Seq. ID 1500833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1662:

Met	Val	Tyr	Asp	Phe	Ile	Glu	Thr	Asn	Val	Pro	Leu	Val	Gln	Asn	Ile
1				5					10					15	
Ile	Met	Gly	Ile	Leu	Ser	Ser	Pro	Ala	Phe	Asp	Gly	Val	Thr	Val	Lys
				20				25					30		
Gly	Phe	Val	Ala	Asp	Phe	Phe	Cys	Leu	Pro	Met	Ile	Asp	Val	Ala	Lys
				35			40					45			
Asp	Ala	Ser	Leu	Pro	Phe	Thr	Val	Phe	Leu	Thr	Ser	Asn	Ser	Gly	Phe
				50			55					60			


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Leu Ala Met Met Gln Tyr Leu Ala Tyr Gly His Lys Lys Asp Thr Ser
65              70              75              80
Val Phe Ala Arg Asn Ser Glu Glu Met Leu Ser Ile Pro Gly Phe Val
              85              90              95
Asn Pro Val Pro Ala Lys Val Leu Pro Ser Ala Leu Phe Ile Glu Asp
              100             105             110
Gly Tyr Asp Ala Asp Val Lys Leu Ala Ile Leu Phe Thr Lys Ala Asn
              115             120             125
Gly Ile Leu Val Asn Thr Ser Phe Asp Ile Glu Pro Thr Ser Leu Asn
130              135             140             145
His Phe Leu Glu Glu Glu Asn Tyr Pro Ser Val Tyr Ala Val Gly Pro
145              150             155             160
Ile Phe Asn Pro Lys Ala His Pro His Pro Asp Gln Asp Leu Ala Cys
              165             170             175
Cys Asp Glu Ser Met Lys Trp Leu Asp Ala Gln Pro Glu Ala Ser Val
              180             185             190
Val Phe Leu Cys Phe Gly Ser Met Gly Ser Leu Arg Gly Pro Leu Val
              195             200             205
Lys Glu Ile Ala His Gly Leu Glu Leu Cys Gln Tyr Arg Phe Leu Trp
210              215             220             225
Ser Leu Arg Thr Glu Glu Val Thr Asn Asp Asp Leu Leu Pro Xaa Gly
225              230             235             240
Phe Met Asp Arg Val Ser Gly Arg Gly Met Ile Cys Gly Trp Ser Pro
              245             250             255
Gln Val Glu Ile Leu Ala His Lys Ala Val Gly Gly Phe Val Ser His
260              265             270             275
Cys Gly Trp Asn Ser Ile Val Glu Ser Leu Trp Phe Gly Val Pro Ile
275              280             285             290
Val Thr Trp Pro Asn Val Cys Arg Ala Thr Ala Gln Cys Val Ser Asp
290              295             300             305
Gly Glu Gly Thr Glu Ala Arg Ser Gly Ala Glu Thr Arg Leu
305              310             315

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(2) INFORMATION FOR SEQ ID NO:1663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..301
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1663:

```

Met Gly Ile Leu Ser Ser Pro Ala Phe Asp Gly Val Thr Val Lys Gly
1              5              10              15
Phe Val Ala Asp Phe Phe Cys Leu Pro Met Ile Asp Val Ala Lys Asp
              20              25              30
Ala Ser Leu Pro Phe Tyr Val Phe Leu Thr Ser Asn Ser Gly Phe Leu
35              40              45
Ala Met Met Gln Tyr Leu Ala Tyr Gly His Lys Lys Asp Thr Ser Val
50              55              60
Phe Ala Arg Asn Ser Glu Glu Met Leu Ser Ile Pro Gly Phe Val Asn
65              70              75              80
Pro Val Pro Ala Lys Val Leu Pro Ser Ala Leu Phe Ile Glu Asp Gly
              85              90              95
Tyr Asp Ala Asp Val Lys Leu Ala Ile Leu Phe Thr Lys Ala Asn Gly
100             105             110
Ile Leu Val Asn Thr Ser Phe Asp Ile Glu Pro Thr Ser Leu Asn His
115             120             125
Phe Leu Glu Glu Glu Asn Tyr Pro Ser Val Tyr Ala Val Gly Pro Ile

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	130						135						140					
Phe	Asn	Pro	Lys	Ala	His	Pro	His	Pro	Asp	Gln	Asp	Leu	Ala	Cys	Cys			
145					150					155					160			
Asp	Glu	Ser	Met	Lys	Trp	Leu	Asp	Ala	Gln	Pro	Glu	Ala	Ser	Val	Val			
				165					170						175			
Phe	Leu	Cys	Phe	Gly	Ser	Met	Gly	Ser	Leu	Arg	Gly	Pro	Leu	Val	Lys			
			180					185					190					
Glu	Ile	Ala	His	Gly	Leu	Glu	Leu	Cys	Gln	Tyr	Arg	Phe	Leu	Trp	Ser			
		195					200					205						
Leu	Arg	Thr	Glu	Glu	Val	Thr	Asn	Asp	Asp	Leu	Leu	Pro	Xaa	Gly	Phe			
		210				215					220							
Met	Asp	Arg	Val	Ser	Gly	Arg	Gly	Met	Ile	Cys	Gly	Trp	Ser	Pro	Gln			
225					230					235					240			
Val	Glu	Ile	Leu	Ala	His	Lys	Ala	Val	Gly	Gly	Phe	Val	Ser	His	Cys			
				245					250					255				
Gly	Trp	Asn	Ser	Ile	Val	Glu	Ser	Leu	Trp	Phe	Gly	Val	Pro	Ile	Val			
			260					265					270					
Thr	Trp	Pro	Asn	Val	Cys	Arg	Ala	Thr	Ala	Gln	Cys	Val	Ser	Asp	Gly			
		275					280						285					
Glu	Gly	Thr	Glu	Ala	Arg	Ser	Gly	Ala	Glu	Thr	Arg	Leu						
290						295					300							

(2) INFORMATION FOR SEQ ID NO:1664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..276
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1500835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1664:

| (X1) SEQUENCE DESCRIPTION |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|---------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met                       | Ile | Asp | Val | Ala | Lys | Asp | Ala | Ser | Leu | Pro | Phe | Tyr | Val | Phe | Leu |  |
| 1                         |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Thr                       | Ser | Asn | Ser | Gly | Phe | Leu | Ala | Met | Met | Gln | Tyr | Leu | Ala | Tyr | Gly |  |
|                           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| His                       | Lys | Lys | Asp | Thr | Ser | Val | Phe | Ala | Arg | Asn | Ser | Glu | Glu | Met | Leu |  |
|                           |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |  |
| Ser                       | Ile | Pro | Gly | Phe | Val | Asn | Pro | Val | Pro | Ala | Lys | Val | Leu | Pro | Ser |  |
|                           |     |     | 50  |     |     | 55  |     |     |     |     |     | 60  |     |     |     |  |
| Ala                       | Leu | Phe | Ile | Glu | Asp | Gly | Tyr | Asp | Ala | Asp | Val | Lys | Leu | Ala | Ile |  |
| 65                        |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Leu                       | Phe | Thr | Lys | Ala | Asn | Gly | Ile | Leu | Val | Asn | Thr | Ser | Phe | Asp | Ile |  |
|                           |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Glu                       | Pro | Thr | Ser | Leu | Asn | His | Phe | Leu | Glu | Glu | Glu | Asn | Tyr | Pro | Ser |  |
|                           |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val                       | Tyr | Ala | Val | Gly | Pro | Ile | Phe | Asn | Pro | Lys | Ala | His | Pro | His | Pro |  |
|                           |     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |  |
| Asp                       | Gln | Asp | Leu | Ala | Cys | Cys | Asp | Glu | Ser | Met | Lys | Trp | Leu | Asp | Ala |  |
|                           |     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |  |
| Gln                       | Pro | Glu | Ala | Ser | Val | Val | Phe | Leu | Cys | Phe | Gly | Ser | Met | Gly | Ser |  |
| 145                       |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Leu                       | Arg | Gly | Pro | Leu | Val | Lys | Glu | Ile | Ala | His | Gly | Leu | Glu | Leu | Cys |  |
|                           |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Gln                       | Tyr | Arg | Phe | Leu | Trp | Ser | Leu | Arg | Thr | Glu | Glu | Val | Thr | Asn | Asp |  |
|                           |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Asp                       | Leu | Leu | Pro | Xaa | Gly | Phe | Met | Asp | Arg | Val | Ser | Gly | Arg | Gly | Met |  |
|                           |     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Ile                       | Cys | Gly | Trp | Ser | Pro | Gln | Val | Glu | Ile | Leu | Ala | His | Lys | Ala | Val |  |
|                           |     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |  |

Gly Gly Phe Val Ser His Cys Gly Trp Asn Ser Ile Val Glu Ser Leu  
225 230 235 240  
Trp Phe Gly Val Pro Ile Val Thr Trp Pro Asn Val Cys Arg Ala Thr  
245 250 255  
Ala Gln Cys Val Ser Asp Gly Glu Gly Thr Glu Ala Arg Ser Gly Ala  
260 265 270  
Glu Thr Arg Leu  
275

(2) INFORMATION FOR SEQ ID NO:1665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..566
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1665:

|                                                                      |     |
|----------------------------------------------------------------------|-----|
| actacgaatt tagcacatag ccggagctcc gatactgtca tcttgctccg acgaagcgat    | 60  |
| tcccggcccaa ccaatcgtcc tcggttggtg tcaactttgt ctatgattact tagtcacagt  | 120 |
| ggcgctctttt ccaattcccg atcaaaagat ccgaggcac agcttcaagg tccaaggagt    | 180 |
| tggttaacact gggaatgctt taacatgtgt tgctcgtttg ggtttgcctt gtcgaacttt   | 240 |
| ggctaaagggt gctgatgatt ctacacggcg atatatggta gaagaactcg aatctagcgg   | 300 |
| tgttgataact tcgttttggta tgagtgcctaa agatggagct tcacatttta attacgtcat | 360 |
| tgtagataaac caaacgaata ctctactcttg tatttacact ccaggatatt ctccctttgt  | 420 |
| accagatgac ctactgaat ctctactctt agatgttctt gatggagtaa gagtctata      | 480 |
| tgtaaatgga aggtcccgctg aagccgaatt gcttcttgcg caaaaggcac atagcaagaa   | 540 |
| ataaccaat cttaattaat gcagag                                          |     |

(2) INFORMATION FOR SEQ ID NO:1666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1666:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ser Ser Cys Ser Asp Glu Ala Ile Pro Gly Gln Pro Ile Val Leu |  |
| 1 5 10 15                                                       |  |
| Gly Cys Gly Gln Leu Cys Leu Asp Tyr Leu Val Thr Val Ala Ser Phe |  |
| 20 25 30                                                        |  |
| Pro Ile Pro Asp Gln Lys Ile Arg Gly Thr Ser Phe Lys Val Gln Gly |  |
| 35 40 45                                                        |  |
| Val Gly Asn Thr Gly Asn Ala Leu Thr Cys Val Ala Arg Leu Gly Leu |  |
| 50 55 60                                                        |  |
| Pro Cys Arg Ile Leu Ala Lys Val Ala Asp Asp Ser His Gly Arg Tyr |  |
| 65 70 75 80                                                     |  |
| Met Val Glu Glu Leu Glu Ser Ser Gly Val Asp Thr Ser Phe Cys Met |  |
| 85 90 95                                                        |  |
| Ser Ala Lys Asp Gly Ala Ser His Phe Asn Tyr Val Ile Val Asp Asn |  |
| 100 105 110                                                     |  |
| Gln Thr Asn Thr Arg Thr Cys Ile Tyr Thr Pro Gly Tyr Pro Pro Leu |  |
| 115 120 125                                                     |  |
| Leu Pro Asp Asp Leu Thr Glu Ser Leu Leu Leu Asp Val Leu Asp Gly |  |
| 130 135 140                                                     |  |
| Val Arg Val Leu Tyr Val Asn Gly Arg Ser Arg Glu Ala Glu Leu Leu |  |

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(i) SEQUENCE CHARACTERISTICS:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 94 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..94
(D) OTHER INFORMATION
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1667:

Met Val Glu Glu Leu Glu Ser Ser Gly Val Asp Thr Ser Phe Cys Met															
1 5 10 15															
Ser Ala Lys Asp Gly Ala Ser His Phe Asn Tyr Val Ile Val Asp Asn															
20 25 30															
Gln Thr Asn Thr Arg Thr Cys Ile Tyr Thr Pro Gly Tyr Pro Pro Leu															
35 40 45															
Leu Pro Asp Asp Leu Thr Glu Ser Leu Leu Leu Asp Val Leu Asp Gly															
50 55 60															
Val Arg Val Leu Tyr Val Asn Gly Arg Ser Arg Glu Ala Glu Leu Leu															
65 70 75 80															
Leu Ala Gln Lys Ala His Ser Lys Lys Tyr Thr Asn Leu Asn															
85 90															

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..581

(D) OTHER INFORMATION: / Ceres Seq. ID 1500847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1668:

(X1) SEQUENCE DESCRIPTION: SEQ ID: 407						
aataaaca	aaataaat	aacaagatc	tgtcatgt	tccacggcga	gaaatatctt	60
tgccagcggg	aaccgaaagt	cgaatagctt	gcacgcggcg	gtctccaccg	ctcttaagat	120
aaccctctg	gaacgaant	ggaagtggc	tattctctct	ctataacct	cggagtccgc	180
gccacagaaa	caccgcggcg	taatgaagaa	ggaggagcaa	cggtggggta	aagagagagc	240
gaagccgcg	rtttttaaga	agtgcagcga	ccggcgagct	ccgttttact	accagccgac	300
acgcctcatg	aatcagccgt	ttgatcgctg	aaattaacgg	tctcttaata	ttaggcttat	360
caacaaataa	cataaatatt	tgaattcttt	taatttgtat	ccgatataat	tgacaaatag	420
catatttttt	ttttatttaa	catataccat	tttatgcagt	atgtatgttg	ggtttgatgt	480
tgttatgtcc	ttgaacacct	gaatttaaat	actaataat	atgatgtatt	gtttctgata	540
ctgtgtaatg	ttgaagacac	tacgaagatt	ccgcgtgtaa	t		

(2) INFORMATION FOR SEQ ID NO:1669:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..11

(D) OTHER INFORMATION: / Ceres Seq. ID 1500848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1669:

```

Ile Asn Lys Lys Leu Ile Gln Gln Asp Pro Ala Met Ser Ser Thr Ala
1           5           10           15
Arg Asn Ile Ser Gly Ser Gly Asn Arg Lys Ser Ser Arg Leu Gln Arg
20           25           30
Arg Ala Pro Pro Pro Leu Lys Ile Asn Pro Cys Glu Arg Xaa Trp Lys
35           40           45
Val Ala Ile Pro Leu Leu Ser Pro Thr Glu Ser Pro Pro Gln Lys Pro
50           55           60
Pro Ala Val Met Lys Arg Glu Glu Gln Arg Trp Gly Lys Glu Ala Glu
65           70           75           80
Lys Pro Pro Xaa Phe Lys Lys Trp Gln His Pro Ala Ala Pro Phe Tyr
85           90           95
Tyr Gln Pro Ala Pro Ser Ser Asn Gln Pro Phe Ala Trp Pro Asn
100          105          110

```

(2) INFORMATION FOR SEQ ID NO:1670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1670:

```

Met Ser Ser Thr Ala Arg Asn Ile Ser Gly Ser Gly Asn Arg Lys Ser
1           5           10           15
Ser Arg Leu Gln Arg Arg Ala Pro Pro Pro Leu Lys Ile Asn Pro Cys
20           25           30
Glu Arg Xaa Trp Lys Val Ala Ile Pro Leu Leu Ser Pro Thr Glu Ser
35           40           45
Pro Pro Gln Lys Pro Pro Ala Val Met Lys Arg Glu Glu Gln Arg Trp
50           55           60
Gly Lys Glu Ala Glu Lys Pro Pro Xaa Phe Lys Lys Trp Gln His Pro
65           70           75           80
Ala Ala Pro Phe Tyr Tyr Gln Pro Ala Pro Ser Ser Asn Gln Pro Phe
85           90           95
Ala Trp Pro Asn
100

```

(2) INFORMATION FOR SEQ ID NO:1671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..517
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671:

```

gcataatcag ctgtcaggtc agattccccg agatcttggt gagctctcct ttctgtcaac 60
catgaacttc gccacaaca atctcgaagg tccaatgcc a cgcggaacac aatttcaaag 120
ccaaaactgt tcttcattca tggacaaccc caagctttac ggtcttgatg atactctgac 180
aaaaactcat gtccaaatc ctagaccaca agaattagag aaagtatcat agccggaaga 240
agagcaagtg attaactgga catcagcagc aatagcgtat ggaccttggt tgttttgcgg 300
attagtgatt ggacatatct tcatttcgca taagcaggag tggttaatgg aaaagtttcc 360
tagaacaacg ccacagattg tcatcagaag cgtctgttga acacgtgc at atgtatgtgt 420
ttgtgaaaaa ctctttctgt tgcgttgtaa tgttctaata tatggttttt taataaacgt 480
ctttggtggc ggtaactgatt tgatacatat tgggtttg

```

(2) INFORMATION FOR SEQ ID NO:1672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672:

His	Asn	Gln	Leu	Ser	Gly	Gln	Ile	Pro	Arg	Asp	Leu	Gly	Glu	Leu	Ser	
1				5					10					15		
Phe	Leu	Ser	Thr	Met	Asn	Phe	Ala	His	Asn	Asn	Leu	Glu	Gly	Pro	Met	
				20				25						30		
Pro	Arg	Gly	Thr	Gln	Phe	Gln	Ser	Gln	Asn	Cys	Ser	Ser	Phe	Met	Asp	
				35			40					45				
Asn	Pro	Lys	Leu	Tyr	Gly	Leu	Asp	Asp	Ile	Cys	Arg	Lys	Thr	His	Val	
				50			55				60					
Pro	Asn	Pro	Arg	Pro	Gln	Glu	Leu	Glu	Lys	Val	Ser	Glu	Pro	Glu	Glu	
65					70					75					80	
Glu	Gln	Val	Ile	Asn	Trp	Thr	Ser	Ala	Ala	Ile	Ala	Tyr	Gly	Pro	Gly	
				85					90					95		
Val	Phe	Cys	Gly	Leu	Val	Ile	Gly	His	Ile	Phe	Ile	Ser	His	Lys	Gln	
				100				105					110			
Glu	Trp	Leu	Met	Glu	Lys	Phe	Arg	Asn	Lys	Pro	Arg	Val	Val	Ile		
				115			120					125				
Arg	Ser	Ala	Arg													
				130												

(2) INFORMATION FOR SEQ ID NO:1673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673:

Met	Asn	Phe	Ala	His	Asn	Asn	Leu	Glu	Gly	Pro	Met	Pro	Arg	Gly	Thr	
1				5					10					15		
Gln	Phe	Gln	Ser	Gln	Asn	Cys	Ser	Ser	Phe	Met	Asp	Asn	Pro	Lys	Leu	
				20				25					30			
Tyr	Gly	Leu	Asp	Asp	Ile	Cys	Arg	Lys	Thr	His	Val	Pro	Asn	Pro	Arg	
				35			40					45				
Pro	Gln	Glu	Leu	Glu	Lys	Val	Ser	Glu	Pro	Glu	Glu	Glu	Gln	Val	Ile	
				50			55				60					
Asn	Trp	Thr	Ser	Ala	Ala	Ile	Ala	Tyr	Gly	Pro	Gly	Val	Phe	Cys	Gly	
65				70					75					80		
Leu	Val	Ile	Gly	His	Ile	Phe	Ile	Ser	His	Lys	Gln	Glu	Trp	Leu	Met	
				85				90					95			
Glu	Lys	Phe	Arg	Arg	Asn	Lys	Pro	Arg	Val	Val	Ile	Arg	Ser	Ala	Arg	
				100				105					110			

(2) INFORMATION FOR SEQ ID NO:1674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..101
(D) OTHER INFORMATION: / Ceres Seq. ID 1500857
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674:
Met Pro Arg Gly Thr Gln Phe Gln Ser Gln Asn Cys Ser Ser Phe Met
1 5 10 15
Asp Asn Pro Lys Leu Tyr Gly Leu Asp Asp Ile Cys Arg Lys Thr His
20 25 30
Val Pro Asn Pro Arg Pro Gln Glu Leu Glu Lys Val Ser Glu Pro Glu
35 40 45
Glu Glu Gln Val Ile Asn Trp Thr Ser Ala Ala Ile Ala Tyr Gly Pro
50 55 60
Gly Val Phe Cys Gly Leu Val Ile Gly His Ile Phe Ile Ser His Lys
65 70 75 80
Gln Glu Trp Leu Met Glu Lys Phe Arg Arg Asn Lys Pro Arg Val Val
85 90 95
Ile Arg Ser Ala Arg
100

(2) INFORMATION FOR SEQ ID NO:1675:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 615 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..615
(D) OTHER INFORMATION: / Ceres Seq. ID 1500862
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675:
gataaatattt cattttctrtc gttttctttct ttctaagttt cgatgtcagt tcctaattctc 60
tatggcgcttc atgatagcca aatggtaact ttggtggcct aatgtatgtc acgtaaaatta 120
tccacgtggc actcactttt ttgcattctt ctcaaaatat atcaaaaggag acttcataaaa 180
gaaagaattct ttagtgtgga gagactaaaa ggacaccaca agcttatttc ataagaaact 240
tcaaattaga atcagaaca agagcatcct tcttcattta cacaggtaaa ttagggtgtaa 300
aaatggtgat gagaagtggt gatctacgat cagataccgt tactagaccg acagatgcga 360
tgcgagaagc aatgtgtaac gcagagggtg atgatgacgt cctcggatat gacccaacg 420
ctagacgtct tgaagaggag atggctaaga tgatggggaa agaggctgct ctgtctegtc 480
catccgggac aatggggaa ctgatcagcg tgatggttca ctgcgacgtg agaggcagcg 540
aggtgattct tggcgacaat tgtcacatcc atgtttacga gaatggaggg atatcgacta 600
tcgggggagt gcatc

(2) INFORMATION FOR SEQ ID NO:1676:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..104
(D) OTHER INFORMATION: / Ceres Seq. ID 1500863
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676:
Met Val Met Arg Ser Val Asp Leu Arg Ser Asp Thr Val Thr Arg Pro
1 5 10 15
Thr Asp Ala Met Arg Glu Ala Met Cys Asn Ala Glu Val Asp Asp Asp

20 25 30
Val Leu Gly Tyr Asp Pro Thr Ala Arg Arg Leu Glu Glu Met Ala
35 40 45
Lys Met Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met
50 55 60
Gly Asn Leu Ile Ser Val Met Val His Cys Asp Val Arg Gly Ser Glu
65 70 75 80
Val Ile Leu Gly Asp Asn Cys His Ile His Val Tyr Glu Asn Gly Gly
85 90 95
Ile Ser Thr Ile Gly Gly Val His
100

(2) INFORMATION FOR SEQ ID NO:1677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677:

Met Arg Ser Val Asp Leu Arg Ser Asp Thr Val Thr Arg Pro Thr Asp
1 5 10 15
Ala Met Arg Glu Ala Met Cys Asn Ala Glu Val Asp Asp Asp Val Leu
20 25 30
Gly Tyr Asp Pro Thr Ala Arg Arg Leu Glu Glu Glu Met Ala Lys Met
35 40 45
Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met Gly Asn
50 55 60
Leu Ile Ser Val Met Val His Cys Asp Val Arg Gly Ser Glu Val Ile
65 70 75 80
Leu Gly Asp Asn Cys His Ile His Val Tyr Glu Asn Gly Gly Ile Ser
85 90 95
Thr Ile Gly Gly Val His
100

(2) INFORMATION FOR SEQ ID NO:1678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1678:

Met Arg Glu Ala Met Cys Asn Ala Glu Val Asp Asp Val Leu Gly
1 5 10 15
Tyr Asp Pro Thr Ala Arg Arg Leu Glu Glu Glu Met Ala Lys Met Met
20 25 30
Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met Gly Asn Leu
35 40 45
Ile Ser Val Met Val His Cys Asp Val Arg Gly Ser Glu Val Ile Leu
50 55 60
Gly Asp Asn Cys His Ile His Val Tyr Glu Asn Gly Gly Ile Ser Thr
65 70 75 80
Ile Gly Gly Val His
85

(2) INFORMATION FOR SEQ ID NO:1679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..643
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679:

atttttttagg	ttgtttcagc	tggtttacgg	agtcgctttt	gagatatcga	tcttacgaag	60
aagcaaaaat	ggcggtcccg	ttgctttacca	agaaggttgt	gaagaagagg	tctactaagt	120
tcatacagacc	ccagagtgac	cgtagaatca	ccgtcaagga	aagctggagg	aggccaaaagg	180
gtattgattca	aaggatgaga	agaaagtcca	aagggtgtgac	tttgatgccc	aatggttggt	240
acggatctga	caagaagact	cgtaactatc	ttcccaatgg	attcaagaaa	ttcgtttgttc	300
acaacacaag	tgagctcgag	ttgtttgatga	tgacacaacag	gacttactgt	gctgagattg	360
ctcacacagt	ctccactaag	aagagaaaagg	caattgttga	gagagcttct	cagctagacg	420
ttgttgtttac	caacaggctt	gctaggctcc	gtagccaaga	agacgagtga	agaagaatct	480
tgccgactac	ttagttgttt	cttctgtttt	gttgcatctc	ctttttgtta	taagacgatt	540
tttgattact	gctgtgtttg	tggtttgagt	gaacaaacat	gagttttggt	tttagtatga	600
aacagatcaa	gttaagacct	ttgttaag	ctatttcgga	ttc		

(2) INFORMATION FOR SEQ ID NO:1680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680:

Ph	Leu	Gly	Leu	Phe	Ser	Cys	Phe	Thr	Glu	Ser	Leu	Leu	Arg	Tyr	Arg	
1			5					10					15			
Ser	Tyr	Glu	Glu	Ala	Lys	Met	Ala	Val	Pro	Leu	Leu	Thr	Lys	Lys	Val	
			20					25					30			
Val	Lys	Lys	Arg	Ser	Thr	Lys	Phe	Ile	Arg	Pro	Gln	Ser	Asp	Arg	Arg	
			35				40					45				
Ile	Thr	Val	Lys	Glu	Ser	Trp	Arg	Arg	Pro	Lys	Gly	Ile	Asp	Ser	Arg	
			50				55				60					
Met	Arg	Arg	Lys	Phe	Lys	Gly	Val	Thr	Leu	Met	Pro	Asn	Val	Gly	Tyr	
			65				70			75					80	
Gly	Ser	Asp	Lys	Lys	Thr	Arg	His	Tyr	Leu	Pro	Asn	Gly	Phe	Lys	Lys	
							85			90				95		
Phe	Val	Val	His	Asn	Thr	Ser	Glu	Leu	Glu	Leu	Leu	Met	Met	His	Asn	
							100			105				110		
Arg	Thr	Tyr	Cys	Ala	Glu	Ile	Ala	His	Asn	Val	Ser	Thr	Lys	Lys	Arg	
							115			120				125		
Lys	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gln	Leu	Asp	Val	Val	Val	Thr	Asn	
							130			135				140		
Arg	Leu	Ala	Arg	Leu	Arg	Ser	Gln	Glu	Asp	Glu						
							145			150				155		

(2) INFORMATION FOR SEQ ID NO:1681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..133
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500868
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681:
Met Ala Val Pro Leu Leu Thr Lys Lys Val Val Lys Lys Arg Ser Thr
1 5 10 15
Lys Phe Ile Arg Pro Gln Ser Asp Arg Arg Ile Thr Val Lys Glu Ser
 20 25 30
Trp Arg Arg Pro Lys Gly Ile Asp Ser Arg Met Arg Arg Lys Phe Lys
 35 40 45
Gly Val Thr Leu Met Pro Asn Val Gly Tyr Gly Ser Asp Lys Lys Thr
50 55 60
Arg His Tyr Leu Pro Asn Gly Phe Lys Lys Phe Val Val His Asn Thr
65 70 75
Ser Glu Leu Glu Leu Leu Met Met His Asn Arg Thr Tyr Cys Ala Glu
 85 90 95
Ile Ala His Asn Val Ser Thr Lys Lys Arg Lys Ala Ile Val Glu Arg
 100 105 110
Ala Ser Gln Leu Asp Val Val Val Thr Asn Arg Leu Ala Arg Leu Arg
115 120 125
Ser Gln Glu Asp Glu
130

(2) INFORMATION FOR SEQ ID NO:1682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1682:

Met Arg Arg Lys Phe Lys Gly Val Thr Leu Met Pro Asn Val Gly Tyr
1 5 10 15
Gly Ser Asp Lys Lys Thr Arg His Tyr Leu Pro Asn Gly Phe Lys Lys
 20 25 30
Phe Val Val His Asn Thr Ser Glu Leu Glu Leu Leu Met Met His Asn
35 40 45
Arg Thr Tyr Cys Ala Glu Ile Ala His Asn Val Ser Thr Lys Lys Arg
50 55 60
Lys Ala Ile Val Glu Arg Ala Ser Gln Leu Asp Val Val Val Thr Asn
65 70 75
Arg Leu Ala Arg Leu Arg Ser Gln Glu Asp Glu
 85 90

(2) INFORMATION FOR SEQ ID NO:1683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..493
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1683:

tacctacccc ctgcgcttgc acaaaatcct tcttgatccg cacaggaagg tggaagggtcc

cggcagaaga acttggcggg cgaaaggcga aaccgcagtg ctcccrggcg ggcgcggaca 120
cggcatggag cgagagcgnc aggcagtgcc gaggaacagg aaggtggtgc tgcgcgggta 180
catcgaccgc gcgcccaggg aggaagacat ggagctcgtc gacggcrgcg ccgtggagct 240
gcgcgtcccc gadggcggcg gcggccccgc ggtgctggtg aagaacctct acctatcctg 300
cgacccttac atgcgcggca ggaatgcggga ctccgcaac tcctacatcc cgcccttcaa 360
acctggatca cctattgang ggttggcgt ggggargggtg gtcgactcca ctcatccagg 420
attcagtgcc ggtgacgttg ttccgggat gactggatgg gaggactaca gtctgatcac 480
caatcctgaa cag

(2) INFORMATION FOR SEQ ID NO:1684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1684:

Thr	Tyr	Pro	Leu	Arg	Leu	His	Lys	Ile	Leu	Leu	Asp	Pro	His	Arg	Lys
1			5					10						15	
Val	Glu	Gly	Pro	Gly	Arg	Arg	Thr	Trp	Arg	Ala	Lys	Gly	Glu	Thr	Asp
			20					25					30		
Val	Leu	Xaa	Gly	Gly	Arg	Arg	His	Gly	Met	Glu	Arg	Glu	Xaa	Gln	Ala
			35					40					45		
Val	Ala	Arg	Asn	Arg	Lys	Val	Val	Leu	Arg	Gly	Tyr	Ile	Asp	Arg	Ala
			50				55					60			
Pro	Arg	Glu	Glu	Asp	Met	Glu	Leu	Val	Asp	Gly	Xaa	Ala	Val	Glu	Leu
65					70					75				80	
Arg	Val	Pro	Xaa	Gly	Gly	Gly	Gly	Pro	Ala	Val	Leu	Val	Lys	Asn	Leu
			85					90					95		
Tyr	Leu	Ser	Cys	Asp	Pro	Tyr	Met	Arg	Gly	Arg	Met	Arg	Asp	Phe	Arg
			100					105					110		
Asn	Ser	Tyr	Ile	Pro	Pro	Phe	Lys	Pro	Gly	Ser	Pro	Ile	Xaa	Gly	Phe
			115				120						125		
Gly	Val	Gly	Xaa	Val	Val	Asp	Ser	Thr	His	Pro	Gly	Phe	Ser	Ala	Gly
			130				135					140			
Asp	Val	Val	Ser	Gly	Met	Thr	Gly	Trp	Glu	Asp	Tyr	Ser	Leu	Ile	Thr
					150					155				160	
Asn	Pro	Glu	Gln												

(2) INFORMATION FOR SEQ ID NO:1685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1685:

Met	Glu	Arg	Glu	Xaa	Gln	Ala	Val	Ala	Arg	Asn	Arg	Lys	Val	Val	Leu
1			5					10					15		
Arg	Gly	Tyr	Ile	Asp	Arg	Ala	Pro	Arg	Glu	Glu	Asp	Met	Glu	Leu	Val
			20					25					30		
Asp	Gly	Xaa	Ala	Val	Glu	Leu	Arg	Val	Pro	Xaa	Gly	Gly	Gly	Gly	Pro
			35				40					45			
Ala	Val	Leu	Val	Lys	Asn	Leu	Tyr	Leu	Ser	Cys	Asp	Pro	Tyr	Met	Arg

50	55	60
Gly Arg Met Arg Asp Phe Arg Asn Ser Tyr Ile Pro Pro Phe Lys Pro		
65	70	75
Gly Ser Pro Ile Xaa Gly Phe Gly Val Gly Xaa Val Val Asp Ser Thr		80
	85	90
His Pro Gly Phe Ser Ala Gly Asp Val Val Ser Gly Met Thr Gly Trp		95
	100	105
Glu Asp Tyr Ser Leu Ile Thr Asn Pro Glu Gln		110
	115	120

(2) INFORMATION FOR SEQ ID NO:1686:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1500880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686:

Met Glu Leu Val Asp Gly Xaa Ala Val Glu Leu Arg Val Pro Xaa Gly	
1	5
Gly Gly Gly Pro Ala Val Leu Val Lys Asn Leu Tyr Leu Ser Cys Asp	10
	15
20	25
Pro Tyr Met Arg Gly Arg Met Arg Asp Phe Arg Asn Ser Tyr Ile Pro	30
	35
40	45
Pro Phe Lys Pro Gly Ser Pro Ile Xaa Gly Phe Gly Val Gly Xaa Val	50
	55
60	65
Val Asp Ser Thr His Pro Gly Phe Ser Ala Gly Asp Val Val Ser Gly	70
	75
80	85
Met Thr Gly Trp Glu Asp Tyr Ser Leu Ile Thr Asn Pro Glu Gln	90
	95

(2) INFORMATION FOR SEQ ID NO:1687:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 535 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..535

(D) OTHER INFORMATION: / Ceres Seq. ID 1500881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687:

aagtacagagg	gacattgcat	tggggaacta	cagaaaaagg	tccgaatcga	atccgtgggtg	60
cactgccccct	tctctcccaca	caagccgcgcg	ccgcgcgcgt	gaggactccg	gcgaatggcg	120
tcccgcgtcg	cctcgggcct	cctccgcgcg	cgcgcgcggc	ccacactagg	cctcctaagg	180
agttatgcac	atgtcagaag	ctacacacagt	caactttcag	ctttggtttc	tgctacatct	240
gaatgctcaa	atctgccgag	aagatgctat	tacttaccta	atccctctcc	ataccaagtt	300
tggagtaggt	catttgcttc	agacaacgga	gacaagtttg	aggctgttgt	gcccttcagt	360
gggtgaatctg	taactgatgg	aactcttgct	aacttcttaa	agaaacctgg	agacagagtc	420
gaggtgatg	aaactatagc	gcagattgaa	actgataagg	tcactataga	tgctcgcaagt	480
cctgargctg	gtgttattga	aaagctcatt	gctagtgaag	gcgcacacgt	tacttc	

(2) INFORMATION FOR SEQ ID NO:1688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1500882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1688:

```
Val Arg Gly Thr Leu His Trp Gly Thr Thr Glu Lys Gly Pro Asn Arg
1      5      10      15
Ile Arg Gly Ala Leu Pro Leu Pro Pro Gln Ala Ala Ala Ala Ala
20      25      30
Val Arg Thr Pro Ala Asn Gly Val Pro Arg Arg Leu Gly Pro Pro Pro
35      40      45
Pro Pro Arg Arg Arg His Thr Arg Pro Pro Lys Glu Leu Cys Thr Cys
50      55      60
Gln Lys Leu Gln Gln Ser Thr Phe Ser Phe Gly Phe Cys Tyr Ile
65      70      75
```

(2) INFORMATION FOR SEQ ID NO:1689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1500883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1689:

```
Met Ala Ser Arg Val Ala Ser Gly Leu Leu Arg Arg Ala Gly Ala
1      5      10      15
Thr Leu Gly Leu Leu Arg Ser Tyr Ala His Val Arg Ser Tyr Asn Ser
20      25      30
Gln Leu Ser Ala Leu Val Ser Ala Thr Ser Glu Cys Ser Asn Leu Pro
35      40      45
Arg Arg Cys Tyr Tyr Leu Pro Asn Pro Ser Pro Tyr Gln Val Trp Ser
50      55      60
Arg Ser Phe Ala Ser Asp Asn Gly Asp Lys Phe Glu Ala Val Val Pro
65      70      75      80
Phe Met Gly Glu Ser Val Thr Asp Gly Thr Leu Ala Asn Phe Leu Lys
85      90      95
Lys Pro Gly Asp Arg Val Glu Ala Asp Glu Pro Ile Ala Gln Ile Glu
100      105      110
Thr Asp Lys Val Thr Ile Asp Val Ala Ser Pro Xaa Ala Gly Val Ile
115      120      125
Glu Lys Leu Ile Ala Ser Glu Gly Asp Thr Val Thr
130      135      140
```

(2) INFORMATION FOR SEQ ID NO:1690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1500884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1690:

```
ataccgcaac cagctattga gctactgect ctgaccaagt cccaagctgc gctgcgcctg 60
ctatgtcgct gctctcgccc gtatcggggg tctcatcage cactgcgcgc cactgtcgtag 120
acgactgcct cggcatcgct cagctctctta gcgatggcac cgtgacgcgc tccgsgacta 180
ctccgacatc cctctctcgg gcgaggtgcc gtccaacctg cccgtccagt ggaaggacgt 240
```

cgtctacgac ccgcgcgaac gcgtccgcct ccgcatgtac agggccaccg acaccgaagg 300
cggcaggacg accaacaaca agctgcgcgt gctagtctac ttccacggcg gcggcttctg 360
catctgcagc ttcgagatgc cccacttcca ccgcggcggg ctccgcctcg ccgcgagct 420
cccgccgcctc gtgcctctmcg ccgactacmg cctggggccc gagcaccgcc t

(2) INFORMATION FOR SEQ ID NO:1691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691:

Ile Pro Gln Pro Ala Ile Glu Leu Leu Pro Leu Thr Lys Ser Gln Ala
1 5 10 15
Ala Leu Arg Leu Leu Cys Arg Arg Pro Arg Pro Tyr Arg Arg Ser His
20 25 30
Gln Pro Leu Arg Arg Thr Ser Trp Thr Thr Ala Ser Ala Ser Cys Ser
35 40 45
Phe Leu Ala Met Ala Pro
50

(2) INFORMATION FOR SEQ ID NO:1692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692:

Met Ser Ser Ser Pro Val Ser Ala Val Ser Ser Ala Thr Ala Pro
1 5 10 15
His Val Val Asp Asp Cys Leu Gly Ile Val Gln Leu Leu Ser Asp Gly
20 25 30
Thr Val Thr Arg Ser Xaa Thr Thr Pro Thr Ser Leu Ser Trp Ala Arg
35 40 45
Cys Arg Pro Thr Cys Pro Ser Ser Gly Arg Thr Ser Ser Thr Thr Pro
50 55 60
Arg Thr Arg Ser Ala Ser Ala Cys Thr Gly Pro Pro Thr Pro Thr Ala
65 70 75 80
Ala Gly Arg Pro Thr Thr Ser Cys Arg Cys
85 90

(2) INFORMATION FOR SEQ ID NO:1693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693:

Met Tyr Arg Pro Thr Asp Thr Asp Gly Gly Arg Thr Thr Asn Asn Lys

1 5 10 15
Leu Pro Val Leu Val Tyr Phe His Gly Gly Phe Cys Ile Cys Ser
20 25 30
Phe Glu Met Pro His Phe His Ala Gly Gly Leu Arg Leu Ala Ala Glu
35 40 45
Leu Pro Ala Leu Val Leu Xaa Ala Asp Tyr Xaa Leu Gly Pro Glu His
50 55 60

Arg
65

(2) INFORMATION FOR SEQ ID NO:1694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..591
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694:

cttcgcgtgc ttttccttcc tctctcttcc cctttctctc cccaagcag gcggggcgag 60
cgagccaccg aggcgtctct cctctcgtcc atccgtttcc tctcccccct gcttcccggc 120
gtgcctccct cccctccctg tgcgcctctt ttcctgcgcg agggaggacc gtggggacca 180
ccaccaccag caccaccacc tccatccgtg cgctctcgcg tctcgtctgc ggtgctcctc 240
ctctctctcc tgctcccggg gcgggcgggc tcttttcca cctcctgctg gtgcmagggc 300
cgggaggcgg tmgcgagggt ggcgcgcgat gggctcgcmg gggamgggtc ggcgggacac 360
gcmcacctca gtaataatga aaatrggcgg ttmatttatg gagttgcgag tctctctggt 420
aaaagagcat cgatggaggga cttctatgag gcaagaatag acgamtgtga ttgagagaaa 480
attggaatgt tcgggtgata tgatggtcac ggaggagtcc gagcagctga gtatgttaag 540
cagcaccttt tcagcaatatt aatcaaacac ccaagttca tcaactgatac c

(2) INFORMATION FOR SEQ ID NO:1695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695:

Leu Pro Leu Leu Phe Leu Ser Pro Leu Ser Pro Phe Leu Ser Pro Ser
1 5 10 15
Arg Arg Gly Glu Arg Ala Gln Gln Ala Ser Leu Leu Ser Ser Ile Arg
20 25 30
Phe Leu Leu Pro Leu Leu Pro Gly Ser Pro Pro Ser Pro Pro Cys Ala
35 40 45
Pro Leu Phe Met Arg Glu Gly Pro Trp Gly Pro Pro Pro Pro Ala
50 55 60
Pro Pro Pro Pro Ser Val Arg Leu Ser Leu Ser Leu Val Val Leu Leu
65 70 75 80
Leu Leu Leu Leu Leu Pro Gly Arg Ala Ala Ser Phe Ser Thr Ser Cys
85 90 95
Trp Cys Xaa Gly Arg Glu Gly Xaa Ala Glu Val Ala Arg Met Gly Leu
100 105 110
Xaa Gly Xaa Gly Ser Ala Asp Xaa Xaa His Leu Ser Asn Asn Glu Asn
115 120 125
Xaa Arg Xaa Ile Tyr Gly Val Ala Ser Ser Pro Gly Lys Arg Ala Ser
130 135 140

Met Glu Asp Phe Tyr Glu Ala Arg Ile Asp Xaa Val Asp Gly Glu Lys
145 150 155 160
Ile Gly Met Phe Gly Val Tyr Asp Gly His Gly Gly Val Arg Ala Ala
165 170 175
Glu Tyr Val Lys Gln His Leu Phe Ser Asn Leu Ile Lys His Pro Lys
180 185 190
Phe Ile Thr Asp Thr
195

(2) INFORMATION FOR SEQ ID NO:1696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1696:

Phe Arg Cys Phe Ser Phe Leu Leu Ser Pro Leu Ser Ser Pro Gln Ala
1 5 10 15
Gly Gly Ala Ser Glu Pro Ser Arg Arg Leu Ser Ser Arg Pro Ser Val
20 25 30
Ser Ser Ser Pro Cys Phe Pro Ala Arg Leu Pro Pro Leu Pro Val Arg
35 40 45
Leu Phe Ser Cys Ala Arg Arg Asp Arg Gly Asp His His His Gln His
50 55 60
His His Leu His Pro Cys Ala Ser Arg Ser Arg Trp Trp Cys Ser Ser
65 70 75 80
Ser Ser Ser Cys Ser Arg Gly Gly Arg Pro Pro Phe Pro Pro Pro Ala
85 90 95
Gly Xaa Arg Ala Gly Arg Ala Xaa Arg Arg Trp Arg Ala Trp Gly Ser
100 105 110
Xaa Gly Xaa Gly Arg Arg Thr Xaa Xaa Thr Ser Val Ile Met Lys Xaa
115 120 125
Gly Gly Xaa Phe Met Glu Leu Arg Val Leu Leu Val Lys Glu His Arg
130 135 140
Trp Arg Thr Ser Met Arg Gln Glu
145 150

(2) INFORMATION FOR SEQ ID NO:1697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697:

Met Arg Glu Glu Gly Pro Trp Gly Pro Pro Pro Ala Pro Pro Pro
1 5 10 15
Pro Ser Val Arg Leu Ser Leu Ser Leu Val Val Leu Leu Leu Leu
20 25 30
Leu Leu Pro Gly Arg Ala Ala Ser Phe Ser Thr Ser Cys Trp Cys Xaa
35 40 45
Gly Arg Glu Gly Xaa Ala Glu Val Ala Arg Met Gly Leu Xaa Gly Xaa
50 55 60
Gly Ser Ala Asp Xaa Xaa His Leu Ser Asn Asn Glu Asn Xaa Arg Xaa

65	70	75	80
Ile Tyr Gly Val Ala Ser Ser Pro Gly Lys Arg Ala Ser Met Glu Asp			
	85	90	95
Phe Tyr Glu Ala Arg Ile Asp Xaa Val Asp Gly Glu Lys Ile Gly Met			
	100	105	110
Phe Gly Val Tyr Asp Gly His Gly Gly Val Arg Ala Ala Glu Tyr Val			
	115	120	125
Lys Gln His Leu Phe Ser Asn Leu Ile Lys His Pro Lys Phe Ile Thr			
	130	135	140
Asp Thr			
145			

(2) INFORMATION FOR SEQ ID NO:1698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..654
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1698:

ctccgcgcgtc	gocgtgtccac	tttccccgtg	cttctccgcc	gtcgaggccg	cgtcccgagt	60
cgaagagacc	acgactcaga	tggccagccc	ctgggtccgg	cccgaggtgt	accgctgttt	120
cgcggcaacg	ggcgtggccg	tggcctctgt	cggatttcag	ctcttcgcga	acatcaccgg	180
caaccgggaa	gtcagggtaa	acaaggcagg	gagggcagct	ggtgtgcttg	agaacctatga	240
ggaggggagg	cgttacgcc	tgcattggcct	aacgcctacc	ctcctatggg	ttctttcagc	300
agcactggcc	tcactatttc	ttctaaatta	ccaagattct	cggacatgta	cactctcaca	360
atagcaagtg	cgagtcacaca	gtctatctct	gcaaacaaagc	cagttcatatt	cactaagagc	420
gtaacaaagt	ggtttacaaa	ggaaggagtt	cttgtggagg	gcctgttctg	gaaggatgtc	480
gagaagctga	ttgatgacta	caacagtgg	cgcaagagta	aatgaattgg	tagctcgtgt	540
ctctggccat	ctggggagac	atcgcgtgt	agagaaatcc	gtcaaatgtt	agcttaatat	600
gaacaggcat	ttttgtata	ctgtaccggt	tgaccagtga	atgaatgatg	ttct	

(2) INFORMATION FOR SEQ ID NO:1699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1699:

Ser	Ala	Val	Ala	Cys	Pro	Leu	Ser	Pro	Cys	Phe	Ser	Ala	Val	Glu	Ala
1		5		10		15		20		25		30		35	
Ala	Ser	Gln	Cys	Glu	Glu	Thr	Thr	Gln	Met	Ala	Ser	Arg	Trp	Val	
		20		25		30		35		40		45		50	
Arg	Pro	Glu	Val	Tyr	Pro	Leu	Phe	Ala	Ala	Thr	Gly	Val	Ala	Val	Gly
		35		40		45		50		55		60		65	
Ile	Cys	Gly	Phe	Gln	Leu	Phe	Arg	Asn	Ile	Thr	Gly	Asn	Pro	Glu	Val
		50		55		60		65		70		75		80	
Arg	Val	Asn	Lys	Ala	Gly	Arg	Ala	Ala	Gly	Val	Leu	Glu	Asn	His	Glu
		70		75		80		85		90		95		100	
Glu	Gly	Arg	Arg	Tyr	Ala	Met	His	Gly	Leu	Thr	Pro	Thr	Leu	Leu	Trp
		85		90		95		100		105		110		115	
Val	Leu	Ser	Ala	Ala	Leu	Ala	Ser	Leu	Phe	Leu	Leu	Asn	Tyr	Gln	Asp
		100		105		110		115		120		125		130	
Ser	Arg	Thr	Cys	Thr	Leu	Ser	Gln								

115 120
(2) INFORMATION FOR SEQ ID NO:1700:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..94
(D) OTHER INFORMATION: / Ceres Seq. ID 1500902
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1700:
Met Ala Ser Arg Trp Val Arg Pro Glu Val Tyr Pro Leu Phe Ala Ala
1 5 10 15
Thr Gly Val Ala Val Gly Ile Cys Gly Phe Gln Leu Phe Arg Asn Ile
20 25 30
Thr Gly Asn Pro Glu Val Arg Val Asn Lys Ala Gly Arg Ala Ala Gly
35 40 45
Val Leu Glu Asn His Glu Glu Gly Arg Arg Tyr Ala Met His Gly Leu
50 55 60
Thr Pro Thr Leu Leu Trp Val Leu Ser Ala Ala Leu Ala Ser Leu Phe
65 70 75 80
Leu Leu Asn Tyr Gln Asp Ser Arg Thr Cys Thr Leu Ser Gln
85 90

(2) INFORMATION FOR SEQ ID NO:1701:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..79
(D) OTHER INFORMATION: / Ceres Seq. ID 1500903
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1701:
Met Gly Ser Phe Ser Ser Thr Gly Leu Thr Ile Ser Ser Lys Leu Pro
1 5 10 15
Arg Phe Ser Asp Met Tyr Thr Leu Thr Ile Ala Ser Ala Asp Pro Gln
20 25 30
Ser Ile Ser Ala Asn Lys Pro Val His Phe Thr Lys Ser Val Thr Lys
35 40 45
Trp Phe Thr Lys Glu Gly Val Leu Val Glu Gly Leu Phe Trp Lys Asp
50 55 60
Val Glu Lys Leu Ile Asp Asp Tyr Asn Ser Glu Arg Lys Ser Lys
65 70 75

(2) INFORMATION FOR SEQ ID NO:1702:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..465
(D) OTHER INFORMATION: / Ceres Seq. ID 1500907
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1702:
acacaacacc agtaagcaag caccgccagc acgcacaagc agggcaaaagt ctcgaccatc
gctctgaggg attaatggcg gcgggaggag gaggcgggcg catcgcgacg agaaggcccc

tgctgctgag gcgttcggcg ggcacctgga ggcgggcggag atgacggagg cggaggagga 180
acacagcggc gtcgaagtccc ggctgtcggg tctgctgtgg cagcgcgggg cggcgtagca 240
cgcggtggttc agctgcgcggt cgaaccaggt ggcgaggtg ctgctgacgc tgcctactc 300
gttcggcgac tggggatgct garcggcggt ctgttcacag tcttctacgg cctgctgggc 360
agctggacgg cgtacctgat cagcatcctg tacctggagt accgcaccg tcgggagerc 420
gagaaggccg cggacttcgc gaaccacgtg atccagtggg tcgag

(2) INFORMATION FOR SEQ ID NO:1703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1703:

Thr Thr Pro Val Ser Lys His Arg Gln His Ala Gln Gly Lys Ala
1 5 10 15
Leu Asp His Arg Ser Glu Gly Leu Met Ala Ala Gly Gly Gly Gly Gly
20 25 30
Gly Ile Ala Thr Arg Arg Pro Leu Leu Arg Arg Ser Ala Gly Thr
35 40 45
Trp Arg Arg Arg Arg
50

(2) INFORMATION FOR SEQ ID NO:1704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1704:

Met Thr Glu Ala Glu Glu Glu His Ser Gly Val Lys Ser Arg Leu Ser
1 5 10 15
Gly Leu Leu Trp His Gly Gly Ser Ala Tyr Asp Ala Trp Phe Ser Cys
20 25 30
Ala Ser Asn Gln Val Ala Gln Val Leu Leu Thr Leu Pro Tyr Ser Phe
35 40 45
Ala His Trp Gly Cys
50

(2) INFORMATION FOR SEQ ID NO:1705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1705:

Met Leu Xaa Gly Val Leu Phe Gln Leu Phe Tyr Gly Leu Leu Gly Ser
1 5 10 15
Trp Thr Ala Tyr Leu Ile Ser Ile Leu Tyr Leu Glu Tyr Arg Thr Arg

20 25 30
Arg Glu Xaa Glu Lys Ala Ala Asp Phe Arg Asn His Val Ile Gln Trp
35 40 45
Phe Glu
50

(2) INFORMATION FOR SEQ ID NO:1706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..548
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1706:

gttacatccc	accatttget	gttcaccttc	cctcccgttt	gcctcctctc	gctgtctcgt	60
agctttcttc	ctccggcgac	ggctgggcga	gcggccgcga	gtcgggccct	tcgtcggcga	120
cgagcatcca	cgtgcggcgc	gcccatcttt	ccgctccttc	ccttactcgc	gctcggcaca	180
caggcgacgg	cgccggcgcc	gctcaggatc	gggctatcac	cgacggggtc	cggtctctcc	240
gcccgctctc	cgccactcgc	ctcgcgcctc	cgctccgggt	cctccgcaca	ccggccggcg	300
atctgcgaag	ggttggatga	tgggcgcgat	ctgaaggatg	ctgatttcta	taagcagcaa	360
gctaaacttc	ttttcaagaa	cttgtcaaaa	gggcatcatg	aagcttcacg	gatgtmaatt	420
gagacagggc	cctactattt	ccactacatt	attgarggca	gagtatgtta	tctgactatg	480
tgtgamcgct	cttatccgaa	gaaacttgca	ttccagtacc	tagaagatct	gaaaaatgaa	540
tttgagag						

(2) INFORMATION FOR SEQ ID NO:1707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1707:

Val Thr Ser His His Leu Leu Phe Thr Phe Pro Pro Val Cys Leu Leu	
1 5 10 15	
Ser Leu Ser Arg Ser Phe Phe Pro Pro Ala Thr Ala Gly Arg Ala Ala	
20 25 30	
Ala Ser Arg Ala Leu Arg Arg Arg Arg Ala Ser Thr Cys Ala Ala Pro	
35 40 45	
His Leu Pro Leu Leu Pro Leu Leu Ala Leu Gly Thr Gln Ala Thr Ala	
50 55 60	
Ala Ala Ala Leu Arg Ile Gly Leu Ser Pro Thr Gly Ser Gly Phe Ser	
65 70 75 80	
Ala Arg Leu Ser Pro Leu Ala Ser Arg Pro Arg Leu Arg Ser Ser Ala	
85 90 95	
His Arg Pro Ala Ile Leu Gln Gly Leu Asp Asp Gly Arg Asp Leu Lys	
100 105 110	
Asp Ala Asp Phe Tyr Lys Gln Gln Ala Lys Leu Leu Phe Lys Asn Leu	
115 120 125	
Ser Lys Gly His His Glu Ala Ser Arg Met Xaa Ile Glu Thr Gly Pro	
130 135 140	
Tyr Tyr Phe His Tyr Ile Ile Xaa Gly Arg Val Cys Tyr Leu Thr Met	
145 150 155 160	
Cys Xaa Arg Ser Tyr Pro Lys Lys Leu Ala Phe Gln Tyr Leu Glu Asp	
165 170 175	

Leu Lys Asn Glu Phe Glu
180

(2) INFORMATION FOR SEQ ID NO:1708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1708:

Leu	His	Pro	Thr	Ile	Cys	Cys	Ser	Pro	Ser	Leu	Pro	Phe	Ala	Ser	Ser	
1				5				10							15	
Arg	Cys	Leu	Val	Ala	Ser	Phe	Leu	Arg	Arg	Arg	Leu	Gly	Glu	Arg	Pro	
			20					25					30			
Pro	Val	Gly	Pro	Phe	Val	Gly	Asp	Glu	His	Pro	Pro	Ala	Arg	Arg	Pro	
			35				40					45				
Ile	Phe	Arg	Ser	Phe	Pro	Tyr	Ser	Arg	Ser	Ala	His	Arg	Arg	Arg	Arg	
			50				55				60					
Arg	Arg	Arg	Ser	Gly	Ser	Gly	Tyr	His	Arg	Arg	Gly	Pro	Ala	Ser	Pro	
			65				70				75				80	
Pro	Ala	Ser	Arg	His	Ser	Pro	Arg	Ala	Leu	Ala	Ser	Gly	Pro	Pro	His	
				85					90					95		
Thr	Gly	Arg	Arg	Ser	Cys	Lys	Gly	Trp	Met	Met	Gly	Glu	Ile			
				100				105					110			

(2) INFORMATION FOR SEQ ID NO:1709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..790
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1709:

atgctctacc	ggagtagcgc	aactcgcgca	gcaaatcctc	ctatctccaa	gcctccaatc	60
tgtgaacggt	gaaccccaat	cgaatgacgc	cgacggsagc	ctcctcctcc	cggtcccccc	120
atgtctctct	atctccgatg	tgccgcgcct	ccagctcccc	ccgcgcggcg	gccaccggcc	180
tgcgccctcg	tggaaagggt	tggagtgccg	ctccgtacag	acgcggatgg	tctctctttt	240
cgttgggagc	agaacacgcc	gcagaaacgt	tatatgtgct	tccctgttcc	gagttggagc	300
tcccgaagca	ctggctcattg	gagtagtcgc	cttgttggtg	tccggcccca	agggtctagc	360
agaggtagcc	aggaatttgg	ggaagacttt	gcgtgctttc	caaccaacca	ttagagagat	420
acagggatga	tcaaaggaggt	tcaggagcac	tcttgaacga	gaaatcgga	ttgatgaggt	480
ttcccgatcg	acgaattata	cacccacgac	catgaataac	aaccaacaac	ctgctgcgca	540
ctcaaatatc	aagcctgcac	ctgcacctta	caccagcgat	gaacttgtga	aagtaactga	600
agaacaaatt	gctgcacatc	ctgctgcaga	gagttatcgt	cagttgtgtc	gggtgtgtcc	660
cttaaacctt	atttgtggtt	ggttggtact	tttggtgtgg	ttattttttt	ggacctcggt	720
atagtcgggt	ggttcaatgt	tatcgcggt	actggcaaac	cttaagtgtat	acggtattct	780
ctctttcggt						

(2) INFORMATION FOR SEQ ID NO:1710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1500927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1710:

Cys Ser Thr Gly Val Ala Gln Leu Arg Lys Gln Ile Leu Leu Ser Pro
1 5 10 15
Ser Leu Gln Ser Val Asn Gly Glu Pro Gln Ser Asn Asp Ala Asp Xaa
20 25 30
Ser Leu Leu Leu Pro Ala Pro Phe Val Ser Ile Ser Asp Val Arg
35 40 45
Arg Leu Gln Leu Pro Pro Arg Gly Gly His Arg Pro Arg Pro Cys Trp
50 55 60
Lys Gly Leu Glu Cys Gly Ser Val Gln Thr Arg Met Val Ser Ser Phe
65 70 75 80
Val Gly Ser Arg Thr Arg Arg Arg Asn Val Ile Cys Ala Ser Leu Phe
85 90 95
Gly Val Gly Ala Pro Glu Ala Leu Val Ile Gly Val Val Ala Leu Leu
100 105 110
Val Phe Gly Pro Lys Gly Leu Ala Glu Val Ala Arg Asn Leu Gly Lys
115 120 125
Thr Leu Arg Ala Phe Gln Pro Thr Ile Arg Glu Ile Gln Asp Val Ser
130 135 140
Arg Glu Phe Arg Ser Thr Leu Glu Arg Glu Ile Gly Ile Asp Glu Val
145 150 155 160
Ser Gln Ser Thr Asn Tyr Thr Pro Thr Thr Met Asn Asn Asn Gln Gln
165 170 175
Pro Ala Ala Asp Ser Asn Ile Lys Pro Ala Pro Ala Pro Tyr Thr Ser
180 185 190
Asp Glu Leu Val Lys Val Thr Glu Glu Gln Ile Ala Ala Ser Ala Ala
195 200 205
Ala Glu Ser Tyr Arg Gln Leu Val Arg Cys Val Arg Leu Asn Phe Ile
210 215 220
Cys Gly Trp Leu Val Leu Leu Trp Trp Leu Phe Trp Thr Ser
225 230 235

(2) INFORMATION FOR SEQ ID NO:1711:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1500928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1711:

Met Val Ser Ser Phe Val Gly Ser Arg Thr Arg Arg Arg Asn Val Ile
1 5 10 15
Cys Ala Ser Leu Phe Gly Val Gly Ala Pro Glu Ala Leu Val Ile Gly
20 25 30
Val Val Ala Leu Leu Val Phe Gly Pro Lys Gly Leu Ala Glu Val Ala
35 40 45
Arg Asn Leu Gly Lys Thr Leu Arg Ala Phe Gln Pro Thr Ile Arg Glu
50 55 60
Ile Gln Asp Val Ser Arg Glu Phe Arg Ser Thr Leu Glu Arg Glu Ile
65 70 75 80
Gly Ile Asp Glu Val Ser Gln Ser Thr Asn Tyr Thr Pro Thr Thr Met
85 90 95
Asn Asn Asn Gln Gln Pro Ala Ala Asp Ser Asn Ile Lys Pro Ala Pro
100 105 110

Ala Pro Tyr Thr Ser Asp Glu Leu Val Lys Val Thr Glu Glu Gln Ile
115 120 125
Ala Ala Ser Ala Ala Ala Glu Ser Tyr Arg Gln Leu Val Arg Cys Val
130 135 140
Arg Leu Asn Phe Ile Cys Gly Trp Leu Val Leu Trp Trp Leu Phe
145 150 155 160
Phe Trp Thr Ser

(2) INFORMATION FOR SEQ ID NO:1712:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..482

(D) OTHER INFORMATION: / Ceres Seq. ID 1500929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1712:

aaggattttt	gcaccgtgcc	tctgcctcca	ggattgtcgt	gcgcgcctc	caccattttc	60
gccgcgcgc	cccgcacacc	acctccaagg	atccttgccc	cgcgccctgt	actcctcgcg	120
tccgcatctc	cgcgtccatt	tccgctgcgc	gcgatgcgt	cgcacgtgtc	gcgcgcctcg	180
gcgcgcgggc	cgcgattacm	cccctcccca	tcaccacctc	gctgtggtgt	acccccgtcc	240
ttggcgccgc	caccccgcac	cccgtccgag	attggctctt	ccaccgctcc	ccctggagat	300
gagcgctcgc	ttagggttag	gcgtccaacg	gttgacctt	ccaccacaag	cgagaggaga	360
tcgctggaag	aggggggctg	ggagacgaac	aggaacacgg	tccacatctg	ggtgcmctcg	420
cmtccacatc	tctcgaatcc	tgamgcacac	acagcgctcc	cgcmctcggt	agaccgcgac	480

gc

(2) INFORMATION FOR SEQ ID NO:1713:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1500930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1713:

Lys	Asp	Phe	Cys	Thr	Val	Pro	Leu	Pro	Pro	Gly	Leu	Ser	Cys	Arg	Ala
1			5					10					15		
Ser	Thr	Ile	Phe	Ala	Ala	Ala	Pro	Pro	Thr	Pro	Pro	Pro	Arg	Ile	Leu
			20					25					30		
Ala	Pro	Ala	Pro	Val	Leu	Leu	Ala	Ser	Ala	Ser	Pro	Ala	Pro	Phe	Pro
			35					40					45		
Leu	Pro	Ala	Met	Arg	Ser	His	Val	Ser	Pro	Pro	Ser	Ala	Arg	Gly	Pro
			50					55				60			
Arg	Leu	Xaa	Pro	Ser	Pro	Ser	Pro	Pro	Arg	Cys	Gly	Val	Pro	Pro	Ser
			70					75						80	
Leu	Ala	Pro	Pro	Pro	Arg	Thr	Pro	Ser	Glu	Ile	Gly	Ser	Ser	Thr	Ala
			85					90						95	
Pro	Pro	Gly	Asp	Glu	Arg	Ser	Leu	Arg	Val	Arg	Arg	Pro	Thr	Val	Val
			100					105					110		
Pro	Ser	Thr	Thr	Ser	Glu	Arg	Arg	Ser	Leu	Glu	Glu	Gly	Gly	Trp	Glu
			115					120					125		
Thr	Asn	Arg	Asn	Thr	Val	His	Ile	Trp	Val	Xaa	Ser	Xaa	Pro	Thr	Leu
			130					135					140		
Ser	Asn	Pro	Xaa	Ala	His	Thr	Ala	Pro	Pro	Xaa	Ser				
			145					150					155		

(2) INFORMATION FOR SEQ ID NO:1714:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1500931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1714:

```
Arg Ile Phe Ala Pro Cys Leu Cys Leu Gln Asp Cys Arg Ala Ala Pro
1      5      10      15
Pro Pro Phe Ser Pro Pro Arg Pro Arg His His Leu Gln Gly Ser Leu
20      25      30
Pro Pro Pro Leu Tyr Ser Ser Arg Pro His Leu Pro Leu His Phe Arg
35      40      45
Cys Pro Arg Cys Ala Arg Thr Cys Arg Arg Pro Arg Pro Ala Gly Arg
50      55      60
Asp Tyr Xaa Pro Pro His His His Leu Ala Val Val Tyr Pro Arg Pro
65      70      75      80
Trp Arg Arg His Pro Ala Pro Arg Pro Arg Leu Ala Leu Pro Pro Leu
85      90      95
Pro Leu Glu Met Ser Ala Arg Leu Gly Leu Gly Val Gln Arg Leu Tyr
100      105      110
Pro Pro Pro Gln Ala Arg Gly Asp Arg Trp Lys Arg Gly Ala Gly Arg
115      120      125
Arg Thr Gly Thr Arg Ser Thr Ser Gly Cys Xaa Arg Xaa Pro Leu Ser
130      135      140
Arg Ile Leu Xaa Pro Thr Gln Arg Leu Arg Xaa Arg Glu Thr Ala Thr
145      150      155      160
```

(2) INFORMATION FOR SEQ ID NO:1715:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1500932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1715:

```
Met Arg Ser His Val Ser Pro Pro Ser Ala Arg Gly Pro Arg Leu Xaa
1      5      10      15
Pro Ser Pro Ser Pro Pro Arg Cys Gly Val Pro Pro Ser Leu Ala Pro
20      25      30
Pro Pro Arg Thr Pro Ser Glu Ile Gly Ser Ser Thr Ala Pro Pro Gly
35      40      45
Asp Glu Arg Ser Leu Arg Val Arg Arg Pro Thr Val Val Pro Ser Thr
50      55      60
Thr Ser Glu Arg Arg Ser Leu Glu Glu Gly Gly Trp Glu Thr Asn Arg
65      70      75      80
Asn Thr Val His Ile Trp Val Xaa Ser Xaa Pro Thr Leu Ser Asn Pro
85      90      95
Xaa Ala His Thr Ala Pro Pro Xaa Ser
100      105
```

(2) INFORMATION FOR SEQ ID NO:1716:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..463
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500945
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1716:
aatcaacaca ccaccaccac cagcagcaca tcaatttagc tagttccagg aacacgcgag 60
gaaaccgcag catggccaac aaccgcattc tcgacgagta caaccccgcc gtcgaatgga 120
gccgctccga cgaggcgagc gccgtccgga tctcgctccc agggttcaag agggaggaca 180
tacgctgtct ggtggacagc cagggccacc tgcggagcgc cgcgagcggg cacatcgccg 240
gcaacaggtg gaggcgttcc cagacggagc tcgacctccc cgccaactgc aacgccgagc 300
gcatccgcgc caagttcgcg aacgacaggc tcaccatcac gtcctcccaag agcacctctc 360
cggcgcccat tcgcgcgcgc ccgcagaggg cgacagtga ggcgcgcgtc acgtgctcgg 420
cgaggcttcc gccggtgact gctaggccag tggcgaggcc tgc
(2) INFORMATION FOR SEQ ID NO:1717:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..153
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500946
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1717:
Ser Thr His His Gln Gln His Ile Asn Leu Ala Ser Ser Arg
1 5 10 15
Asn Thr Arg Gly Asn Arg Ser Met Ala Asn Asn Arg Ile Phe Asp Glu
20 25 30
Tyr Asn Pro Ala Val Glu Trp Ser Arg Ser Asp Glu Ala Asp Ala Val
35 40 45
Arg Ile Ser Leu Pro Gly Phe Lys Arg Glu Asp Ile Arg Val Leu Val
50 55 60
Asp Ser His Gly His Leu Arg Thr Arg Gly Glu Arg His Ile Ala Gly
65 70 75 80
Asn Arg Trp Ser Arg Phe Gln Thr Asp Val Asp Leu Pro Ala Asn Cys
85 90 95
Asn Ala Asp Gly Ile Arg Ala Lys Phe Glu Asn Asp Arg Leu Thr Ile
100 105 110
Thr Leu Pro Lys Ser Thr Ser Ser Ala Pro Ile Pro Ala Pro Pro Gln
115 120 125
Arg Pro His Val Lys Ala Pro Ser Thr Ser Ser Ala Arg Leu Pro Pro
130 135 140
Val Thr Ala Arg Pro Val Ala Arg Pro
145 150
(2) INFORMATION FOR SEQ ID NO:1718:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1500947
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1718:
Met Ala Asn Asn Arg Ile Phe Asp Glu Tyr Asn Pro Ala Val Glu Trp
1 5 10 15
Ser Arg Ser Asp Glu Ala Asp Ala Val Arg Ile Ser Leu Pro Gly Phe
20 25 30
Lys Arg Glu Asp Ile Arg Val Leu Val Asp Ser His Gly His Leu Arg
35 40 45
Thr Arg Gly Glu Arg His Ile Ala Gly Asn Arg Trp Ser Arg Phe Gln
50 55 60
Thr Asp Val Asp Leu Pro Ala Asn Cys Asn Ala Asp Gly Ile Arg Ala
65 70 75 80
Lys Phe Glu Asn Asp Arg Leu Thr Ile Thr Leu Pro Lys Ser Thr Ser
85 90 95
Ser Ala Pro Ile Pro Ala Pro Pro Gln Arg Pro His Val Lys Ala Pro
100 105 110
Ser Thr Ser Ser Ala Arg Leu Pro Pro Val Thr Ala Arg Pro Val Ala
115 120 125
Arg Pro
130

(2) INFORMATION FOR SEQ ID NO:1719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1719:

Met Glu Pro Leu Arg Arg Gly Gly Arg Arg Pro Asp Leu Ala Pro Arg
1 5 10 15
Val Gln Glu Gly Gly His Thr Arg Ala Gly Gly Gln Pro Arg Pro Pro
20 25 30
Ala Asp Ala Arg Arg Ala Ala His Arg Arg Gln Gln Val Glu Pro Leu
35 40 45
Pro Asp Gly Arg Arg Pro Pro Arg Gln Leu Gln Arg Arg Arg His Pro
50 55 60
Arg Gln Val Arg Glu Arg Gln Ala His His His Ala Pro Gln Glu His
65 70 75 80
Leu Leu Gly Ala His Ser Gly Ala Ala Ala Glu Ala Ala Arg Glu Gly
85 90 95
Ala Val Asp Val Val Gly Glu Ala Ser Ala Gly Asp Cys
100 105

(2) INFORMATION FOR SEQ ID NO:1720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..520
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720:

ctcgacgcca gcaggacacc actcatcttc ttctccccc cctcgtttcc atcgccacca 60
ccctcttctc ctgcggtcct cccccgtccc actccacacc cctcgcctc cgctccact 120
gcagctgcgc ccattgcagag cctcctcctg cccaccgtcg ccgtggcccc ggtggcgcc 180

ccgctcgaggaa ggcgggaatct cccggggacgc ctctccgctcc gcgcctccgc gacgggtggta 240
ggcgccaccgc ggcggggagac ggatcccaag aagcgggtgg tgatcacggg gatggggctg 300
gtctccggtt tcggggaacga tgtagacgct tactacgacc gcctgctagt cggggagagc 360
ggcatcgggc ccacgcacgc cctcgacgct tctaagtccc ccaccgcgtt tgccggctcag 420
atccggggct tctcctccga gggatacatc gacggaaaaga acgacgcgm g ccttgatgat 480
tgccctcgat actgcacgt cagtggcaag aagctctcg

(2) INFORMATION FOR SEQ ID NO:1721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..173
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721:

Leu	Ala	Ala	Ser	Arg	Thr	Pro	Leu	Ile	Phe	Phe	Ser	Pro	Ala	Ser	Phe
1				5				10					15		
Pro	Ser	Pro	Pro	Pro	Ser	Ser	Pro	Ala	Val	Leu	Pro	Arg	Pro	Thr	Pro
			20					25					30		
Thr	Pro	Leu	Ala	Ser	Ala	Ser	Thr	Ala	Ala	Ala	Ala	Met	Gln	Ser	Leu
			35				40					45			
Leu	Leu	Pro	Thr	Ala	Ala	Val	Ala	Pro	Val	Ala	Pro	Pro	Cys	Gly	Arg
			50			55				60					
Arg	Asn	Leu	Pro	Gly	Arg	Leu	Ser	Val	Arg	Ala	Ser	Ala	Thr	Val	Val
65				70					75				80		
Ala	Ala	Pro	Arg	Arg	Glu	Thr	Asp	Pro	Lys	Lys	Arg	Val	Val	Ile	Thr
			85					90				95			
Gly	Met	Gly	Leu	Val	Ser	Val	Phe	Gly	Asn	Asp	Val	Asp	Ala	Tyr	Tyr
			100				105					110			
Asp	Arg	Leu	Leu	Val	Gly	Glu	Ser	Gly	Ile	Gly	Pro	Ile	Asp	Arg	Phe
			115			120						125			
Asp	Ala	Ser	Lys	Phe	Pro	Thr	Arg	Phe	Ala	Gly	Gln	Ile	Arg	Gly	Phe
			130			135					140				
Ser	Ser	Glu	Gly	Tyr	Ile	Asp	Gly	Lys	Asn	Asp	Arg	Xaa	Leu	Asp	Asp
145				150					155				160		
Cys	Leu	Arg	Tyr	Cys	Ile	Val	Ser	Gly	Lys	Lys	Ala	Leu			
			165					170							

(2) INFORMATION FOR SEQ ID NO:1722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722:

Arg	Ser	Gln	Gln	Asp	Thr	Thr	His	Leu	Leu	Leu	Pro	Arg	Leu	Val	Ser
1				5				10					15		
Ile	Ala	Thr	Thr	Leu	Phe	Ser	Cys	Gly	Pro	Pro	Pro	Ser	His	Ser	His
			20					25					30		
Pro	Pro	Arg	Leu	Arg	Leu	His	Cys	Ser	Cys	Arg	His	Ala	Glu	Pro	Pro
			35			40						45			
Pro	Ala	His	Arg	Cys	Arg	Gly	Pro	Gly	Gly	Ala	Ser	Val	Arg	Lys	Ala
			50			55				60					
Glu	Ser	Pro	Gly	Thr	Pro	Leu	Arg	Pro	Arg	Leu	Arg	Asp	Gly	Gly	Ser

65		70		75		80
Gly	Thr	Ala	Ala	Gly	Asp	Gly
		85		90		95
Asp	Gly	Ala	Gly	Leu	Arg	Phe
		100		105		110
Pro	Pro	Ala	Ser	Arg	Gly	Glu
		115		120		125
Arg	Phe					
	130					

(2) INFORMATION FOR SEQ ID NO:1723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1723:

Met	Gln	Ser	Leu	Leu	Pro	Thr	Ala	Ala	Val	Ala	Pro	Val	Ala	Pro
1		5		10		15		20		25		30		35
Pro	Cys	Gly	Arg	Arg	Asn	Leu	Pro	Gly	Arg	Leu	Ser	Val	Arg	Ala
		40		45		50		55		60		65		70
Ala	Thr	Val	Val	Ala	Ala	Pro	Arg	Arg	Glu	Thr	Asp	Pro	Lys	Lys
		75		80		85		90		95		100		105
Val	Val	Ile	Thr	Gly	Met	Gly	Leu	Val	Ser	Val	Phe	Gly	Asn	Asp
		110		115		120		125		130		135		140
Asp	Ala	Tyr	Tyr	Asp	Arg	Leu	Leu	Val	Gly	Glu	Ser	Gly	Ile	Gly
		145		150		155		160		165		170		175
Ile	Asp	Arg	Phe	Asp	Ala	Ser	Lys	Phe	Pro	Thr	Arg	Phe	Ala	Gly
		180		185		190		195		200		205		210
Ile	Arg	Gly	Phe	Ser	Ser	Glu	Gly	Tyr	Ile	Asp	Gly	Lys	Asn	Asp
		215		220		225		230		235		240		245
Xaa	Leu	Asp	Asp	Cys	Leu	Arg	Tyr	Cys	Ile	Val	Ser	Gly	Lys	Lys
		250		255		260		265		270		275		280
Leu														

(2) INFORMATION FOR SEQ ID NO:1724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..485
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1724:

aytccctgcag	ctgcagcysr	tgcgtgcgcg	ctactccatc	gtctattaat	tcctcgtgta	60
gctccagcgc	tcggtctaga	caagcctctc	caacatgaag	ctcctgggtt	ggatgcaccg	120
gaagttacga	cagaacagta	atgatgtgtt	caaagagttc	aacaacgctg	gaggtgggac	180
gtgcaactgc	atcacccggc	tggccgcgtc	ggaccgcggc	actttcctcg	ccaccgccaa	240
cgaatacttc	gcgcgcgaca	acgacttcac	caacaatcat	ccatogtcgc	cggccgcgga	300
cctcttcacc	tttgggtggc	gcggcctcct	caccattggc	acgctaggca	tcgcgcgctc	360
gcgtgtctcg	agatgctgat	gaagttgatt	acgacgtcga	cgcgcgatgt	gactccgcat	420
ttgacgacaa	cgacgacac	gcggttkatg	acgaagacca	ggtcgacagc	gocgtcacgc	480
ccacg						

(2) INFORMATION FOR SEQ ID NO:1725:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..94
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500964
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1725:
Met Lys Leu Leu Gly Trp Met His Arg Lys Leu Arg Gln Asn Ser Asn
1 5 10 15
Asp Val Phe Lys Glu Phe Asn Asn Ala Gly Gly Gly Thr Cys Asn Cys
 20 25 30
Ile Thr Gly Leu Ala Ala Ser Asp Pro Ala Thr Phe Leu Ala Thr Ala
 35 40 45
Asn Glu Tyr Phe Ala Ala Asp Asn Asp Phe Thr Asn Asn His Pro Ser
 50 55 60
Ser Pro Ala Ala Asp Leu Phe Thr Phe Gly Gly Ser Gly Leu Leu Thr
65 70 75 80
Ile Gly Thr Leu Gly Ile Ala Pro Ser Arg Val Cys Arg Cys
 85 90
(2) INFORMATION FOR SEQ ID NO:1726:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..88
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500965
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1726:
Met His Arg Lys Leu Arg Gln Asn Ser Asn Asp Val Phe Lys Glu Phe
1 5 10 15
Asn Asn Ala Gly Gly Gly Thr Cys Asn Cys Ile Thr Gly Leu Ala Ala
 20 25 30
Ser Asp Pro Ala Thr Phe Leu Ala Thr Ala Asn Glu Tyr Phe Ala Ala
 35 40 45
Asp Asn Asp Phe Thr Asn Asn His Pro Ser Ser Pro Ala Ala Asp Leu
 50 55 60
Phe Thr Phe Gly Gly Ser Gly Leu Leu Thr Ile Gly Thr Leu Gly Ile
65 70 75 80
Ala Pro Ser Arg Val Cys Arg Cys
 85
(2) INFORMATION FOR SEQ ID NO:1727:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..68
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500966
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1727:
Met Met Cys Ser Lys Ser Ser Thr Thr Leu Glu Val Gly Arg Ala Thr
1 5 10 15

Ala Ser Pro Gly Trp Pro Arg Arg Thr Arg Pro Leu Ser Ser Pro Pro
20 25 30
Pro Thr Asn Thr Ser Pro Pro Thr Thr Thr Ser Pro Thr Ile Ile His
35 40 45
Arg Arg Arg Pro Pro Thr Ser Ser Pro Leu Val Ala Ala Ala Ser Ser
50 55 60
Pro Leu Ala Arg
65

(2) INFORMATION FOR SEQ ID NO:1728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..410
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1728:

tccgttcggy	tccttctctcc	ccctatctag	ctagccttcc	cgttctctgca	tcgcggcgga	60
gatggggcgc	tccaccacgc	cgcctgcgtc	ggcggcgggc	ctgcttctgc	tgctgctcgc	120
gccgctcgcc	gcggcgggcg	acagcatgtc	gacgtctctc	tacggcgagc	ggasmdgmsn	180
aggaggcgcg	gcggatgtac	gccgagtggg	tggcgggcga	cgcccgagacc	tacaacgccg	240
tcggagggag	gagcgcaggt	tcgaggtggt	cagggacaac	ctccgctacg	tcgacgccca	300
caacgcgcgc	gccgagggcg	gcgtccactc	cttccgcctc	gggctcaacc	gettccgcga	360
ctctaccaac	gacgagtacc	gcrcamcta	cttcggcgctc	aggagcaggg		

(2) INFORMATION FOR SEQ ID NO:1729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729:

Arg Ser Xaa Pro Ser Ser Pro Tyr Leu Ala Ser Leu Pro Val Pro Ala	
1 5 10 15	
Ser Arg Arg Arg Trp Ala Pro Pro Pro Arg Arg Ser Arg Arg Arg Arg	
20 25 30	
Arg Cys Phe Cys Cys Cys Ser Arg Arg Ser Pro Arg Arg Thr Ala	
35 40 45	
Cys Arg Ser Ser Pro Thr Ala Ser Gly Xaa Xaa Xaa Glu Ala Arg Arg	
50 55 60	
Met Tyr Ala Glu Trp Met Ala Ala His Gly Arg Thr Tyr Asn Ala Val	
65 70 75 80	
Xaa Arg Arg Ser Ala Gly Ser Arg Cys Ser Gly Thr Thr Ser Ala Thr	
85 90 95	
Ser Thr Pro Thr Thr Pro Pro Pro Xaa Arg Ala Ser Thr Pro Ser Ala	
100 105 110	
Ser Gly Ser Thr Ala Ser Pro Thr Ser Pro Thr Thr Ser Thr Xaa Pro	
115 120 125	
Xaa Thr Ser Ala Ser Gly Ala Gly	
130 135	

(2) INFORMATION FOR SEQ ID NO:1730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..116
(D) OTHER INFORMATION: / Ceres Seq. ID 1500976
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730:
Met Gly Ala Ser Thr Pro Leu Ala Ser Ala Ala Leu Leu Leu
1 5 10 15
Leu Leu Leu Ala Pro Leu Ala Ala Ala Asp Ser Met Ser Ile Val
20 25 30
Ser Tyr Gly Glu Arg Xaa Xaa Xaa Gly Gly Ala Ala Asp Val Arg Arg
35 40 45
Val Asp Gly Gly Ala Arg Pro Asp Leu Gln Arg Arg Arg Xaa Glu Glu
50 55 60
Arg Arg Phe Glu Val Phe Arg Asp Asn Leu Arg Tyr Val Asp Ala His
65 70 75 80
Asn Ala Ala Ala Xaa Ala Gly Val His Ser Phe Arg Leu Gly Leu Asn
85 90 95
Arg Phe Ala Asp Leu Thr Asn Asp Glu Tyr Arg Xaa Xaa Tyr Leu Gly
100 105 110
Val Arg Ser Arg
115
(2) INFORMATION FOR SEQ ID NO:1731:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..88
(D) OTHER INFORMATION: / Ceres Seq. ID 1500977
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1731:
Met Ser Ile Val Ser Tyr Gly Glu Arg Xaa Xaa Xaa Gly Gly Ala Ala
1 5 10 15
Asp Val Arg Arg Val Asp Gly Gly Ala Arg Pro Asp Leu Gln Arg Arg
20 25 30
Arg Xaa Glu Glu Arg Arg Phe Glu Val Phe Arg Asp Asn Leu Arg Tyr
35 40 45
Val Asp Ala His Asn Ala Ala Ala Xaa Ala Gly Val His Ser Phe Arg
50 55 60
Leu Gly Leu Asn Arg Phe Ala Asp Leu Thr Asn Asp Glu Tyr Arg Xaa
65 70 75 80
Xaa Tyr Leu Gly Val Arg Ser Arg
85
(2) INFORMATION FOR SEQ ID NO:1732:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..485
(D) OTHER INFORMATION: / Ceres Seq. ID 1500985
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732:
agcacatcga tcagtcgcgt gtctaggttt cctctctcac catagcgccc gctctgtcgc

ccttcgttca cctctccttc ctctctctccc tgcctgccag ggagagggga agtcagaggc 120
acggagtggc gcagagcaga cgcacgtgaa ccattngtag ctgtccctgt cgtcgtcgtc 180
gtcgtcaacg aatccacaca aggaaaggat ggagaagaag ccgaccatcc tcatgaacag 240
gtacgagctc gggcgacgc tcgggcaggg caccttcgcc aaggtgtacc acggccggaa 300
cctcgcgtcc ggcgaaagcg tggccatcaa ggtcatcgac aaggagaagg tgatgcgcgt 360
cgccatgata gaccagatca agcgcgagat ctccgctcat gcctcgtcc gccaccctaa 420
cgtcgtcgag ctgcacgagg gtgatggcca gcaagagcaa gatatacttc gccatggagt 480
acgtc

(2) INFORMATION FOR SEQ ID NO:1733:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..52
(D) OTHER INFORMATION: / Ceres Seq. ID 1500986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733:

Ala His Arg Ser Val Ala Cys Leu Gly Phe Leu Ser His His Ser Ala
1 5 10 15
Arg Ser Val Ala Leu Arg Ser Pro Leu Leu Pro Leu Leu Pro Ala Cys
20 25 30
Gln Gly Glu Gly Lys Ser Glu Ala Arg Ser Gly Ala Glu Gln Thr His
35 40 45
Val Asn His Xaa
50

(2) INFORMATION FOR SEQ ID NO:1734:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..92
(D) OTHER INFORMATION: / Ceres Seq. ID 1500987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734:

Met Glu Lys Lys Pro Thr Ile Leu Met Asn Arg Tyr Glu Leu Gly Arg
1 5 10 15
Thr Leu Gly Gln Gly Thr Phe Ala Lys Val Tyr His Gly Arg Asn Leu
20 25 30
Ala Ser Gly Glu Ser Val Ala Ile Lys Val Ile Asp Lys Glu Lys Val
35 40 45
Met Arg Val Gly Met Ile Asp Gln Ile Lys Arg Glu Ile Ser Val Met
50 55 60
Arg Leu Val Arg His Pro Asn Val Val Gln Leu His Glu Gly Asp Gly
65 70 75 80
Gln Gln Glu Gln Asp Ile Leu Arg His Gly Val Arg
85 90

(2) INFORMATION FOR SEQ ID NO:1735:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..84
(D) OTHER INFORMATION: / Ceres Seq. ID 1500988
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1735:
Met Asn Arg Tyr Glu Leu Gly Arg Thr Leu Gly Gln Gly Thr Phe Ala
1 5 10 15
Lys Val Tyr His Gly Arg Asn Leu Ala Ser Gly Glu Ser Val Ala Ile
20 25 30
Lys Val Ile Asp Lys Glu Lys Val Met Arg Val Gly Met Ile Asp Gln
35 40 45
Ile Lys Arg Glu Ile Ser Val Met Arg Leu Val Arg His Pro Asn Val
50 55 60
Val Gln Leu His Glu Gly Asp Gly Gln Gln Glu Gln Asp Ile Leu Arg
65 70 75 80
His Gly Val Arg

(2) INFORMATION FOR SEQ ID NO:1736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..462
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1736:

aacatctcct cacttcaacac cactcccgcc attgtctctgc gccctttctgc accgccacac 60
acaccccgct ccaatccaat ggcgccctgc caagccgtcc tcgcggtcgt ggctcctcgcc 120
ggcgctgtcc cgctcgccct ctctcgcggg ctgcggccttg gccaccaccg ccacagccga 180
cccgaggcgg caccgtcaacg caccgctcgg aggtggcgcg tggctctcgg ccacagccac 240
cttctacggc ggccggcgacg cgtccggcac catgggcgga cgtgtgggta cggaacacct 300
tacagccagg ggtacggcac caacacggcg gcgctgagca cggcgctctt caacaacggc 360
ctcagctcgg gcgctcgtt cgaggtcggg tgcgagcgcg cggggggcgcg cggccgctcg 420
trcmtgcmgg gctccgtcgt ggtgacggcc accaactctt gc

(2) INFORMATION FOR SEQ ID NO:1737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1737:

Asn Ile Ser Ser Leu His Thr Thr Pro Ala Ile Val Leu Arg Leu Ser
1 5 10 15
Ala Pro Pro His Thr Pro Arg Ser Asn Pro Met Ala Pro Arg Gln Ala
20 25 30
Val Leu Ala Val Val Leu Ala Ala Leu Leu Pro Leu Ala Leu Ser
35 40 45
Arg Gly Leu Arg Leu Gly His His Arg Pro Ala Ala Pro Glu Ala Ala
50 55 60
Arg Ser Arg Thr Ala Arg Arg Trp Arg Val Val Leu Gly Pro Arg His
65 70 75 80
Leu Leu Arg Arg Arg Arg Val Arg His His Gly Arg Thr Cys Gly
85 90 95
Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn Thr Ala Ala Leu
100 105 110

Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala Cys Phe Glu
115 120 125
Val Arg Cys Xaa Ala Ala Gly Gly Gly Arg Ser Xaa Xaa Gly
130 135 140
Ser Val Val Val Thr Ala Thr Asn Phe Cys
145 150

(2) INFORMATION FOR SEQ ID NO:1738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738:

His Leu Leu Thr Ser His His Ser Arg His Cys Pro Ala Pro Phe Cys
1 5 10 15
Thr Ala Thr His Thr Pro Leu Gln Ser Asn Gly Ala Ser Pro Ser Arg
20 25 30
Pro Arg Gly Arg Gly Pro Arg Arg Ala Ala Pro Ala Arg Pro Leu Ser
35 40 45
Arg Ala Ala Ala Trp Pro Pro Pro Ser Arg Thr Arg Gly Arg Thr
50 55 60
Val Thr His Arg Ser Glu Val Ala Arg Gly Pro Arg Pro Thr Pro Pro
65 70 75 80
Ser Thr Ala Ala Ala Thr Arg Pro Ala Pro Trp Ala Asp Val Trp Val
85 90 95
Arg Gln Pro Leu Gln Pro Gly Val Arg His Gln His Gly Gly Ala Glu
100 105 110
His Gly Ala Leu Gln Gln Arg Pro Gln Leu Arg Arg Leu Leu Arg Gly
115 120 125
Ala Val Arg Xaa Gly Gly Gly Arg Arg Pro Leu Xaa Xaa Xaa Gly Leu
130 135 140
Arg Arg Gly Asp Gly His Gln Leu Leu
145 150

(2) INFORMATION FOR SEQ ID NO:1739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739:

Met Ala Pro Arg Gln Ala Val Leu Ala Val Val Leu Ala Ala Leu
1 5 10 15
Leu Pro Leu Ala Leu Ser Arg Gly Leu Arg Leu Gly His His Arg Pro
20 25 30
Ala Ala Pro Glu Ala Ala Arg Ser Arg Thr Ala Arg Arg Trp Arg Val
35 40 45
Val Leu Gly Pro Arg His Leu Leu Arg Arg Arg Arg Arg Val Arg His
50 55 60
His Gly Arg Thr Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly
65 70 75 80
Thr Asn Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser

	85						90							95
Cys	Gly	Ala	Cys	Phe	Glu	Val	Arg	Cys	Xaa	Ala	Ala	Gly	Gly	Gly
			100					105					110	
Arg	Ser	Xaa	Xaa	Xaa	Gly	Ser	Val	Val	Val	Thr	Ala	Thr	Asn	Phe
		115					120						125	Cys

(2) INFORMATION FOR SEQ ID NO:1740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..436
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1740:

ggctatccag	gctccagtcg	tcccgcgatt	agttgtactg	tacattgttc	ctgcgaagac	60
actgggtcgt	ccgggtcaat	cggcagcttg	aacaagccat	ggcggcgcac	cggccgaacg	120
ccgcgcgcgc	gctgctcgcc	aagctcgacg	ccaccgccac	gcgcgcgcgc	aasgcanaca	180
agtaccctt	cttctgcgcc	gtgctcgcat	ccatgacctc	cgtgctcatg	ggctacaacg	240
tcgcggtgac	gagcggcgcg	cagatcttca	tggcgggagga	cctcgggatg	agcgacgcgc	300
agatcgaggt	gctctcgggg	gtcatcaaca	tatactcgct	cgtcggcgcg	ctgctggcag	360
gctggacatc	cgaccgtctc	ggcggcgccc	tcaccatcgt	cctcgccaac	gccttcttcc	420
tcgtcggccc	gctcgc					

(2) INFORMATION FOR SEQ ID NO:1741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1741:

Gly	Tyr	Pro	Gly	Ser	Ser	Arg	Pro	Arg	Ile	Ser	Cys	Thr	Val	His	Cys
1			5					10					15		
Ser	Cys	Glu	Asp	Thr	Gly	Ser	Ser	Gly	Ser	Ile	Gly	Ser	Leu	Asn	Lys
			20				25						30		
Pro	Trp	Arg	Arg	Thr	Gly	Arg	Thr	Pro	Arg	Arg	Arg	Cys	Ser	Pro	Ser
		35					40					45			
Ser	Thr	Pro	Pro	Pro	Arg	Arg	Arg	Arg	Xaa	Xaa	Thr	Ser	Thr	Pro	Ser
		50				55					60				
Ser	Ala	Pro	Cys	Ser	His	Pro									
65			70												

(2) INFORMATION FOR SEQ ID NO:1742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1742:

```

Met Ala Ala His Arg Pro Asn Ala Ala Ala Pro Leu Leu Ala Lys Leu
1          5          10          15
Asp Ala Thr Ala Thr Pro Pro Ala Xaa Ala Xaa Lys Tyr Pro Phe Phe
20          25          30
Cys Ala Val Leu Ala Ser Met Thr Ser Val Leu Met Gly Tyr Asn Val
35          40          45
Ala Val Thr Ser Gly Ala Gln Ile Phe Met Ala Glu Asp Leu Gly Met
50          55          60
Ser Asp Ala Gln Ile Glu Val Leu Ser Gly Val Ile Asn Ile Tyr Ser
65          70          75          80
Leu Val Gly Ala Leu Leu Ala Gly Trp Thr Ser Asp Arg Leu Gly Arg
85          90          95
Arg Leu Thr Ile Val Leu Ala Asn Ala Phe Phe Leu Val Gly Pro Leu
100          105          110

```

(2) INFORMATION FOR SEQ ID NO:1743:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501008

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1743:

```

Met Thr Ser Val Leu Met Gly Tyr Asn Val Ala Val Thr Ser Gly Ala
1          5          10          15
Gln Ile Phe Met Ala Glu Asp Leu Gly Met Ser Asp Ala Gln Ile Glu
20          25          30
Val Leu Ser Gly Val Ile Asn Ile Tyr Ser Leu Val Gly Ala Leu Leu
35          40          45
Ala Gly Trp Thr Ser Asp Arg Leu Gly Arg Arg Leu Thr Ile Val Leu
50          55          60
Ala Asn Ala Phe Phe Leu Val Gly Pro Leu
65          70

```

(2) INFORMATION FOR SEQ ID NO:1744:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 528 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..528
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501016

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744:

```

aagacttcgt cgtcaccacaa aaaataaagc agaaaaaac agagagtagt agactacgac      60
agcgctccgtc gaaccggagg gtcggaggcg gaggcgaaga tgaggaaagaa gctcggcacc      120
cggttccccc cggtcgaat caaaaagata atgcaagcag atgaggatgt tggaaagatt      180
gcattagcag tgacctgttt agtctcgagg gctcttgaat tgtttttaca agatttaatt      240
gaccggactt atgaaattac tcttcaaaagt ggagcgaaga cactgaattc cttccacctg      300
aagcaatgtg tgaagaggta cagttctttt gatttcctaa gataaaagag tggttacctag aagaagaag      360
ccagatcttg gtgtgtctga ttcagtgtga gatgaaagag tggttacctag aagaagaag      420
tcaaatggca gtgaccacaga gaatgatgaa tcaagatcta gtaaaatggc tataaganat      480
gcaaatacca ncnccagagg gacgtdggar gggtcgaggg agagggggc

```

(2) INFORMATION FOR SEQ ID NO:1745:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..143
(D) OTHER INFORMATION: / Ceres Seq. ID 1501017
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1745:
Met Arg Lys Lys Leu Gly Thr Arg Phe Pro Ala Ala Arg Ile Lys Lys
1 5 10 15
Ile Met Gln Ala Asp Glu Asp Val Gly Lys Ile Ala Leu Ala Val Pro
20 25 30
Val Leu Val Ser Arg Ala Leu Glu Leu Phe Leu Gln Asp Leu Ile Asp
35 40 45
Arg Thr Tyr Glu Ile Thr Leu Gln Ser Gly Ala Lys Thr Leu Asn Ser
50 55 60
Phe His Leu Lys Gln Cys Val Lys Arg Tyr Ser Ser Phe Asp Phe Leu
65 70 75 80
Thr Glu Val Val Ser Lys Val Pro Asp Leu Gly Gly Ala Asp Ser Cys
85 90 95
Gly Asp Glu Arg Val Leu Pro Arg Arg Arg Lys Ser Asn Gly Ser Asp
100 105 110
Pro Glu Asn Asp Glu Ser Arg Ser Lys Met Ala Ile Arg Xaa Ala
115 120 125
Asn Thr Xaa Xaa Arg Gly Thr Xaa Xaa Gly Ser Arg Gln Arg Ala
130 135 140
(2) INFORMATION FOR SEQ ID NO:1746:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..126
(D) OTHER INFORMATION: / Ceres Seq. ID 1501018
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1746:
Met Gln Ala Asp Glu Asp Val Gly Lys Ile Ala Leu Ala Val Pro Val
1 5 10 15
Leu Val Ser Arg Ala Leu Glu Leu Phe Leu Gln Asp Leu Ile Asp Arg
20 25 30
Thr Tyr Glu Ile Thr Leu Gln Ser Gly Ala Lys Thr Leu Asn Ser Phe
35 40 45
His Leu Lys Gln Cys Val Lys Arg Tyr Ser Ser Phe Asp Phe Leu Thr
50 55 60
Glu Val Val Ser Lys Val Pro Asp Leu Gly Gly Ala Asp Ser Cys Gly
65 70 75 80
Asp Glu Arg Val Leu Pro Arg Arg Arg Lys Ser Asn Gly Ser Asp Pro
85 90 95
Glu Asn Asp Glu Ser Arg Ser Ser Lys Met Ala Ile Arg Xaa Ala Asn
100 105 110
Thr Xaa Xaa Arg Gly Thr Xaa Xaa Gly Ser Arg Gln Arg Ala
115 120 125
(2) INFORMATION FOR SEQ ID NO:1747:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 538 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..538
(D) OTHER INFORMATION: / Ceres Seq. ID 1501023

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747:

atccgcctcc	gaaccacaga	ggccacgacc	cactactaca	tcagtccacc	gccaccgcgc	60
accgcgagtc	cgcgacagac	atccgcgccc	cggcctcact	ctcactcccc	agtcccccacc	120
gtgccgccac	aagcgacgcg	acgcagccac	gcaggagag	ggaaatggcc	acggccgcga	180
ctgccacggc	ggggagtaga	gcagccgtgc	tgtctgtct	ctcgctggcg	ctggcgctgg	240
cgtcgccgcc	ctccgacgcc	ggcgccggcg	gcgactgcc	cttcccggcc	gtgttcaact	300
tcggcgactc	caactcggac	acggcgccgc	tgtcatcgct	cttcggcgcc	gcaccgccgc	360
caaacggcag	gaccttcttc	ggcatgcccg	cmggccgcta	ctgcgatggt	cgctcgtca	420
tcgacttcat	cgtgaaacc	tggggctgac	tcacctcagt	gcgtacctga	actcgatcgg	480
aagcaacttc	acacagggag	ccaactttgc	aacagctggt	tcatgatca	gaagacag	

- (2) INFORMATION FOR SEQ ID NO:1748:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..179
(D) OTHER INFORMATION: / Ceres Seq. ID 1501024

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748:

Ile	Arg	Leu	Arg	Thr	His	Glu	Ala	Thr	Thr	His	Tyr	Tyr	Ile	Ser	Pro
1			5					10					15		
Pro	Pro	Pro	Arg	Thr	Ala	Ser	Pro	Arg	Gln	Thr	Ser	Ala	Pro	Arg	Pro
			20					25				30			
His	Ser	His	Ser	Pro	Val	Pro	Thr	Val	Pro	Pro	Gln	Ala	Thr	Arg	Arg
		35					40				45				
Ser	His	Ala	Gly	Arg	Gly	Lys	Trp	Pro	Arg	Pro	Arg	Leu	Pro	Arg	Arg
	50					55				60					
Gly	Val	Glu	Gln	Pro	Cys	Cys	Cys	Cys	Ser	Arg	Trp	Arg	Trp	Arg	Trp
	65				70				75					80	
Arg	Cys	Gly	Pro	Pro	Thr	Pro	Ala	Arg	Ala	Ala	Thr	Ala	Thr	Ser	Arg
			85					90						95	
Pro	Cys	Ser	Thr	Ser	Ala	Thr	Pro	Thr	Arg	Thr	Arg	Ala	Ala	Cys	His
			100					105				110			
Arg	Ser	Ser	Ala	Pro	His	Arg	Arg	Pro	Thr	Ala	Gly	Pro	Ser	Ser	Ala
			115				120					125			
Cys	Pro	Xaa	Ala	Ala	Thr	Ala	Met	Val	Ala	Ser	Ser	Ser	Thr	Ser	Ser
			130			135					140				
Leu	Lys	Pro	Gly	Ala	Asp	Ser	Pro	Gln	Cys	Val	Pro	Glu	Leu	Asp	Arg
					150					155				160	
Lys	Gln	Leu	His	Thr	Gly	Ser	Gln	Leu	Cys	Asn	Ser	Trp	Phe	Ile	Asp
					165				170					175	
Gln	Lys	Thr													

- (2) INFORMATION FOR SEQ ID NO:1749:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1501025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749:

```
Pro Pro Pro Asn Pro Arg Gly His Asp Pro Leu Leu His Gln Ser Thr
1      5      10      15
Ala Thr Ala His Arg Glu Ser Ala Thr Asp Ile Arg Ala Pro Ala Ser
20      25      30
Leu Ser Leu Pro Ser Pro His Arg Ala Ala Thr Ser Asp Ala Thr Gln
35      40      45
Pro Arg Arg Glu Arg Glu Met Ala Thr Ala Ala Thr Ala Thr Ala Gly
50      55      60
Ser Arg Ala Ala Val Leu Leu Leu Ser Leu Ala Leu Ala Leu Ala
65      70      75      80
Leu Arg Pro Ser Asp Ala Gly Ala Gly Gly Asp Cys His Phe Pro Ala
85      90      95
Val Phe Asn Phe Gly Asp Ser Asn Ser Asp Thr Gly Gly Leu Ser Ser
100      105      110
Leu Phe Gly Ala Ala Pro Pro Pro Asn Gly Arg Thr Phe Phe Gly Met
115      120      125
Pro Xaa Gly Arg Tyr Cys Asp Gly Arg Leu Val Ile Asp Phe Ile Ala
130      135      140
Glu Thr Trp Gly
145
```

(2) INFORMATION FOR SEQ ID NO:1750:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1501026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750:

```
Met Ala Thr Ala Ala Thr Ala Thr Ala Gly Ser Arg Ala Ala Val Leu
1      5      10      15
Leu Leu Leu Ser Leu Ala Leu Ala Leu Ala Leu Arg Pro Ser Asp Ala
20      25      30
Gly Ala Gly Gly Asp Cys His Phe Pro Ala Val Phe Asn Phe Gly Asp
35      40      45
Ser Asn Ser Asp Thr Gly Gly Leu Ser Ser Leu Phe Gly Ala Ala Pro
50      55      60
Pro Pro Asn Gly Arg Thr Phe Phe Gly Met Pro Xaa Gly Arg Tyr Cys
65      70      75      80
Asp Gly Arg Leu Val Ile Asp Phe Ile Ala Glu Thr Trp Gly
85      90
```

(2) INFORMATION FOR SEQ ID NO:1751:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 487 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..487

(D) OTHER INFORMATION: / Ceres Seq. ID 1501027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1751:

```
acctccctcag tcaggccgctc ccgcgccgac gtcaacggag acgtgtcaac ggcggcggtg
agaagacccta taaccttcta gatttttttc cgctgcctca atggatctct gggagagggc
```

60
120

(2) INFORMATION FOR SEQ ID NO:1752:

(A) LENGTH: 88 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lipid

MOLECULE TYPE: peptide

(IX) FEATURE:
(A) NAM

(A) NAME/KEY: peptide
(B) LOCATION: 1-88

(B) LOCATION: 1..88
(D) OTHER INFORMATION:

(D) OTHER INFORMATION: 7 Ceres Seq. ID 1501028
SEQUENCE DESCRIPTION: SEQ ID NO:1752:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732:
Ser Ser Gln Ala Val Pro Arg Arg Arg Gln Ar

(2) INFORMATION FOR SEQ ID NO:1753:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

```
{ix} FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1501029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1753:

(2) INFORMATION FOR SEQ ID NO:1754:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..513
(D) OTHER INFORMATION: / Ceres Seq. ID 1501037
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1754:
gtgctgcccgc cagatctaac caaaccccgcc gccctcctca cgcgtccggcg agctacggac 60
tcagcagatc accgtcgctc gagttgtacc tgaaggcggtg ccgctggaac cggccgcgag 120
ataagggcgcg cggaagcgcg ggcgcagcatg ccggtggcag cgtcgcccat ctacttcctc 180
aaccttcgcg gggacgtcct catcaaccgc ctctaccgtg atgatgttgg gggaaatatg 240
gttgatcgctg tcagaatgca tatcatgcaa acaaaagaac ttggcacatg ccctgttcgt 300
caaataggag gctgctcctt cctttatatg aggatcagta atgtttacat tgtgatcgta 360
gttagcagca atgctaatgt tgcattgtct tcaaaatttg ttgctgaggg ggtggctctc 420
ttcaagtctc acttcgggtg agcttttgat gaagacgcta tcaggaataa ctttgttttt 480
atatatgaac ttcttgatga gatcatggat ttt
(2) INFORMATION FOR SEQ ID NO:1755:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..122
(D) OTHER INFORMATION: / Ceres Seq. ID 1501038
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1755:
Met Pro Val Ala Ala Ser Ala Ile Tyr Phe Leu Asn Leu Arg Gly Asp
1 5 10 15
Val Leu Ile Asn Arg Leu Tyr Arg Asp Asp Val Gly Gly Asn Met Val
20 25 30
Asp Ala Phe Arg Met His Ile Met Gln Thr Lys Glu Leu Gly Thr Cys
35 40 45
Pro Val Arg Gln Ile Gly Gly Cys Ser Phe Leu Tyr Met Arg Ile Ser
50 55 60
Asn Val Tyr Ile Val Ile Val Val Ser Ser Asn Ala Asn Val Ala Cys
65 70 75 80
Xaa Phe Lys Phe Val Val Glu Ala Val Ala Leu Phe Lys Ser Tyr Phe
85 90 95
Gly Gly Ala Phe Asp Glu Asp Ala Ile Arg Asn Asn Phe Val Leu Ile
100 105 110
Tyr Glu Leu Leu Asp Glu Ile Met Asp Phe
115 120
(2) INFORMATION FOR SEQ ID NO:1756:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..92
(D) OTHER INFORMATION: / Ceres Seq. ID 1501039
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1756:
Met Val Asp Ala Phe Arg Met His Ile Met Gln Thr Lys Glu Leu Gly
1 5 10 15

Thr Cys Pro Val Arg Gln Ile Gly Gly Cys Ser Phe Leu Tyr Met Arg
20 25 30
Ile Ser Asn Val Tyr Ile Val Ile Val Val Ser Ser Asn Ala Asn Val
35 40 45
Ala Cys Xaa Phe Lys Phe Val Val Glu Ala Val Ala Leu Phe Lys Ser
50 55 60
Tyr Phe Gly Gly Ala Phe Asp Glu Asp Ala Ile Arg Asn Asn Phe Val
65 70 75 80
Leu Ile Tyr Glu Leu Leu Asp Glu Ile Met Asp Phe
85 90

(2) INFORMATION FOR SEQ ID NO:1757:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1501040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1757:

Met His Ile Met Gln Thr Lys Glu Leu Gly Thr Cys Pro Val Arg Gln
1 5 10 15
Ile Gly Gly Cys Ser Phe Leu Tyr Met Arg Ile Ser Asn Val Tyr Ile
20 25 30
Val Ile Val Val Ser Ser Asn Ala Asn Val Ala Cys Xaa Phe Lys Phe
35 40 45
Val Val Glu Ala Val Ala Leu Phe Lys Ser Tyr Phe Gly Gly Ala Phe
50 55 60
Asp Glu Asp Ala Ile Arg Asn Asn Phe Val Leu Ile Tyr Glu Leu Leu
65 70 75 80
Asp Glu Ile Met Asp Phe
85

(2) INFORMATION FOR SEQ ID NO:1758:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..405

(D) OTHER INFORMATION: / Ceres Seq. ID 1501058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758:

accagtcgcc ttacatccca cacacaacgc gcaccacacc acaccacacc acccgagcgc 60
aacgtccgag accaaactcc gatccccact atgcccggcg acgggggagcg gctggcgccg 120
gccgtccact tctggggcgga gcacccggcc acggaggcgcg agttctactc ggcgcacggc 180
acggaggcgcg agccctccta cttcaccacg ccgacgcgcg gcgcccggcg gctcttcacg 240
cgcgctgga ggccccgcgc gcccgadcg cccaggcgcg tcgtgttcat ggtccacggc 300
tacggcaatg acatcagctg gaagttccag tccacggcgg tcttctctcg gcgggtccggg 360
ttcgctgct tcgcggcgga cctcccgggc cagcgcgct cccac

(2) INFORMATION FOR SEQ ID NO:1759:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..135
(D) OTHER INFORMATION: / Ceres Seq. ID 1501059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1759:

Thr	Ser	Pro	Leu	Tyr	Ile	His	Thr	Gln	Arg	Ala	Pro	His	His	Thr	Thr
1				5				10						15	
Pro	Pro	Asp	Ala	Asn	Val	Arg	Asp	Gln	Thr	Pro	Ile	Pro	Thr	Met	Pro
			20					25					30		
Ala	Asp	Gly	Glu	Ala	Leu	Ala	Pro	Ala	Val	His	Phe	Trp	Gly	Glu	His
			35					40					45		
Pro	Ala	Thr	Glu	Ala	Glu	Phe	Tyr	Ser	Ala	His	Gly	Thr	Glu	Gly	Glu
			50				55				60				
Pro	Ser	Tyr	Phe	Thr	Thr	Pro	Asp	Ala	Gly	Ala	Arg	Arg	Leu	Phe	Thr
				70					75					80	
Arg	Ala	Trp	Arg	Pro	Arg	Ala	Pro	Xaa	Arg	Pro	Arg	Ala	Leu	Val	Phe
				85					90					95	
Met	Val	His	Gly	Tyr	Gly	Asn	Asp	Ile	Ser	Trp	Thr	Phe	Gln	Ser	Thr
				100				105					110		
Ala	Val	Phe	Leu	Ala	Arg	Ser	Gly	Phe	Ala	Cys	Phe	Ala	Ala	Asp	Leu
				115				120					125		
Pro	Gly	His	Gly	Arg	Ser	His									
				130				135							

(2) INFORMATION FOR SEQ ID NO:1760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..134
(D) OTHER INFORMATION: / Ceres Seq. ID 1501060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1760:

Pro	Val	Pro	Phe	Thr	Ser	Thr	His	Asn	Ala	His	His	Thr	Thr	Pro	His
1				5				10						15	
His	Pro	Thr	Pro	Thr	Ser	Glu	Thr	Lys	Leu	Arg	Ser	Pro	Leu	Cys	Arg
				20				25					30		
Arg	Thr	Gly	Arg	Arg	Trp	Arg	Arg	Pro	Ser	Thr	Ser	Gly	Ala	Ser	Thr
				35			40					45			
Arg	Pro	Arg	Arg	Arg	Ser	Ser	Thr	Arg	Arg	Thr	Ala	Arg	Arg	Ala	Ser
				50			55				60				
Pro	Pro	Thr	Ser	Pro	Arg	Pro	Thr	Arg	Ala	Pro	Gly	Gly	Ser	Ser	Arg
				70					75					80	
Ala	Arg	Gly	Gly	Pro	Ala	Arg	Pro	Xaa	Gly	Pro	Gly	Arg	Ser	Cys	Ser
				85				90						95	
Trp	Ser	Thr	Ala	Thr	Ala	Met	Thr	Ser	Ala	Gly	Arg	Ser	Ser	Pro	Arg
				100				105					110		
Arg	Ser	Ser	Ser	Arg	Gly	Pro	Gly	Ser	Pro	Ala	Ser	Arg	Pro	Thr	Ser
				115				120					125		
Arg	Ala	Thr	Ala	Ala	Pro										
				130											

(2) INFORMATION FOR SEQ ID NO:1761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1501061

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1761:

Met Pro Ala Asp Gly Glu Ala Leu Ala Pro Ala Val His Phe Trp Gly
1 5 10 15
Glu His Pro Ala Thr Glu Ala Glu Phe Tyr Ser Ala His Gly Thr Glu
20 25 30
Gly Glu Pro Ser Tyr Phe Thr Thr Pro Asp Ala Gly Ala Arg Arg Leu
35 40 45
Phe Thr Arg Ala Trp Arg Pro Arg Ala Pro Xaa Arg Pro Arg Ala Leu
50 55 60
Val Phe Met Val His Gly Tyr Gly Asn Asp Ile Ser Trp Thr Phe Gln
65 70 75 80
Ser Thr Ala Val Phe Leu Ala Arg Ser Gly Phe Ala Cys Phe Ala Ala
85 90 95
Asp Leu Pro Gly His Gly Arg Ser His
100 105

(2) INFORMATION FOR SEQ ID NO:1762:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..503

(D) OTHER INFORMATION: / Ceres Seq. ID 1501090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1762:

aactcaaacg agtccattt tggcaaggct tcggagtacc aaactggcga attgcgacgt 60
tgccggaatt gtaatggcaa taattccttc ctccctcggt cccattttct cctcttttcta 120
ggttttacc cctcatcggt cctcgctcca cggccatggt gaggatgaag caggtaaaaga 180
tctcggtaaa gaaggacgtg gattcgatca caatccgcgg cactaacaag gtcgtccatg 240
tgccgcaactg cgtgctgatg cgggcgtcgg actcggacaa gcagccgat gtrgcgcggg 300
tgagagaagt ggargccgac ggacgcggca gctgncgggt rcaggtrcgc tggactacc 360
gccctgagga atccaaagggc ggtcgcggc agttccacgg gcaccaaggag cttttccatt 420
ccgatcattt cgacctacag arcgcccaca ccatcgaggg gaaatgtgtt gtccactott 480
tcaagaacta caccaagcct gat

(2) INFORMATION FOR SEQ ID NO:1763:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1501091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1763:

Met Val Arg Met Lys Gln Val Lys Ile Ser Val Lys Lys Asp Val Asp
1 5 10 15
Ser Tyr Thr Ile Arg Gly Thr Asn Lys Val Val His Val Gly Asp Cys
20 25 30
Val Leu Met Arg Ala Ser Asp Ser Asp Lys Gln Pro Tyr Xaa Ala Arg
35 40 45
Val Glu Lys Met Xaa Ala Asp Gly Arg Gly Xaa Xaa Arg Xaa Gln Xaa
50 55 60
Arg Trp Tyr Trp Arg Pro Glu Glu Ser Lys Gly Gly Arg Arg Gln Phe
65 70 75 80
His Gly Ala Lys Glu Leu Phe Leu Ser Asp His Phe Asp Leu Gln Xaa

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 547 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..547
(D) OTHER INFORMATION: / Ceres Seq. ID 1501115
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1766:
acgccaccgc cacctccacc tctcgaaac cgccgcgacc gatcgagcga abwnccttc 60
cgccgcccgc gccgaacccc tagctcctct tacgccatgg ccaccgtgtc gctcactccg 120
caggcggtct tctccaccga gtcggcgccg gccttggctt ctgccaccat cctccgtctc 180
ccgccaaact tegtacgccg gctcagcacc aaggcacgac gcaactgcag caacatcgcc 240
gtcgcgcaga tegtgcgcgc cgcttggttc gactgctcgc ctgctgcgcg cctccgcggc 300
ggcggnatgtc agcgcaattc ctaacgctaa gtttgcgcas cgtccgcccgt cgtattggcc 360
gagcgtaacc tgctcggttc cgacgcgcgc ctccgcgtcc acggggggga raggctkkgg 420
agaaggatag ccaacggatgc tatcaccacg ccggtagtga acacgtcggc ctactggttc 480
aacaactcgc aagagctaata cgactttaan ggggggargc atgctagctt cgagtattgg 540
aggtatkc

(2) INFORMATION FOR SEQ ID NO:1767:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..107
(D) OTHER INFORMATION: / Ceres Seq. ID 1501116
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767:
Thr Pro Pro Pro Pro Pro Pro Pro Arg Asn Arg Arg Asp Arg Ser Ser
1 5 10 15
Glu Xaa Xaa Phe Pro Arg Arg Arg Arg Asn Pro Ser Ser Ser Tyr Ala
20 25 30
Met Ala Thr Val Ser Leu Thr Pro Gln Ala Val Phe Ser Thr Glu Ser
35 40 45
Gly Gly Ala Leu Ala Ser Ala Thr Ile Leu Arg Phe Pro Pro Asn Phe
50 55 60
Val Arg Gln Leu Ser Thr Lys Ala Arg Arg Asn Cys Ser Asn Ile Gly
65 70 75 80
Val Ala Gln Ile Val Ala Ala Ala Trp Ser Asp Cys Leu Ala Ala Arg
85 90 95
Arg Leu Arg Xaa Ala Xaa Cys Gln Arg Asn Ser
100 105

(2) INFORMATION FOR SEQ ID NO:1768:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..142
(D) OTHER INFORMATION: / Ceres Seq. ID 1501117
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1768:
Arg His Arg His Leu His Leu Leu Glu Thr Ala Ala Thr Asp Arg Ala
1 5 10 15
Xaa Xaa Pro Ser Arg Ala Asp Ala Glu Thr Leu Ala Pro Leu Thr Pro
20 25 30
Trp Pro Pro Cys Arg Ser Leu Arg Arg Ser Ser Pro Pro Ser Pro

35	40	45
Ala Ala Pro Trp Leu Leu Pro Pro Ser Ser Ala Ser Arg Gln Thr Ser		
50	55	60
Tyr Ala Ser Ser Ala Pro Arg His Asp Ala Thr Ala Ala Thr Ser Ala		
65	70	75
Ser Arg Arg Ser Ser Pro Pro Arg Gly Pro Thr Ala Ser Leu Leu Ala		
85	90	95
Ala Ser Ala Xaa Arg Xaa Val Ser Ala Ile Pro Asn Ala Lys Val Ala		
100	105	110
Xaa Arg Pro Pro Ser Tyr Trp Pro Ser Val Thr Cys Ser Ala Pro Thr		
115	120	125
Pro Ala Ser Pro Ser Thr Arg Gly Xaa Gly Xaa Glu Glu Gly		
130	135	140

(2) INFORMATION FOR SEQ ID NO:1769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1769:

Met Ala Thr Val Ser Leu Thr Pro Gln Ala Val Phe Ser Thr Glu Ser	
1	5
Gly Gly Ala Leu Ala Ser Ala Thr Ile Leu Arg Phe Pro Pro Asn Phe	
20	25
Val Arg Gln Leu Ser Thr Lys Ala Arg Arg Asn Cys Ser Asn Ile Gly	
35	40
Val Ala Gln Ile Val Ala Ala Ala Trp Ser Asp Cys Leu Ala Ala Arg	
50	55
Arg Leu Arg Xaa Ala Xaa Cys Gln Arg Asn Ser	
65	70
	75

(2) INFORMATION FOR SEQ ID NO:1770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..921
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1770:

artagcttc	cwccrrctc	crggggtcc	gcrgctccgc	tagtccgctc	cgccgcaccg	60
gcccggctcg	gaggggcgt	tcggggagg	cgaacgganc	gccagcggtt	ccgttttggt	120
ggcgtggagg	cgaactgctg	ctggagcgct	accggggtt	ctcccggtta	ctagcgctcg	180
cgatctgatg	atcgctggct	agtgctctg	ccagartccc	agccagcgct	cctccgcat	240
gatccargcg	gtgatgtga	tcagcaccca	ggccaagccc	cgctctctca	agttctacag	300
tttccagcca	cccagagaac	atcaggacct	cgctcgctgt	gtctccaat	tactctctgc	360
aaggcccgag	agcgcagaca	attttgtcaa	ggtggactcc	atctttggcc	cgggaaacaaa	420
aatgtctcac	aagcatttgg	gccacactat	actttgtttt	tgtctttgat	agctctgaga	480
acgagcttgc	catgctcgac	ctcgtacaag	tgtttgttga	aacattggac	agatgcttca	540
agaatgtatg	cgagcttgac	atcgtattta	acttcaacaa	gctgcacacc	attttgatg	600
agatgatata	ggggggagac	gtgatcgaaa	caagttccga	acagataatg	aaatctgtgg	660
aagagattga	aagcgtggag	aaacaatcga	gcacaaccag	cttcataccc	aagtcgatta	720
cagagcggtt	taccgcttga	gcttcacact	gtttccagaa	caatgtgaca	tttaaggtgt	780
gaacagaact	gagatatata	attcagttct	atttagtttc	tcgcataaga	ccctgtatgc	840

ccccgccccc cggtgtgatt ctgtaagcct gtaacctgga tatgaatgcg gcatctgcag 900
tccaataata ctgcctgcgt t

(2) INFORMATION FOR SEQ ID NO:1771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1771:

Met	Ile	Xaa	Ala	Val	Met	Val	Ile	Ser	Thr	Gln	Ala	Lys	Pro	Arg	Leu	
1				5					10					15		
Leu	Lys	Phe	Tyr	Ser	Phe	Gln	Pro	Pro	Glu	Lys	His	Gln	Asp	Leu	Val	
			20						25					30		
Arg	Cys	Val	Phe	Gln	Leu	Leu	Ser	Ala	Arg	Pro	Glu	Ser	Ala	Ser	Asn	
			35					40					45			
Phe	Val	Lys	Val	Asp	Ser	Ile	Phe	Gly	Pro	Gly	Thr	Lys	Met	Val	Tyr	
			50				55					60				
Lys	His	Leu	Gly	His	Thr	Ile	Leu	Cys	Phe	Cys	Leu					
65					70						75					

(2) INFORMATION FOR SEQ ID NO:1772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1772:

Met	Val	Ile	Ser	Thr	Gln	Ala	Lys	Pro	Arg	Leu	Leu	Lys	Phe	Tyr	Ser	
1				5					10					15		
Phe	Gln	Pro	Pro	Glu	Lys	His	Gln	Asp	Leu	Val	Arg	Cys	Val	Phe	Gln	
			20					25						30		
Leu	Leu	Ser	Ala	Arg	Pro	Glu	Ser	Ala	Ser	Asn	Phe	Val	Lys	Val	Asp	
			35					40					45			
Ser	Ile	Phe	Gly	Pro	Gly	Thr	Lys	Met	Val	Tyr	Lys	His	Leu	Gly	His	
			50				55					60				
Thr	Ile	Leu	Cys	Phe	Cys	Leu										
65					70											

(2) INFORMATION FOR SEQ ID NO:1773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1773:

Met	Leu	Asp	Leu	Val	Gln	Val	Phe	Val	Glu	Thr	Leu	Asp	Arg	Cys	Phe	
1				5					10					15		
Lys	Asn	Val	Cys	Glu	Leu	Asp	Ile	Val	Phe	Asn	Phe	Asn	Lys	Leu	His	

(2) INFORMATION FOR SEQ ID NO:1774:

(A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..352
(D) OTHER INFORMATION: / Ceres Seq. ID 1501123

acagagggat	cgtcatccgc	cccaccaca	actgctcag	atccaggcac	ggcacggcac	60
ggcgccagcg	ccgaacccaag	cccgctctct	ctctctctct	gtccctctcct	cactcgcggc	120
gacgtgcaca	gacaacgcga	cgcgcgcgca	satnancgt	gtccaaggca	cgacagccgc	180
agccaaccaa	tgcgctccgt	ccgggtctcg	tggtggcccg	aatggccctc	ctcgatcagc	240
tctggggcga	gacggtggcc	ggccctccgc	cgagatccac	ctctggcaag	ctccgcaagt	300
actctctctt	ctccccctcc	tgtctctcgt	ctgctctcat	cctggctccc	gc	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..117
(D) OTHER INFORMATION: / Ceres Seq. ID 1501124

[illegible]

(2) INFORMATION FOR SEQ ID NO:1776:

(A) LENGTH: 116 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..116
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501125
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1776:
Arg Gly Ile Val Ile Arg Pro Thr His Asn Cys Ser Arg Ser Arg His
1 5 10 15
Gly Thr Ala Arg Gln Pro Gly Gln Pro Lys Pro Val Phe Ser Ser Leu
 20 25 30
Ser Ser Val Pro His Ser Pro Arg Arg Asp Lys Thr Thr Arg Arg Ala
 35 40 45
Arg Xaa Xaa Xaa Ser Ser Lys Ala Arg Arg Gly Gln Pro Thr Asn Arg
50 55 60
Val Arg Pro Gly Leu Val Val Ala Gly Met Gly Leu Leu Asp Gln Leu
65 70 75 80
Trp Asp Glu Thr Val Ala Gly Pro Arg Pro Asp Ser Gly Leu Gly Lys
 85 90 95
Leu Arg Lys Tyr Ser Ser Phe Ser Ser Pro Ser Ser Ser Ser Ser
100 105 110
Ile Leu Ala Pro
115

(2) INFORMATION FOR SEQ ID NO:1777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1777:

acaaacgaac	aaggcattaa	tctctccaa	tctccagtg	atcccgggta	accaaataca	60
atcagccctt	tcttttgcta	cggttttgta	tttcatcgtg	tcgcccaaga	aaatcgaagg	120
aacgcgcgcg	caccggccgc	aacaaagcaa	agcaggcctc	cggtctccctg	aactgacttc	180
agaagtccac	aacgcaccca	gcacagacag	aagaccctcg	ccggacgcgc	gtcttcgcgc	240
gggacaactc	aatcccagag	ccaggatggc	ccgctacgat	cgcgcgatca	ccgtgttttc	300
accgcagcgc	cacctcttcc	aggtcagagta	cgccctcgag	gccgtccgca	agggcaacgc	360
cgctgtcggc	gtccgcggcg	tcgacaccgt	cgctctcgcg	gtcgagaaga	atgccaccgc	420
caagctccag	gactccaggt	ccgtregcaa	gatcgtkagc	ctggacaccc	acatcgcg	

(2) INFORMATION FOR SEQ ID NO:1778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1778:

Gln Thr Asn Lys Ala Leu Ile Ser Ser Asn Pro Pro Val Ile Pro Gly
1 5 10 15
Asn Gln Ile Lys Ser Ala Leu Ser Phe Ala Thr Val Leu Tyr Phe Ile
 20 25 30
Val Ser Pro Lys Lys Ile Glu Gly Thr Arg Arg His Arg Pro Gln Gln
35 40 45
Ser Lys Ala Gly Leu Arg Leu Pro Glu Leu Thr Ser Glu Val Thr Asn

50	55	60
Ala Pro Ser Thr Asp Arg Arg Pro Ser Pro Asp Ala Arg Ser Arg Arg		
65	70	75
Gly Gln Leu Asn Pro Glu Ala Arg Met Ala Arg Tyr Asp Arg Ala Ile		80
	85	90
Thr Val Phe Ser Pro Asp Gly His Leu Phe Gln Val Glu Tyr Ala Leu		95
	100	105
Glu Ala Val Arg Lys Gly Asn Ala Ala Val Gly Val Arg Gly Val Asp		110
	115	120
Thr Val Val Leu Gly Val Glu Lys Lys Ser Thr Pro Lys Leu Gln Asp		125
	130	135
Ser Arg Ser Xaa Arg Lys Ile Xaa Ser Leu Asp Thr His Ile		140
145	150	155

(2) INFORMATION FOR SEQ ID NO:1779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..442
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1779:

atcatgcatt	cttcatggcg	acgggtgacca	gtttgagctt	ctcaggcagc	tgcagacacg	60
ggccacgcta	tactgcccgg	ccggcgccag	ttctcgtagt	agtcagctac	ttaatgatca	120
gctagctaga	gcattcgcgna	gattacaagt	ngcggcgggc	atggcggtgg	cgcggttccc	180
ttctcggcgc	gccttcgccc	ctccttgcc	agtgcgtaca	aggagagcct	tctcctcggt	240
ggtggccatg	gcttcgcgag	ccccgggtgag	agctccacg	aggaagccct	tcgcccctcc	300
tcgcgaggtg	caacgcgccg	tggcgcacto	gctgcccccg	cagaagcggg	agatcttcga	360
gtgcgtcgag	tcgtggcgcg	cggacaacat	ccgtgtgtgc	ctcaagcccg	tggagagggtc	420
ctggcagccg	cagactacct	gc				

(2) INFORMATION FOR SEQ ID NO:1780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1780:

Ser Cys Ile Leu His Gly Asp Gly Asp Gln Phe Glu Leu Leu Arg Gln		
1	5	10
Leu Gln Thr Arg Ala Thr Leu Tyr Cys Pro Ala Gly Gly Ser Ser Arg		15
	20	25
Ser Ser Gln Leu Leu Asn Asp Gln Leu Ala Arg Ala Ser Xaa Arg Leu		30
	35	40
Gln Xaa Ala Ala Gly Met Ala Val Ala Ala Phe Pro Ser Cys Gly Ala		45
	50	55
Phe Ala Pro Pro Cys Leu Val Ser Thr Arg Arg Ala Phe Ser Ser Val		60
65	70	75
Val Ala Met Ala Ser Ala Ala Pro Val Arg Ala Pro Ser Arg Lys Pro		80
	85	90
Phe Ala Pro Pro Arg Glu Val His Arg Pro Val Ala His Ser Leu Pro		95
	100	105
Pro Gln Lys Arg Glu Ile Phe Glu Ser Leu Xaa Ser Trp Ala Ala Asp		110
	115	120
		125

Asn Ile Leu Val Leu Leu Lys Pro Val Glu Arg Ser Trp Gln Pro Gln
130 135 140
Thr Thr Cys
145

(2) INFORMATION FOR SEQ ID NO:1781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1781:

Met Ala Val Ala Ala Phe Pro Ser Cys Gly Ala Phe Ala Pro Pro Cys
1 5 10 15
Leu Val Ser Thr Arg Arg Ala Phe Ser Ser Val Val Ala Met Ala Ser
20 25 30
Ala Ala Pro Val Arg Ala Pro Ser Arg Lys Pro Phe Ala Pro Pro Arg
35 40 45
Glu Val His Arg Pro Val Ala His Ser Leu Pro Pro Gln Lys Arg Glu
50 55 60
Ile Phe Glu Ser Leu Xaa Ser Trp Ala Ala Asp Asn Ile Leu Val Leu
65 70 75 80
Leu Lys Pro Val Glu Arg Ser Trp Gln Pro Gln Thr Thr Cys
85 90

(2) INFORMATION FOR SEQ ID NO:1782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..464
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1782:

atcgccgcgcgttctctctcctctctctcccgcccccttcac tccaccaacg aacccccacgc 60
aggcgagcagc acgcgcgaasc gcaagggaag cacaacacat annngccggg catggcgagc 120
cgggcggaagc tggagaaggcg cgggcggcgag aggaaggagc ccggcaaggt gccgtgcggc 180
ctgtaccgcgc agcagcargg ggagcgggag tnggtgccct ggctcgtccc cgtcatcttc 240
gtcgccagca tcaccgctct cgtgctcaacc atgtacgcc acaactgcmc cgcgcgagc 300
accaacaagt ggtgcggccg ctctctcgmm cgcttctcct tccagccgct gcgacagaac 360
cgctctcttg ggccctcttc cgccacgctc accaagatgg gggccctggt gtgggagaag 420
gtgggtgacc gccaccaggg ctggcgccct ctctccagca tgtk

(2) INFORMATION FOR SEQ ID NO:1783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1783:

Ile Ala Arg Xaa Pro Leu Leu Ser Ser Pro Ala Pro Ser Leu His Gln

1	5	10	15
Arg Thr Pro Arg Arg Gln Gln His Ala Gln Xaa Gln Gly Arg His Lys			
	20	25	30
His Xaa Xaa Pro Gly Met Ala Thr Arg Ala Asp Val Glu Lys Gly Gly			
	35	40	45
Pro Ala Arg Lys Glu Pro Gly Lys Val Pro Ser Pro Leu Tyr Pro Gln			
	50	55	60
His Xaa Gly Glu Arg Glu Xaa Val Pro Trp Leu Val Pro Val Ile Phe			
	65	70	75
Val Ala Ser Ile Thr Val Phe Val Val Thr Met Tyr Ala Asn Asn Cys			
	85	90	95
Xaa Ala Arg Asp Thr Asn Lys Cys Val Ala Arg Phe Leu Xaa Arg Phe			
	100	105	110
Ser Phe Gln Pro Leu Arg Gln Asn Pro Leu Phe Gly Pro Ser Ser Ala			
	115	120	125
Thr Leu Thr Lys Met Gly Ala Leu Val Trp Glu Lys Val Val His Arg			
	130	135	140
His Gln Gly Trp Arg Leu Leu Ser Ser Met			
	145	150	

(2) INFORMATION FOR SEQ ID NO:1784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1501144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1784:

Ser Pro Xaa Val Leu Ser Ser Pro Pro Arg Pro Leu His Ser Thr Asn			
1	5	10	15
Glu Pro His Ala Gly Ser Ser Thr Arg Xaa Arg Lys Glu Gly Thr Asn			
	20	25	30
Thr Xaa Xaa Arg Ala Trp Arg Arg Gly Arg Thr Trp Arg Arg Ala Gly			
	35	40	45
Arg Arg Gly Arg Ser Pro Ala Arg Cys Arg Arg Arg Cys Thr Arg Ser			
	50	55	60
Thr Xaa Gly Ser Gly Ser Xaa Cys Pro Gly Ser Ser Pro Ser Ser Ser			
	65	70	75
Ser Pro Ala Ser Pro Ser Ser Ser Ser Pro Cys Thr Pro Thr Thr Xaa			
	85	90	95
Pro Arg Ala Thr Pro Thr Ser Ala Ser Pro Ala Ser Ser Xaa Ala Ser			
	100	105	110
Pro Ser Ser Arg Cys Asp Arg Thr Arg Ser Ser Gly Pro Pro Pro Pro			
	115	120	125
Arg Ser Pro Arg Trp Gly Pro Trp Cys Gly Arg Arg Trp Cys Thr Ala			
	130	135	140
Thr Arg Ala Gly Ala Ser Ser Pro Ala Cys			
	145	150	

(2) INFORMATION FOR SEQ ID NO:1785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1501145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1785:

Arg Pro Xaa Ser Ser Pro Leu Leu Pro Gly Pro Phe Thr Pro Pro Thr
1 5 10 15
Asn Pro Thr Gln Ala Ala Ala Arg Ala Xaa Ala Arg Lys Ala Gln Thr
20 25 30
Leu Xaa Ala Gly His Gly Asp Ala Gly Gly Arg Gly Glu Gly Arg Ala
35 40 45
Gly Glu Glu Gly Ala Arg Gln Gly Ala Val Ala Ala Val Pro Ala Ala
50 55 60
Arg Xaa Gly Ala Gly Xaa Gly Ala Leu Ala Arg Pro Arg His Leu Arg
65 70 75 80
Arg Gln His His Arg Leu Arg Arg His His Val Arg Gln Gln Leu Xaa
85 90 95
Arg Ala Arg His Gln Gln Val Arg Arg Pro Leu Pro Arg Xaa Leu Leu
100 105 110
Leu Pro Ala Ala Ala Thr Glu Pro Ala Leu Arg Ala Leu Leu Arg His
115 120 125
Ala His Gln Asp Gly Gly Pro Gly Val Gly Glu Gly Gly Ala Pro Pro
130 135 140
Pro Gly Leu Ala Pro Pro Leu Gln His
145 150

(2) INFORMATION FOR SEQ ID NO:1786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..480
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1786:

ttctcgccct accatcgccct gaccgcagcg cccgttttct cctgaaaaca gaaggtcccg 60
gcctccggca tcgccaaaa aggggaaaaa aggagagata acacacacac acacaaaacc 120
caatccctcg cggcgccgat ggaccctgca tcggcgggct ccggcgggaa ctccctcccg 180
tcctcgcgcc ccgacgggca gaagcggcgc gtgtgctact tctacgaccc ggatgtgggc 240
aactactact acgggcaggg ccattccgat aagccgcacc gcattccgat gacgactcg 300
ctgtggtggc gctacggcct cctcaaccag atgcagggtgt accgccccaa ccggtcccg 360
gaccgcgacc tctgcgcgtt ccacgcgcag gactacatca acttctcgct cctcgctcacg 420
ccggaacgc agcaggacca gatccgctg ctcaagcgct tcaacgtcgg cgaggactgc 480

(2) INFORMATION FOR SEQ ID NO:1787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1787:

Met Asp Pro Ser Ser Ala Gly Ser Gly Gly Asn Ser Leu Pro Ser Val
1 5 10 15
Gly Pro Asp Gly Gln Lys Arg Arg Val Cys Tyr Phe Tyr Asp Pro Asp
20 25 30
Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His Arg
35 40 45

Ile Arg Met Thr His Ser Leu Leu Ala Arg Tyr Gly Leu Leu Asn Gln
50 55 60
Met Gln Val Tyr Arg Pro Asn Pro Ala Arg Asp Arg Asp Leu Cys Arg
65 70 75 80
Phe His Ala Asp Asp Tyr Ile Asn Phe Leu Arg Ser Val Thr Pro Glu
85 90 95
Thr Gln Gln Asp Gln Ile Arg Leu Leu Lys Arg Phe Asn Val Gly Glu
100 105 110
Asp Cys

(2) INFORMATION FOR SEQ ID NO:1788:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1501165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1788:

Met Lys Pro His Arg Ile Arg Met Thr His Ser Leu Leu Ala Arg Tyr
1 5 10 15
Gly Leu Leu Asn Gln Met Gln Val Tyr Arg Pro Asn Pro Ala Arg Asp
20 25 30
Arg Asp Leu Cys Arg Phe His Ala Asp Asp Tyr Ile Asn Phe Leu Arg
35 40 45
Ser Val Thr Pro Glu Thr Gln Gln Asp Gln Ile Arg Leu Leu Lys Arg
50 55 60
Phe Asn Val Gly Glu Asp Cys
65 70

(2) INFORMATION FOR SEQ ID NO:1789:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1501166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1789:

Met Thr His Ser Leu Leu Ala Arg Tyr Gly Leu Leu Asn Gln Met Gln
1 5 10 15
Val Tyr Arg Pro Asn Pro Ala Arg Asp Arg Asp Leu Cys Arg Phe His
20 25 30
Ala Asp Asp Tyr Ile Asn Phe Leu Arg Ser Val Thr Pro Glu Thr Gln
35 40 45
Gln Asp Gln Ile Arg Leu Leu Lys Arg Phe Asn Val Gly Glu Asp Cys
50 55 60

(2) INFORMATION FOR SEQ ID NO:1790:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 520 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..520

(D) OTHER INFORMATION: / Ceres Seq. ID 1501167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1790:

atctcaacttt	ctttctcgct	gcgtccgcc	tgctctcgct	ttccttctct	ctgctttgct	60
tttgtgtcgt	cgatgtcgaa	aactccttcc	agaccaagct	tcgctctgtg	tcgggttgca	120
ccagttactca	cgggccacgt	cgaggagag	gaaggagtag	gaggcgagg	cgagggttgc	180
aaaaaatggt	cgggagcatg	caggcggttg	accagcggtg	ccggataaag	gcgttgctcg	240
cattgcgcc	stcctcgcca	tgctctagcc	gctggccctg	ctccgcctt	tcattggcgc	300
gcgtggccgg	ggcgtccgat	gttgcggcct	ccgcgttggtg	gctagcggtg	aaaggggaag	360
gcggcggtgt	caagrtttct	acgggtgccg	gcgctctgc	ccatggtcgc	caacaggaag	420
agatagcca	cgcgccggac	gcaggagccc	ggggcggtg	tacgagctga	tcaccaggtg	480
gtgaacatgt	tccatctctt	gcctattctg	ttcctctctg			

(2) INFORMATION FOR SEQ ID NO:1791:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1501168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1791:

Leu	Thr	Phe	Phe	Leu	Ala	Ala	Ser	Ala	Met	Leu	Ser	Leu	Ser	Phe	Ser
1			5					10					15		
Leu	Leu	Cys	Phe	Cys	Val	Val	Asp	Val	Glu	Asn	Ser	Phe	Gln	Thr	Lys
			20					25				30			
Leu	Arg	Leu	Leu	Ser	Ala	Cys	Thr	Ser	Pro	His	Gly	Pro	Arg	Arg	Gly
			35				40					45			
Arg	Arg	Arg	Asp	Arg	Arg	Arg	Arg	Arg	Leu	Gln	Lys	Met	Val	Gly	
			50				55			60					
Ser	Met	Gln	Ala	Val	Asp	Pro	Ala	Gly	Arg	Ile	Ser	Ala	Leu	Leu	Ala
			65		70			75						80	
Leu	Arg	Xaa	Ser	Ser	Pro	Cys	Ser	Ser	Arg	Trp	Pro	Cys	Ser	Ala	Leu
			85					90					95		
Ser	Leu	Ala	Arg	Val	Ala	Gly	Ala	Ser	Asp	Val	Ala	Ala	Ser	Ala	Leu
			100					105					110		
Gly	Leu	Ala	Gly	Lys	Gly	Glu	Gly	Gly	Gly	Val	Ser	Xaa	Ser	Thr	Gly
			115				120					125			
Ala	Gly	Arg	Leu	Ala	His	Gly	Arg	His	Thr	Lys	Glu	Asp	Ser	His	Ala
			130				135				140				
Pro	Asp	Ala	Gly	Gly	Arg	Gly	Gly	Cys	Thr	Ser					
			145		150					155					

(2) INFORMATION FOR SEQ ID NO:1792:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1501169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1792:

Met	Leu	Ser	Leu	Ser	Phe	Ser	Leu	Leu	Cys	Phe	Cys	Val	Val	Asp	Val
1			5					10					15		
Glu	Asn	Ser	Phe	Gln	Thr	Lys	Leu	Arg	Leu	Leu	Ser	Ala	Cys	Thr	Ser

aactgcagcgc	agagocacccc	accttactcgt	catctcctgt	cgcctctcagt	cgccagcgcgc	60
ctctctctct	ctctctctctt	ccccccagct	gcgcacatgg	ctctgcgaata	agagaagacac	120
gcgttgtgtg	ttgctgtctgc	tgcctcgtcga	gcgcagacagg	agccatcacgc	ggcgsgsgcgc	180
agcaactctc	cgccgctgtgg	gcgcgcgcgc	ggggcaggacc	atctggccgcg	ggcgccaggagc	240
cgccacacccc	ttcgaactctt	ccacccatcgt	gaacctctctc	aatgcagcta	gcatcacagga	300
gtatggcagc	cgatcgcgca	agggaccgcgc	ttcaccaggag	atggcggsa	gcgtcagcgaag	360
acgctgtgtgt	ccccgcggcga	gcacacacgac	cagcagcggcg	ggcgacagca	gcgcagcagctg	420
gaggtgcgca	aqtacgtggc	gcacgtcagc	cagctgtatgc	ag		

(2) INFORMATION FOR SEQ ID NO:1795:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1501204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1795:

Xaa Cys Ser Gln Ser His Pro Pro Tyr Arg His Pro Arg Ser Leu Leu
1 5 10 15
Ile Ala Ser Ala Ser Ser Ser Ser Ser Phe Phe Pro Thr Ala Ala Asp
20 25 30
Met Ala Ala Gln Glu Glu Lys Thr Ala Val Val Val Ala Ala Ala Ala
35 40 45
Asp Val Ala Thr Glu Glu Pro Thr Pro Ala Xaa Ser Ser Asn Leu Ser
50 55 60
Arg Leu Gly Arg Arg Ala Gly Gln Asp His Arg Arg Pro Ala Gly Leu
65 70 75 80
Arg Gln Pro Leu Arg Leu Leu His His Asp Glu Pro Ser Gln
85 90

(2) INFORMATION FOR SEQ ID NO:1796:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1501205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1796:

Xaa Ala Ala Arg Ala Thr His Leu Ile Val Ile Leu Ala Arg Ser Ser
1 5 10 15
Ser Pro Ala Pro Pro Pro Pro Pro Ser Ser Pro Pro Leu Pro Thr
20 25 30
Trp Leu Arg Lys Lys Arg Arg Pro Leu Leu Leu Leu Leu Pro
35 40 45
Met Ser Arg Gln Arg Ser Leu Arg Arg Xaa Ala Ala Thr Ser Ala
50 55 60
Gly Trp Gly Gly Ala Gln Gly Arg Thr Ile Gly Ala Arg Arg Gly Ser
65 70 75 80
Ala Asn Pro Phe Asp Phe Ser Thr Met Met Asn Leu Leu Asn Asp Pro
85 90
Ser Ile Lys Glu Met Ala Glu Gln Ile Ala Lys Asp Pro Ala Phe Thr
100 105 110
Glu Met Ala Xaa Ser Cys Arg Arg Trp Cys Pro Arg Gly Ser Asn
115 120 125
Ser Ser Ser Arg Arg Gly Ser Ser Ser Ser Trp Thr Arg Arg Ser
130 135 140
Thr Trp Arg Arg Cys Ser Ser
145 150

(2) INFORMATION FOR SEQ ID NO:1797:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..103
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501206
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1797:
Met Ser Arg Gln Arg Ser Leu Arg Arg Arg Xaa Ala Ala Thr Ser Ala
1 5 10 15
Gly Trp Gly Gly Ala Gln Gly Arg Thr Ile Gly Ala Arg Arg Gly Ser
 20 25 30
Ala Asn Pro Phe Asp Phe Ser Thr Met Asn Leu Leu Asn Asp Pro
 35 40 45
Ser Ile Lys Glu Met Ala Glu Gln Ile Ala Lys Asp Pro Ala Phe Thr
 50 55 60
Glu Met Ala Xaa Ser Cys Arg Arg Arg Trp Cys Pro Arg Gly Ser Asn
65 70 75 80
Ser Ser Ser Arg Arg Gly Ser Ser Ser Ser Ser Trp Thr Arg Arg Ser
 85 90 95
Thr Trp Arg Arg Cys Ser Ser
 100

(2) INFORMATION FOR SEQ ID NO:1798:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 509 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..509
(D) OTHER INFORMATION: / Ceres Seq. ID 1501245
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1798:
aataaatcgc ggaattccca acgcccgcacc ttcaaccgcg ggctcccccag tccaatccaa 60
cccaaacccca gtccggcgac gggtccggggc agcgcgcgat cggatcgtcg cgggttcggc 120
ttctcgtcga acggcgcgga ttctctcccc cgatcggagg gcgtyggctg cggcgscctcg 180
gcgtctgata tgcctgcggtc ggtttcttct tgggararga gtgggatgga cggggaagcg 240
atccggtatg gtggcgggcaa cttggcgccc gcctacctt ccggcgccgc caccgcmac 300
gccatcacca tgcaggatcc gaaccagaac cagaaccaga accagaacca gaaccaaagc 360
cagttcctgt tcagcgccaa ctccacggcg ctgcagctgt tcggaagcgc cgcggtcccc 420
acggttggtc ctgctggtta tataavttac actgggaaac acccaccttc ctgttatgaa 480
ccaagcaagt acttcaaca tcggcgccag

(2) INFORMATION FOR SEQ ID NO:1799:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 169 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..169
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501246
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1799:
Asn Lys Ser Arg Asn Ser Gln Arg Arg Thr Phe Thr Ala Gly Leu Pro
1 5 10 15
Ser Pro Ile Gln Pro Asn Pro Ser Pro Ala Thr Val Pro Gly Ser Ala
 20 25 30
Arg Ser Asp Arg Arg Gly Phe Gly Phe Ser Ser Asn Gly Ala Asp Ser
 35 40 45
Cys Pro Arg Ser Glu Gly Xaa Gly Cys Gly Xaa Ser Ala Ser Asp Leu

50	55	60
Leu Arg Ser Ala Ser Ser Trp Xaa Xaa Ser Gly Met Asp Gly Glu Ala		
65	70	75
Ile Arg Met Gly Gly Gly Asn Leu Ala Pro Ala Tyr Leu Ser Gly Ala		80
	85	90
Ala Thr Xaa Thr Ala Ile Thr Met Gln Asp Pro Asn Gln Asn Gln Asn		
	100	105
Gln Asn Gln Asn Gln Asn Gln Ser Gln Phe Leu Phe Ser Ala Asn Ser		110
	115	120
Thr Ala Leu Gln Leu Phe Gly Ser Xaa Ala Val Pro Thr Val Gly Pro		125
	130	135
Ala Gly Tyr Ile Xaa Tyr Thr Gly Lys His Pro Pro Ser Cys Tyr Glu		140
	145	150
Pro Ser Lys Tyr Phe Lys His Arg Arg		155
	165	160

(2) INFORMATION FOR SEQ ID NO:1800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1501247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1800:

Ile Asn Arg Gly Ile Pro Asn Ala Ala Pro Ser Pro Pro Gly Ser Pro		
1	5	10
Val Gln Ser Asn Pro Thr Pro Val Arg Arg Phe Arg Ala Ala Arg		15
	20	25
Asp Arg Ile Val Ala Gly Ser Ala Ser Arg Arg Thr Ala Arg Ile Pro		30
	35	40
Ala Pro Asp Arg Arg Ala Xaa Ala Ala Ala Xaa Arg Arg Leu Ile Cys		45
	50	55
Cys Gly Arg Leu Leu Leu Gly Xaa Xaa Val Gly Trp Thr Gly Lys Arg		60
	65	70
Ser Gly Trp Val Ala Ala Thr Trp Arg Pro Pro Thr Ser Pro Ala Pro		75
	85	90
Pro Pro Xaa Pro Pro Ser Pro Cys Arg Ile Arg Thr Arg Thr Arg Thr		95
	100	105
Arg Thr Arg Thr Arg Thr Lys Ala Ser Ser Cys Ser Ala Pro Thr Pro		110
	115	120
Arg Arg Cys Ser Cys Ser Glu Xaa Pro Arg Ser Pro Arg Leu Val Leu		125
	130	135
		140
Leu Val Ile		
145		

(2) INFORMATION FOR SEQ ID NO:1801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1501248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1801:

Met Asp Gly Glu Ala Ile Arg Met Gly Gly Gly Asn Leu Ala Pro Ala		
1	5	10
		15

Tyr Leu Ser Gly Ala Ala Thr Xaa Thr Ala Ile Thr Met Gln Asp Pro
20 25 30
Asn Gln Asn Gln Asn Gln Asn Gln Ser Gln Phe Leu
35 40 45
Phe Ser Ala Asn Ser Thr Ala Leu Gln Leu Phe Gly Ser Xaa Ala Val
50 55 60
Pro Thr Val Gly Pro Ala Gly Tyr Ile Xaa Tyr Thr Gly Lys His Pro
65 70 75 80
Pro Ser Cys Tyr Glu Pro Ser Lys Tyr Phe Lys His Arg Arg
85 90

(2) INFORMATION FOR SEQ ID NO:1802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..476
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1802:

aacggaactt	agctgcccag	cgcccaaacg	cccaccgccc	ctcccatcaa	cgggcgctaa	60
aggtttctc	gcccgcaacg	cgatgccgaa	gaacaaggga	aaggagggca	agaaccggaa	120
gcggggcaag	aacgargcgg	acgacgagaa	gcgggagctg	gntgttcaag	gaggacgggc	180
aggagtagcg	cgaggtgacg	cgatgctggg	gcaacggccc	ctgcgaggcg	cgctcttctt	240
gaacaccocg	tccgatcttt	gcccagaagg	tctacttggg	catcaataag	aaactctttc	300
ccctcaaac	gattgtggtt	ccatctcttt	ctgtctggaa	aatgttgtca	ccaaactacc	360
ctatttctcg	tccagctttg	gcacgggaag	ataagtgtg	tacttctatt	ctcaagttgt	420
tgctctttgta	ttatgaaatg	tttccaataa	tcagcagttt	ttgatgtatg	gtcgtg	

(2) INFORMATION FOR SEQ ID NO:1803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1803:

Thr	Glu	Leu	Ser	Cys	Arg	Ala	Pro	Lys	Ala	Pro	Pro	Leu	Pro	Ser
1				5				10					15	
Ser	Gly	Ala	Lys	Gly	Phe	Leu	Ala	Arg	Asn	Ala	Met	Pro	Lys	Asn
			20					25					30	
Gly	Lys	Gly	Gly	Lys	Asn	Arg	Lys	Arg	Gly	Lys	Asn	Xaa	Ala	Asp
			35					40				45		
Glu	Lys	Arg	Glu	Leu	Xaa	Val	Gln	Gly	Gly	Arg	Ala	Gly	Val	Arg
			50					55				60		
Gly	Asp	Ala	Asp	Ala	Gly	Gln	Arg	Pro	Leu	Arg	Gly	Ala	Val	Phe
			65					70				75		80
Asn	Thr	Arg	Ser	Asp	Leu	Cys	Pro	Glu	Gly	Leu	Leu	Gly	His	Gln
				85				90					95	

(2) INFORMATION FOR SEQ ID NO:1804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1501261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1804:

```
Arg Asn Leu Ala Ala Glu Arg Pro Lys Pro His Arg Arg Ser His Gln
1          5          10          15
Ala Ala Leu Lys Val Ser Ser Pro Ala Thr Arg Cys Arg Arg Thr Arg
20          25          30
Glu Arg Glu Ala Arg Thr Gly Ser Gly Ala Arg Thr Xaa Arg Thr Thr
35          40          45
Arg Ser Gly Ser Trp Xaa Phe Lys Glu Asp Gly Gln Glu Tyr Ala Gln
50          55          60
Val Thr Arg Met Leu Gly Asn Gly Arg Cys Glu Ala Pro Ser Ser
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:1805:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1501262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1805:

```
Met Pro Lys Asn Lys Gly Lys Gly Gly Lys Asn Arg Lys Arg Gly Lys
1          5          10          15
Asn Xaa Ala Asp Asp Glu Lys Arg Glu Leu Xaa Val Gln Gly Gly Arg
20          25          30
Ala Gly Val Arg Ala Gly Asp Ala Asp Ala Gly Gln Arg Pro Leu Arg
35          40          45
Gly Ala Val Phe Leu Asn Thr Arg Ser Asp Leu Cys Pro Glu Gly Leu
50          55          60
Leu Gly His Gln
65
```

(2) INFORMATION FOR SEQ ID NO:1806:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..479

(D) OTHER INFORMATION: / Ceres Seq. ID 1501268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1806:

```
acgatccac tctcccgcgt caccctcaagg agtcaagggt caaagctaag cttagctcat 60
tgctcaagct tccgtctctt tctctctgcg agactgcaca ctgccaccac gcgcaatggc 120
ggcattccac catctgttgc cggccttgct ccttctaact ctgctccctt ccacccttga 180
ggcgacgtcc tcggcgctgc ttggcatcag ctacggctcg gttggcaaca acctccctgc 240
agctacatca gtgcgcgaga ttgtggcttc cctggggcgtc ggccgcgtcc gactctaega 300
tgctgcagac accaccattc gcgccttcgc caacacgggc gtcgagctcg tcgtcggcgt 360
ccctgacgag tgcctcgcca ctgtctccac cccgaagggc gcmgctcctc gggtccgctc 420
caacatttcc cctgtgcgtc cgggccacaa agatcgctt cctcacagtc ggcaacgag
```

(2) INFORMATION FOR SEQ ID NO:1807:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..159
(D) OTHER INFORMATION: / Ceres Seq. ID 1501269
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1807:
Asp Pro Thr Leu Pro Ala His Leu Lys Glu Ser Arg Cys Lys Ala Lys
1 5 10 15
Leu Ser Ser Leu Leu Lys Leu Pro Ser Leu Ser Leu Cys Glu Thr Ala
20 25 30
His Cys His His Ala Gln Trp Arg His Ser Thr Ile Cys Cys Arg Pro
35 40 45
Cys Ser Phe Tyr Ser Cys Ser Leu Pro Pro Leu Arg Arg Arg Pro Arg
50 55 60
Arg Cys Leu Ala Ser Ala Thr Val Ala Leu Ala Thr Thr Ser Leu Gln
65 70 75 80
Leu His Gln Cys Arg Arg Leu Trp Leu Pro Trp Ala Ser Ala Ala Ser
85 90 95
Asp Ser Thr Met Leu Thr Ala Pro Pro Phe Ala Pro Ser Pro Thr Arg
100 105 110
Ala Ser Ser Ser Ser Ala Ser Leu Thr Ser Ala Ser Pro Leu Ser
115 120 125
Pro Pro Arg Arg Ala Xaa Pro Pro Gly Ser Ala Pro Thr Phe Pro Pro
130 135 140
Ala Leu Pro Ala Thr Lys Ile Ala Phe Leu Thr Val Gly Asn Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:1808:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..121
(D) OTHER INFORMATION: / Ceres Seq. ID 1501270

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1808:

Met Ala Ala Phe His His Leu Leu Pro Ala Leu Leu Leu Leu Leu
1 5 10 15
Leu Pro Ser Thr Pro Glu Ala Thr Ser Ser Ala Leu Leu Gly Ile Ser
20 25 30
Tyr Gly Arg Val Gly Asn Asn Leu Pro Ala Ala Thr Ser Val Pro Gln
35 40 45
Ile Val Ala Ser Leu Gly Val Gly Arg Val Arg Leu Tyr Asp Ala Asp
50 55 60
Ser Thr Thr Ile Arg Ala Phe Ala Asn Thr Gly Val Glu Leu Val Val
65 70 75 80
Gly Val Pro Asp Glu Cys Leu Ala Thr Val Ser Thr Pro Thr Gly Xaa
85 90 95
Ala Ser Trp Val Arg Ser Asn Ile Ser Pro Cys Ala Pro Gly His Lys
100 105 110
Asp Arg Leu Pro His Ser Arg Gln Arg
115 120

(2) INFORMATION FOR SEQ ID NO:1809:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 422 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..422
(D) OTHER INFORMATION: / Ceres Seq. ID 1501280

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1809:

aaggagagag	agagaggcag	agggagagat	tggaggggag	cccctgcccc	aggcaagaga	60
aaccgcggcg	cgcgagagag	gggtgagggt	gagttctcag	aagcccgtag	ggacttggct	120
gctctttgga	aggactatga	ggaaagtcggt	gcagaggggtg	ccgatgacga	gggtgacgag	180
ggagacgact	attgagtagc	tggctaataa	gtagtctctc	ggtggttaat	ggttgggtta	240
ttttgagtat	atactctatg	gttccactcc	attggatact	gctgctgtgt	gtgtttccat	300
ttctttgggt	tgcacagcta	ttcgtccaat	ttcgggtgat	atgcataat	gctattatgt	420

tg

- (2) INFORMATION FOR SEQ ID NO:1810:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..64
(D) OTHER INFORMATION: / Ceres Seq. ID 1501281

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1810:

Lys	Glu	Arg	Glu	Arg	Gly	Arg	Gly	Arg	Asp	Trp	Arg	Glu	Ala	Pro	Ala	
1				5					10					15		
Gln	Gly	Lys	Arg	Asn	Arg	Gly	Ala	Arg	Glu	Arg	Glu	Gly	Glu	Gly	Phe	
				20				25					30			
Ser	Glu	Ala	Arg	Glu	Asp	Leu	Ala	Ala	Leu	Glu	Lys	Asp	Tyr	Glu	Glu	
				35			40					45				
Val	Gly	Ala	Glu	Gly	Ala	Asp	Asp	Glu	Gly	Asp	Glu	Gly	Asp	Asp	Tyr	
				50			55					60				

- (2) INFORMATION FOR SEQ ID NO:1811:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..65
(D) OTHER INFORMATION: / Ceres Seq. ID 1501282

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1811:

Arg	Arg	Glu	Arg	Glu	Ala	Glu	Gly	Glu	Ile	Gly	Gly	Arg	Pro	Leu	Pro	
1				5					10					15		
Lys	Ala	Arg	Glu	Thr	Ala	Ala	Arg	Gly	Glu	Arg	Val	Arg	Val	Ser	Ser	
				20				25					30			
Gln	Lys	Pro	Val	Arg	Thr	Trp	Leu	Leu	Arg	Arg	Thr	Met	Arg	Lys		
				35			40				45					
Ser	Val	Gln	Arg	Val	Pro	Met	Thr	Arg	Val	Thr	Arg	Glu	Thr	Thr	Ile	
				50			55				60					

Glu
65

- (2) INFORMATION FOR SEQ ID NO:1812:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..570
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1812:

ataaagcacc	ctctccttgc	gcgaattcgg	acacggccac	cacacatccc	ttcctctctt	60
tctcctcgag	gctcgagcat	tctgtctgct	ccgacccacc	cgccacaggc	tcggcgggtc	120
ggcgatctcg	ctacccggcg	ggaacatgac	tacttcaagg	cgccttgcgt	acaggaagac	180
cgcaaatgtc	cagaagaaca	tcaccaggag	gggttctgtg	cctgaacca	ctgtcaagaa	240
gggaaatgac	taccctgttg	gccctctagt	gcttgggttc	ttcatctttg	tctgcatctg	300
atcatctgtg	tttcagatca	tcaggacggc	aaccagcgcc	ggggtggctt	gagagccggc	360
ccacatctaa	tccccagtat	agagagttgc	ttgttataca	tgcatccagc	taggattggg	420
tagcagctaa	aatgttaaac	gtgacaagac	tgccctgcac	tccgttcatt	tggtggggcct	480
tgaatctgga	actgaacct	aaggcagaat	catgtacctt	atataaagtg	ttaaatgggt	540
aactggatct	cagtgtttca	tttaatcttc				

(2) INFORMATION FOR SEQ ID NO:1813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1813:

Ile	Lys	His	Pro	Leu	Ala	Arg	Ile	Arg	Thr	Arg	Pro	Pro	His	Ile
1			5				10					15		
Pro	Ser	Ser	Leu	Ser	Pro	Arg	Gly	Ser	Ser	Ile	Arg	Ala	Ala	Thr
			20				25					30		
Pro	Pro	Pro	Gln	Ala	Arg	Arg	Ser	Gly	Asp	Leu	Ala	His	Arg	Glu
			35				40					45		
His	Asp	Tyr	Phe	Lys	Ala	Pro	Cys							
			50				55							

(2) INFORMATION FOR SEQ ID NO:1814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1814:

Lys	Ala	Pro	Ser	Pro	Cys	Ala	Asn	Ser	Asp	Thr	Ala	Thr	Thr	His	Pro
1				5				10					15		
Phe	Leu	Ser	Phe	Ser	Ser	Arg	Leu	Glu	His	Ser	Cys	Cys	Ser	Asp	Pro
				20				25					30		
Thr	Ala	Thr	Gly	Ser	Ala	Val	Arg	Arg	Ser	Arg	Ser	Pro	Ala	Gly	Thr
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:1815:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..68
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501309
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1815:
Met Thr Thr Ser Arg Arg Leu Ala Asp Arg Lys Thr Ala Lys Phe Gln
1 5 10 15
Lys Asn Ile Thr Arg Arg Gly Ser Val Pro Glu Thr Thr Val Lys Lys
 20 25 30
Gly Asn Asp Tyr Pro Val Gly Pro Leu Val Leu Gly Phe Phe Ile Phe
 35 40 45
Val Val Ile Gly Ser Ser Leu Phe Gln Ile Ile Arg Thr Ala Thr Ser
 50 55 60
Gly Gly Val Ala
65

(2) INFORMATION FOR SEQ ID NO:1816:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1036 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1036
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501310
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1816:
aaccacaagag cgaaaatgga tccgcaccag ttcgccccct cccagcagtc ggcgctgacc 60
atggaatcgg cgagatcac gccgcgccgc gccgcgcgcg gcgcacccaa cggcgctgcc 120
cgggctatcg tcgaggacga cgacgaggac gacgaagtcc cggaggtggc cgcctgcata 180
tcgacgatgc tcgaccgcgg gggtagcgtg gagagccacc gcccttctct ggcgcgccgc 240
accgcgctgg agatgctccg cgaccgcggt acgcggttcc ggaggaagag ctgcgcccgga 300
ccctcccgga gttccgcgcc tgggtgggaat acaggccaga rctcgaacgc ctgcctcttc 360
ccactacctc cgctcccgac ccgtccagca aggtgaaagt tgtgtctgt ccacctggac 420
ctgtcaaaat cgacgctatc cggctgatat ataccgaagt caaagatgag aacttgtcca 480
gactgattct gatactgcag ggcaaaataa tgtctacaac cagagaatcc atcaaggagw 540
tctttcgatt taaagttgac acattccaga tcacggaatt actggtgaac atcactaagc 600
atgtctcaa gcccaagcat gaagtgttga ctgcagaggg gaaagctaag ctctgaagg 660
agtaacaatt ggtggattca cagttgcctc gcattgctga gaatgatgct gttgctcgt 720
attacgggct aggcaaggga actgttgta aggttatata cgacagcgag cttaaccggga 780
accatgtgac gtaccgatgc attacctgag gggcccatgt gtttcggtg atgaagtgtc 840
gtaagcagtc tgtaaaaaat tacctctaag aggggcagggt gacactgttc tgctaggcct 900
ttgtaagcac ccaattatgc aggatgaagc tcgctgtaag ctattggtaa aatcatcttg 960
cgccattgcc gtaccttaag tgcttggtgt taatcttggga aacagtgaga caactaatcc 1020
tgtagtgagt tatctc

(2) INFORMATION FOR SEQ ID NO:1817:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1501311
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1817:
Asn Pro Arg Ala Lys Met Asp Pro His Gln Phe Ala Pro Ser Gln Gln
1 5 10 15
Ser Ala Leu Thr Met Glu Ser Ala Glu Ile Thr Ala Ala Ala Ala
20 25 30
Ala Arg Ala Pro Asn Gly Ala Ala Arg Ala Ile Val Glu Asp Asp Asp
35 40 45
Glu Asp Asp Asp Val Pro Glu Val Ala Ala Cys Ile Ser Thr Met Leu
50 55 60
Asp Arg Gly Gly Ser Val Glu Ser His Arg Leu Phe Leu Ala Arg Arg
65 70 75 80
Thr Ala Leu Glu Met Leu Arg Asp Arg Gly Thr Pro Phe Arg Arg Lys
85 90 95
Ser Ser Pro Gly Pro Ser Arg Ser Ser Ala Pro Gly Gly Asn Thr Gly
100 105 110
Gln Xaa Ser Asn Ala Ser Pro Ser Pro Leu Pro Ser Pro Pro Thr Arg
115 120 125
Pro Ala Arg
130

(2) INFORMATION FOR SEQ ID NO:1818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1818:

Met Asp Pro His Gln Phe Ala Pro Ser Gln Gln Ser Ala Leu Thr Met
1 5 10 15
Glu Ser Ala Glu Ile Thr Ala Ala Ala Ala Ala Ala Arg Ala Pro Asn
20 25 30
Gly Ala Ala Arg Ala Ile Val Glu Asp Asp Asp Glu Asp Asp Asp Val
35 40 45
Pro Glu Val Ala Ala Cys Ile Ser Thr Met Leu Asp Arg Gly Gly Ser
50 55 60
Val Glu Ser His Arg Leu Phe Leu Ala Arg Arg Thr Ala Leu Glu Met
65 70 75 80
Leu Arg Asp Arg Gly Thr Pro Phe Arg Arg Lys Ser Ser Pro Gly Pro
85 90 95
Ser Arg Ser Ser Ala Pro Gly Gly Asn Thr Gly Gln Xaa Ser Asn Ala
100 105 110
Ser Pro Ser Pro Leu Pro Ser Pro Pro Thr Arg Pro Ala Arg
115 120 125

(2) INFORMATION FOR SEQ ID NO:1819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1819:

Met Glu Ser Ala Glu Ile Thr Ala Ala Ala Ala Ala Arg Ala Pro

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..543

(D) OTHER INFORMATION: / Ceres Seq. ID 1501324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1822:

gcctcgcgca	ctcgactta	acctagccgc	cagccctcga	cgaccgacgc	gacgtcgct	60
tcgcccctgc	tccaaacct	gcccccttcg	tcgctccggc	ctcggaagga	agatccctca	120
tcgacgttc	tgctgatgc	ctgtctgtca	tcgtttcgag	gagagcctca	gtggctcgat	180
ccttgatgtg	ttgggccccg	tcgaggcgat	tgtaaccact	tcacacaggg	gcaaatgtcg	240
gtcggtcctc	cccccttggg	tctccaccgc	ccaatgctcg	atgctctgat	cgacaaagct	300
cccgctccga	gtctccccc	ctcggtatcct	tccctcgccc	gtgcttgctt	cctcgctcgt	360
ggatactcgc	ccggccccct	catcgctccg	agaacctggc	atgagacacg	ccaccagacg	420
ttgtttacag	tcacgcccag	ttggccatta	ctttgctagt	gtttcacatg	acaggactgc	480
tagaatttgg	tcaattgata	aaatccagcc	tttgcgaata	atggctgggc	atctttctga	540

tgt

(2) INFORMATION FOR SEQ ID NO:1823:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1501325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1823:

Pro	Arg	Ala	Leu	Ala	Leu	Asn	Leu	Ala	Ala	Ser	Pro	Arg	Arg	Pro	Thr	
1			5						10						15	
Arg	Arg	Arg	Leu	Arg	Pro	Cys	Ser	Asn	Pro	Cys	Pro	Leu	Arg	Arg	Arg	Ser
			20					25					30			
Gly	Leu	Gly	Arg	Lys	Ile	Leu	His	Arg	Arg	Ser	Cys	Arg	Cys	Leu	Cys	
		35					40					45				
Cys	His	Arg	Ser	Glu	Glu	Ser	Leu	Ser	Gly	Arg	Ile	Leu	Asp	Val	Leu	
	50					55					60					
Gly	Pro	Val	Glu	Ala	Ile	Val	Thr	Thr	Ser	His	Arg	Gly	Lys	Val	Arg	
	65					70				75				80		
Ser	Val	Leu	Pro	Leu	Trp	Ile	Leu	His	Arg	Gln	Cys	Ser	Met	Pro	Ala	
				85					90					95		
Ser	Thr	Lys	Leu	Pro	Ser	Glu	Val	Ser	Pro	Phe	Arg	Ile	Leu	Pro	Leu	
			100					105					110			
Pro	Val	Leu	Ala	Ser	Ser	Ser	Trp	Asp	Thr	Pro	Pro	Ala	Pro	Ser	Ser	
		115				120						125				
Ser	Arg	Glu	Pro	Gly	Met	Arg	His	Ala	Thr	Arg	Ala	Cys	Leu	Gln	Phe	
	130					135				140						
Ser	Pro	Val	Gly	His	Tyr	Phe	Ala	Ser	Ala	Ser	His	Asp	Arg	Thr	Ala	
	145				150				155						160	
Arg	Ile	Trp	Ser	Ile	Asp	Lys	Ile	Gln	Pro	Leu	Arg	Ile	Met	Ala	Gly	
			165					170						175		

His Leu Ser Asp
180

(2) INFORMATION FOR SEQ ID NO:1824:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 536 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..536

(D) OTHER INFORMATION: / Ceres Seq. ID 1501326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1824:

aatcacccttc	ttcgtttcat	ctctgtatc	wcccccctg	ggtctgctct	gctcccatcc	60
catggagccc	gacgcgccc	aaaaccctag	ccccagcccc	gtccccccgc	ccatctccgc	120
ctactaccag	agcgcgcgcg	aacaccacgc	cgctgtaact	agcgactggc	tcgcccacgc	180
cgccgcgcga	ggcgcgacct	tccccggcgc	cgataccgcc	gatgcmgcmc	cgcccccgtc	240
ccccgggggc	ggcggcgctga	tcgaggagtt	caacttctgg	cgccgcaagc	ccgaggccgc	300
cgaggcggtg	ggcgccatca	tggtctctgc	cgcmgtcatc	cgctccagca	gggcccaccac	360
catgatggag	ctcgagatcg	agctcaagaa	ggcatctgac	aagctcaagt	cctgggatgc	420
tacatccatt	tctcttcttg	ctgcttgtag	ttgtttcatg	cggtttgtaa	cgaggaccctc	480
acatctggag	catgagaagt	ttgatgcgac	aaaatcgcg	ctaattgagc	gaggag	

(2) INFORMATION FOR SEQ ID NO:1825:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1501327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1825:

Ile	Thr	Phe	Phe	Val	Ser	Ser	Ser	Asp	Xaa	Pro	Pro	Xaa	Gly	Leu	Leu
1				5				10					15		
Cys	Ser	His	Pro	Met	Glu	Pro	Asp	Ala	Ala	Gln	Asn	Pro	Ser	Pro	Ser
			20				25					30			
Pro	Val	Pro	Pro	Pro	Ile	Ser	Ala	Tyr	Tyr	Gln	Thr	Arg	Ala	Glu	His
			35				40					45			
His	Ala	Val	Val	Thr	Ser	Asp	Trp	Leu	Ala	His	Ala	Ala	Ala	Ala	Ala
			50			55					60				
Ala	Ala	Phe	Pro	Gly	Ala	Asp	Thr	Ala	Asp	Xaa	Xaa	Pro	Pro	Pro	Ser
65				70						75				80	
Pro	Gly	Gly	Gly	Gly	Val	Ile	Glu	Glu	Phe	Asn	Phe	Trp	Arg	Arg	Lys
				85					90				95		
Pro	Glu	Ala	Ala	Glu	Ala	Val	Ala	Ala	Ile	Met	Ala	Leu	Ala	Xaa	Val
				100				105				110			
Ile	Arg	Ser	Ser	Arg	Ala	Thr	Thr	Met	Met	Glu	Leu	Glu	Ile	Glu	Leu
				115			120					125			
Lys	Lys	Ala	Ser	Asp	Lys	Leu	Lys	Ser	Trp	Asp	Ala	Thr	Ser	Ile	Ser
				130			135				140				
Leu	Ser	Ala	Ala	Cys	Asp	Leu	Phe	Met	Arg	Phe	Val	Thr	Arg	Thr	Ser
145					150					155					160
His	Leu	Glu	His	Glu	Lys	Phe	Asp	Ala	Ala	Lys	Ser	Arg	Leu	Ile	Glu
					165				170					175	

Arg Gly

(2) INFORMATION FOR SEQ ID NO:1826:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1501328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1826:

Met Glu Pro Asp Ala Ala Gln Asn Pro Ser Pro Ser Pro Val Pro Pro

1	5	10	15
Pro Ile Ser Ala Tyr Tyr Gln Thr Arg Ala Glu His His Ala Val Val	20	25	30
Thr Ser Asp Trp Leu Ala His Ala Ala Ala Ala Ala Ala Phe Pro	35	40	45
Gly Ala Asp Thr Ala Asp Xaa Xaa Pro Pro Pro Ser Pro Gly Gly Gly	50	55	60
Gly Val Ile Glu Glu Phe Asn Phe Trp Arg Arg Lys Pro Glu Ala Ala	65	70	75
Glu Ala Val Ala Ala Ile Met Ala Leu Ala Xaa Val Ile Arg Ser Ser	85	90	95
Arg Ala Thr Thr Met Met Glu Leu Glu Ile Glu Leu Lys Lys Ala Ser	100	105	110
Asp Lys Leu Lys Ser Trp Asp Ala Thr Ser Ile Ser Leu Ser Ala Ala	115	120	125
Cys Asp Leu Phe Met Arg Phe Val Thr Arg Thr Ser His Leu Glu His	130	135	140
Glu Lys Phe Asp Ala Ala Lys Ser Arg Leu Ile Glu Arg Gly	145	150	155

(2) INFORMATION FOR SEQ ID NO:1827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..492
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1827:

acactgctc	tcgccactgt	cgctccaccga	tccgtcatgg	cgactgtgc	gccattgttg	60
ctcttccagc	gtctcctcct	cctcctctcc	ctggcgctcg	gcccatggcg	tgaacgtgaa	120
gcccggggag	caccacatcc	tcaacaggca	gagcttcccc	ccgggggttcg	tcttcggcac	180
ggcgctctcg	gcgtaccagg	tggaggggaa	cacgcacagg	tacggggcgcg	ggccctcgat	240
ctgggacacc	ttctctcaagt	atccaggcac	tactctgat	aacgcgaccg	cggacgtgac	300
agtcgacgag	tacaatcgct	acatggatga	tgtggacaat	atggtccggg	ttagcttcga	360
cgcgtaccgc	ttctcgatct	catggctcgc	tattttcccc	agtgggattg	ggaggggttaa	420
caaggatggt	gtggactatt	accacaggct	catcaactac	ttgctggcga	accatattac	480
tcctacgtg	gt					

(2) INFORMATION FOR SEQ ID NO:1828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1828:

Thr Leu Ala Leu Ala Thr Val Val His Arg Ser Val Met Ala Thr Ala	5	10	15
Ala Pro Leu Leu Leu Phe His Gly Leu Leu Leu Leu Ser Leu Ala	20	25	30
Leu Gly Pro Trp Arg Glu Arg Glu Ala Arg Gly Ala Pro His Pro Gln	35	40	45
Gln Ala Glu Leu Pro Pro Gly Val Arg Leu Arg His Gly Val Phe Gly	50	55	60
Val Pro Gly Gly Gly Glu His Ala Gln Val Arg Ala Arg Ala Leu His			

80

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..163

- (D) OTHER INFORMATION: / Ceres Seq. ID 1501331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1829:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1830:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs

- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..409

- (D) OTHER INFORMATION: / Ceres Seq. ID 1501339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1830:

gtcagagtcaa	gaaccttttt	cccccgcttcg	cgcagacagct	cgcgccactac	acacacgcgcg	60
ccacacaccaa	ccatggagcgc	cctccgcgaag	ggaggcgctga	tctcgacctc	gacacgcggtg	120
cgaggccgtga	agctggggcac	ctctgtgctga	aagtcgcggga	tgatccctccc	gtatcagcttg	180
gcacctgcgcg	tgctcgtctc	ccacccgcgct	ctgtcgtcgct	cgctgcctccc	ccctctcggc	240
gcgctcgcgcg	ccacgcgcgcc	ctacagcagct	ctctgcggcgc	tgccctatagc	agcgctgcccc	300
ttctcggcgcc	cggctctcgt	ccgcgscctc	gtgcgcatcgc	tctcagcgcg	ctacgacacc	360
aatcgccctcg	agatgcgctc	ccgcgcgcgc	cagagmcgtgc	tgctctctcg		

(2) INFORMATION FOR SEQ ID NO:1831

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids

- (B) TYPE: amino acid

- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1501340

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1831:

```
Val Glu Ser Arg Thr Phe Leu Pro Arg Ser Arg Xaa Gln Ser Ala Thr
1      5      10      15
Thr His Thr Pro Thr Asn Thr Met Asp Ala Ala Lys Glu Ala
20      25      30
Leu Ile Leu Asp Leu His Ala Val Glu Ala Val Lys Leu Gly Thr Phe
35      40      45
Val Leu Lys Ser Gly Ile Thr Ser Pro Ile Tyr Leu Asp Leu Arg Val
50      55      60
Leu Val Ser His Pro Arg Leu Leu Ala Ser Val Ala Ser Leu Leu Gly
65      70      75      80
Ala Leu Pro Ala Thr Arg Pro Tyr Asp Leu Leu Cys Gly Val Pro Xaa
85      90      95
Thr Ala Leu Pro Phe Ala Ala Ala Leu Ser Val Ala Xaa Ser Val Pro
100      105      110
Met Leu Leu Ser Arg Tyr Asp Thr Lys Arg Val Glu Gly Ala Phe Arg
115      120      125
Xaa Ala Gln Xaa Val Leu Ile Val
130      135
```

- (2) INFORMATION FOR SEQ ID NO:1832:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1501341

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1832:

```
Arg Val Lys Asn Phe Ser Pro Pro Phe Ala Xaa Thr Val Gly His Thr
1      5      10      15
Thr His Ala Ala His Gln His His Gly Arg Arg Arg Glu Gly Ala
20      25      30
Asp Pro Gly Pro Ala Arg Gly Gly Gly Arg Glu Ala Gly His Leu Arg
35      40      45
Ala Gln Val Arg Asp His Leu Pro Asp Leu Pro Gly Pro Ala Arg Ala
50      55      60
Arg Leu Pro Pro Ala Pro Ala Arg Leu Arg Arg Val Pro Pro Arg Arg
65      70      75      80
Ala Pro Gly His Ala Pro Leu Arg Pro Ser Leu Arg Arg Ala Leu Xaa
85      90      95
Ser Ala Ala Leu Arg Gly Arg Ala Leu Arg Arg Xaa Leu Arg Ala His
100      105      110
Ala Ala Gln Pro Leu Arg His Gln Ala Arg Arg Gly Arg Leu Pro Xaa
115      120      125
Arg Pro Xaa Arg Ala His Arg
130      135
```

- (2) INFORMATION FOR SEQ ID NO:1833:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1501342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1833:

Met	Asp	Ala	Ala	Lys	Glu	Ala	Leu	Ile	Leu	Asp	Leu	His	Ala	Val
1				5				10					15	
Glu	Ala	Val	Lys	Leu	Gly	Thr	Phe	Val	Leu	Lys	Ser	Gly	Ile	Thr
			20					25					30	
Pro	Ile	Tyr	Leu	Asp	Leu	Arg	Val	Leu	Val	Ser	His	Pro	Arg	Leu
			35					40					45	
Ala	Ser	Val	Ala	Ser	Leu	Leu	Gly	Ala	Leu	Pro	Ala	Thr	Arg	Pro
			50					55					60	
Asp	Leu	Leu	Cys	Gly	Val	Pro	Xaa	Thr	Ala	Leu	Pro	Phe	Ala	Ala
65								70					75	
Leu	Ser	Val	Ala	Xaa	Ser	Val	Pro	Met	Leu	Leu	Ser	Arg	Tyr	Asp
								85					90	
Lys	Arg	Val	Glu	Gly	Ala	Phe	Arg	Xaa	Ala	Gln	Xaa	Val	Leu	Ile
								100					105	
													110	

(2) INFORMATION FOR SEQ ID NO:1834:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 539 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..539

(D) OTHER INFORMATION: / Ceres Seq. ID 1501345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1834:

agcagcccat	ccccagcagc	actgcctcgt	cgtctcgcat	attggcggtg	gcataccagt	60
cggcattgtg	cccattacca	tgccgcgcgt	gccgcgggcc	gacgatttac	tcattctcga	120
gttcacgcgc	agcaaccgcc	gtatccccca	cgccgtgttc	aactccttca	tcgcctccca	180
atccccacc	tccgccttct	cccgcacctc	acagcgcctc	cgaaaagccc	tagtgcctcg	240
cgccctcgac	gcccctctct	acaccgtggg	cgcctcctgc	tcctccagcc	tcctctctca	300
caaggcgcgca	aaggctctcg	ccgaccgccga	cgcagccgcc	tgtctccccc	accagattcc	360
ttttacagaa	aatgaagaaa	acgatgaggc	tagggctcgc	gtggccgata	tcaagcgctc	420
cctcgacctt	gagtgggcca	acctcccgcm	ctccacgcct	gagctcgtmg	ccggggagcg	480
gtcccaccag	actggtgcgm	ctgcggacca	caccatgcgt	acaaagcttc	gcctgtttcg	

(2) INFORMATION FOR SEQ ID NO:1835:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1501346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1835:

Ser	Ser	Pro	Ser	Pro	Ala	Ala	Leu	Pro	Arg	Arg	Leu	Ala	Tyr	Trp	Arg
1					5						10			15	
Trp	His	His	Arg	Arg	His	Cys	Ala	His	Tyr	His	Ala	Ala	Ala	Ala	Arg
					20						25			30	
Gly	Arg	Arg	Phe	Thr	His	Ser	Arg	Val	His	Arg	Gln	Gln	Pro	Pro	Tyr
					35						40			45	

Pro Pro Arg Arg Val Gln Leu Leu His Arg Leu Pro Ile Pro Thr Leu
50 55 60
Arg Leu Leu Pro His Leu Thr Ala Pro Pro Lys Ser Pro Ser Ala Pro
65 70 75 80
Arg Pro Arg Arg Arg Pro Leu His Arg Gly Arg Leu Leu Leu Leu Gln
85 90 95
Pro Pro Pro Pro Gln Gly Ala Lys Gly Pro Arg Arg Pro Arg Arg Ser
100 105 110
Arg Leu Leu Pro Pro Pro Asp Ser Phe Tyr Arg Lys
115 120

(2) INFORMATION FOR SEQ ID NO:1836:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1501347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1836:

Ala Ala His Pro Gln Gln His Cys Leu Val Val Ser His Ile Gly Val
1 5 10 15
Gly Ile Thr Val Gly Ile Val Pro Ile Thr Met Pro Pro Leu Pro Ala
20 25 30
Ala Asp Asp Leu Leu Ile Leu Glu Phe Ile Ala Ser Asn Arg Arg Ile
35 40 45
Pro His Ala Val Phe Asn Ser Phe Ile Ala Ser Gln Ser Pro Pro Ser
50 55 60
Ala Phe Ser Arg Thr Ser Gln Arg Leu Arg Lys Ala Leu Val Leu Arg
65 70 75 80
Ala Leu Asp Ala Ala Leu Tyr Thr Val Gly Ala Ser Cys Ser Ser Ser
85 90 95
Leu Leu Leu His Lys Ala Arg Lys Val Leu Ala Asp Pro Asp Ala Ala
100 105 110
Ala Cys Phe Pro His Gln Ile Pro Phe Thr Glu Asn Glu Glu Asn Asp
115 120 125
Glu Ala Arg Ala Ala Val Ala Asp Leu Lys Arg Leu Leu Asp Leu Glu
130 135 140
Trp Ala Asn Leu Pro Xaa Ser Thr Leu Glu Leu Xaa Ala Gly Asp Gly
145 150 155 160
Ser His Gln Thr Gly Xaa Ala Ala Asp His Thr Met Arg Thr Lys Leu
165 170 175
Arg Leu Phe

(2) INFORMATION FOR SEQ ID NO:1837:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1501348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1837:

Met Pro Pro Leu Pro Ala Ala Asp Asp Leu Leu Ile Leu Glu Phe Ile
1 5 10 15
Ala Ser Asn Arg Arg Ile Pro His Ala Val Phe Asn Ser Phe Ile Ala

	20		25		30										
Ser	Gln	Ser	Pro	Pro	Ser	Ala	Phe	Ser	Arg	Thr	Ser	Gln	Arg	Leu	Arg
	35		40		45		50		55		60		65		70
Lys	Ala	Leu	Val	Leu	Arg	Ala	Leu	Asp	Ala	Ala	Leu	Tyr	Thr	Val	Gly
	50		55		60		65		70		75		80		85
Ala	Ser	Cys	Ser	Ser	Ser	Leu	Leu	Leu	His	Lys	Ala	Arg	Lys	Val	Leu
	65		70		75		80		85		90		95		100
Ala	Asp	Pro	Asp	Ala	Ala	Ala	Cys	Phe	Pro	His	Gln	Ile	Pro	Phe	Thr
	85		90		95		100		105		110		115		120
Glu	Asn	Glu	Glu	Asn	Asp	Glu	Ala	Arg	Ala	Ala	Val	Ala	Asp	Leu	Lys
	100		105		110		115		120		125		130		135
Arg	Leu	Leu	Asp	Leu	Glu	Trp	Ala	Asn	Leu	Pro	Xaa	Ser	Thr	Leu	Glu
	115		120		125		130		135		140		145		150
Leu	Xaa	Ala	Gly	Asp	Gly	Ser	His	Gln	Thr	Gly	Xaa	Ala	Ala	Asp	His
	130		135		140		145		150		155		160		165
Thr	Met	Arg	Thr	Lys	Leu	Arg	Leu	Phe							
	145		150		155		160		165		170		175		180

(2) INFORMATION FOR SEQ ID NO:1838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..511
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1838:

agccttcacaa	tccttaggag	aaacgtcttg	ccctccactc	caacatcgac	acgactactc	60
gtccgactag	aaccaaactt	ttcaatccat	cggtccgagt	tcagttcaca	cttcacaggc	120
gagcgggacc	atggataccc	aagcacgtcc	ggttcccgcg	gtcaagctcg	gcacccaggg	180
attcgagggtg	tccaagctgg	ggttcgggtg	catggggctg	acgggcgcgt	acaactcccc	240
ctgtggacga	gaggccggca	tcgccgtcat	cgcgcacgct	ttcagccgcg	gagtcacatt	300
gttcgacacc	tccgacgtat	acggggccctc	caccaacgaa	atctctctcg	gcaaggcgct	360
gaagcagctg	ccgcggggagc	aggtgcaggt	ggccaccaag	ttcggggatam	ggcgtgacga	420
gagcggcaacs	ggnacgtgt	gcggccggcc	ggagtaegtt	cgtrcctctg	gcgaggccag	480
cctgcgcgcg	ctcggcatcg	actgcacga	c			

(2) INFORMATION FOR SEQ ID NO:1839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1839:

Ser	Leu	Pro	Ile	Ser	Arg	Arg	Asn	Val	Leu	Pro	Ser	Thr	Pro	Thr	Ser
	1		5		10		15		20		25		30		35
Thr	Arg	Leu	Leu	Val	Arg	Leu	Glu	Pro	Asn	Phe	Ser	Ile	His	Arg	Ser
	35		40		45		50		55		60		65		70
Gln	Phe	Ser	Ser	His	Phe	Thr	Gly	Glu	Arg	Asp	His	Gly	Tyr	Pro	Ser
	50		55		60		65		70		75		80		85
Thr	Ser	Gly	Ser	Pro	Arg	Gln	Ala	Arg	His	Pro	Gly	Ile	Arg	Gly	Val
	65		70		75		80		85		90		95		100
Gln	Ala	Gly	Val	Arg	Val	His	Gly	Ala	Asp	Gly	Arg	Ile	Gln	Leu	Pro
	100		105		110		115		120		125		130		135
Ala	Gly	Arg	Arg	Gly	Arg	His	Arg	Arg	His	Arg	Ala	Arg	Phe	Gln	Pro

(2) INFORMATION FOR SEQ ID NO:1840:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1840:

Asp Thr Gln Ala Arg Pro Val Pro Arg Val Ly

(2) INFORMATION FOR SEO ID NO:1841:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1.,100

(D) OTHER INFORMATION: / Ceres Seq. ID 1501367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1841:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..516
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1842:

atctataaca	gccgccacct	tcccccttat	actgcgcgga	ggcaaccagt	actcgtgcc	60
cgactgccac	ccctcctctt	cttgtgtatc	tccgaatacc	catctcagat	tccaagggcc	120
gcgccgtgta	atccccgggt	ctccccacc	accatatact	tagtatccgc	gcctcaaatc	180
cctcgcaaaa	cgccccgcgc	taagcagttg	ttgtctgccg	tgatttgagc	cgggcggagc	240
gattgatccc	gggaacgaggt	gtctcagctc	ttgatcttga	tcctgatctc	gggaggcggt	300
cctggtttat	tgggtggagc	gaagaagcca	tgataccttc	cgtgaggctc	tctcctggct	360
gtgcagcctt	ctcaggctcc	agcctacgct	caaaattacc	gtcaattcca	tccatctcca	420
gtctcaaaacc	ctccaaatat	gtggctctct	cgctgaaacc	actctaccta	gcaccgctag	480
atggtcgcgcg	cactgcgcgcg	cttaagtctc	ggagac			

(2) INFORMATION FOR SEQ ID NO:1843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1843:

Ile	Tyr	Asn	Ser	Arg	His	Leu	Pro	Pro	Tyr	Thr	Arg	Arg	Gln	Pro
1			5						10				15	
Val	Leu	Val	Pro	Arg	Leu	Pro	Pro	Leu	Phe	Leu	Val	Ile	Ser	Glu
			20					25				30		
Tyr	Pro	Ser	Gln	Ile	Pro	Arg	Ala	Ala	Pro	Cys	Asn	Pro	Arg	Leu
			35				40				45			
Pro	Pro	Thr	Ile	Tyr	Leu	Val	Ser	Ala	Pro	Gln	Ile	Pro	Arg	Glu
			50				55				60			
Pro	Arg	Arg	Lys	Gln	Leu	Leu	Ser	Ala	Val	Ile				
			65			70				75				

(2) INFORMATION FOR SEQ ID NO:1844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1844:

Met	Ile	Pro	Ser	Val	Arg	Leu	Ser	Pro	Gly	Pro	Ala	Ala	Phe	Ser	Gly
1									10					15	
Ser	Ser	Leu	Arg	Ser	Lys	Leu	Pro	Ser	Ile	Pro	Ser	Ile	Ser	Ser	Leu
			20					25					30		
Lys	Pro	Ser	Lys	Tyr	Val	Val	Ser	Leu	Lys	Pro	Leu	Tyr	Leu	Ala	
			35				40					45			

Pro Leu Asp Gly Pro Arg Thr Ala Glu Leu Lys Ser Arg Arg
50 55 60

(2) INFORMATION FOR SEQ ID NO:1845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..529
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1845:

aattctgcaa	agcacgarc	cggttcgttc	tcgaccttc	gtctcgctct	cgccgcgmcg	60
accccgcgga	scctagccta	gccttgcccc	cgaccgcgga	ttccccctcg	gccgcgcgcg	120
gccgcgaccc	gcaccgcgga	tgatgaactg	cgccggaggg	nangaccccg	tgaggagactt	180
cctgatctcc	ggcgccgtcg	acgacgaaga	tctagccatc	ttctgcgacg	gaggacttgg	240
gattgarggt	gtcaatggag	atgcttgttg	atttgagcag	tctaatttgg	gcaaaaggag	300
tagagatgaa	ccatgttcat	ctgggtctaaa	atccaaagct	tgctcgtgaaa	aaatgaggag	360
ggacaagctg	aatgacaggt	tcttgggaatt	aarttcggtt	atgaatcctg	gaaaacaagc	420
aaagttggat	aaagccaata	tcttgarcga	mgcagccctg	atggtggcac	aacttagagg	480
tgaggcagaa	aagcttaaa	aatcaaatga	gaagctgcgg	grgaatatc		

(2) INFORMATION FOR SEQ ID NO:1846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1846:

Met	Met	Asn	Cys	Ala	Gly	Gly	Xaa	Asp	Pro	Val	Glu	Asp	Phe	Leu	Ile
1		5						10						15	
Ser	Gly	Ala	Val	Asp	Asp	Glu	Asp	Leu	Ala	Ile	Phe	Cys	Asp	Gly	Gly
		20						25					30		
Leu	Gly	Ile	Xaa	Gly	Val	Asn	Gly	Asp	Ala	Cys	Gly	Phe	Glu	Gln	Ser
		35						40					45		
Asn	Leu	Gly	Lys	Arg	Ser	Arg	Asp	Glu	Pro	Cys	Ser	Ser	Gly	Leu	Lys
		50						55					60		
Ser	Lys	Ala	Cys	Arg	Glu	Lys	Met	Arg	Arg	Asp	Lys	Leu	Asn	Asp	Arg
65					70					75					80
Phe	Leu	Glu	Leu	Xaa	Ser	Val	Met	Asn	Pro	Gly	Lys	Gln	Ala	Lys	Leu
					85					90				95	
Asp	Lys	Ala	Asn	Ile	Leu	Xaa	Xaa	Ala	Ala	Arg	Met	Val	Ala	Gln	Leu
					100					105				110	
Arg	Gly	Glu	Ala	Glu	Lys	Leu	Lys	Glu	Ser	Asn	Glu	Lys	Leu	Arg	Xaa
					115					120				125	
Asn	Ile														
	130														

(2) INFORMATION FOR SEQ ID NO:1847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..129
(D) OTHER INFORMATION: / Ceres Seq. ID 1501418
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1847:
Met Asn Cys Ala Gly Gly Xaa Asp Pro Val Glu Asp Phe Leu Ile Ser
1 5 10 15
Gly Ala Val Asp Asp Glu Asp Leu Ala Ile Phe Cys Asp Gly Gly Leu
20 25 30
Gly Ile Xaa Gly Val Asn Gly Asp Ala Cys Gly Phe Glu Gln Ser Asn
35 40 45
Leu Gly Lys Arg Ser Arg Asp Glu Pro Cys Ser Ser Gly Leu Lys Ser
50 55 60
Lys Ala Cys Arg Glu Lys Met Arg Arg Asp Lys Leu Asn Asp Arg Phe
65 70 75 80
Leu Glu Leu Xaa Ser Val Met Asn Pro Gly Lys Gln Ala Lys Leu Asp
85 90 95
Lys Ala Asn Ile Leu Xaa Xaa Ala Ala Arg Met Val Ala Gln Leu Arg
100 105 110
Gly Glu Ala Glu Lys Leu Lys Glu Ser Asn Glu Lys Leu Arg Xaa Asn
115 120 125
Ile

(2) INFORMATION FOR SEQ ID NO:1848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..546
(D) OTHER INFORMATION: / Ceres Seq. ID 1501439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1848:

gaggcgatcg catcgagac tcggagccgg caaaacctta aggggaaggt ttctgcaagg 60
aggagggaga tgcaggcgcg cagcacatgc tctggagga gcccttcgcg ctgcgctccg 120
tcctctcccc cgccaagcct aaagtatttc catcactcac caagatagtt gggacgctcg 180
ggcccaattc acactcgggt gagattattc aggaatgcct cactgctgga atgtcagttg 240
cacgatttga tttctcatgg atggatgctg cgtatcacca ggagaccctt gataatttga 300
ggaaaagcggc acagaatgtg aagaagtgtt gccctgtaat gttggatact ctgtgtccag 360
aaattcaggt tcacaattcc actggtgagc caattgagtt gaaagctggg aatcatgtta 420
tcataactcc agatatttct aaagctctct ctgctgagat cctaccaatt aagtttggtg 480
atctggcaaa agctgtgaag aaggkgkata ctctttttat gggccaatat ctcttcacag 540
gaagtg

(2) INFORMATION FOR SEQ ID NO:1849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..153
(D) OTHER INFORMATION: / Ceres Seq. ID 1501440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1849:

Met Leu Leu Glu Glu Pro Phe Arg Leu Ala Ser Val Leu Ser Pro Ala
1 5 10 15
Lys Pro Lys Val Phe Pro Ser Leu Thr Lys Ile Val Gly Thr Leu Gly
20 25 30
Pro Asn Ser His Ser Val Glu Ile Ile Gln Glu Cys Leu Thr Ala Gly

35	40	45
Met Ser Val Ala Arg Phe Asp Phe Ser Trp Met Asp Ala Ala Tyr His		
50	55	60
Gln Glu Thr Leu Asp Asn Leu Arg Lys Ala Ala Gln Asn Val Lys Lys		
65	70	75
Leu Cys Pro Val Met Leu Asp Thr Leu Gly Pro Glu Ile Gln Val His		
85	90	95
Asn Ser Thr Gly Glu Pro Ile Glu Leu Lys Ala Gly Asn His Val Ile		
100	105	110
Ile Thr Pro Asp Ile Ser Lys Ala Leu Ser Ala Glu Ile Leu Pro Ile		
115	120	125
Lys Phe Gly Asp Leu Ala Lys Ala Val Lys Lys Xaa Asp Thr Leu Phe		
130	135	140
Met Gly Gln Tyr Leu Phe Thr Gly Ser		
145	150	

(2) INFORMATION FOR SEQ ID NO:1850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1501441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1850:

Met Ser Val Ala Arg Phe Asp Phe Ser Trp Met Asp Ala Ala Tyr His		
1	5	10
Gln Glu Thr Leu Asp Asn Leu Arg Lys Ala Ala Gln Asn Val Lys Lys		
20	25	30
Leu Cys Pro Val Met Leu Asp Thr Leu Gly Pro Glu Ile Gln Val His		
35	40	45
Asn Ser Thr Gly Glu Pro Ile Glu Leu Lys Ala Gly Asn His Val Ile		
50	55	60
Ile Thr Pro Asp Ile Ser Lys Ala Leu Ser Ala Glu Ile Leu Pro Ile		
65	70	75
Lys Phe Gly Asp Leu Ala Lys Ala Val Lys Lys Xaa Asp Thr Leu Phe		
85	90	95
Met Gly Gln Tyr Leu Phe Thr Gly Ser		
100	105	

(2) INFORMATION FOR SEQ ID NO:1851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1501442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1851:

Met Asp Ala Ala Tyr His Gln Glu Thr Leu Asp Asn Leu Arg Lys Ala		
1	5	10
Ala Gln Asn Val Lys Lys Leu Cys Pro Val Met Leu Asp Thr Leu Gly		
20	25	30
Pro Glu Ile Gln Val His Asn Ser Thr Gly Glu Pro Ile Glu Leu Lys		
35	40	45
Ala Gly Asn His Val Ile Ile Thr Pro Asp Ile Ser Lys Ala Leu Ser		
50	55	60

Ala Glu Ile Leu Pro Ile Lys Phe Gly Asp Leu Ala Lys Ala Val Lys
65 70 75 80
Lys Xaa Asp Thr Leu Phe Met Gly Gln Tyr Leu Phe Thr Gly Ser
85 90 95

(2) INFORMATION FOR SEQ ID NO:1852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..552
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1852:

tcgcatacgg	gagcttgccct	ttctaaatcc	tgagctaaca	ataatcttga	caaaggaaga	60
agggcacaca	gttcaacgca	acgaatatgt	ttatgctggt	ggccttggtg	aatatgttaa	120
atgggtgaat	actgacaaga	aaccctcgca	tgaccgcgatt	gcgttcagaa	aggaggttga	180
tggtataaca	gtggatgtct	cccttcaatg	gtcctctgat	tcctactctg	atacagtgtc	240
aggatacgcg	aacagtatcc	gcactattga	tggtggtact	catattgatg	gtctaaaggc	300
ttcattgacg	agaaccatta	ataaccttgc	aaagaagtcg	aagmtattaa	ggataaggat	360
attacccttga	gtggggagca	tgtaagagaa	ggaatgacat	gcatacttcc	agtgaaggtc	420
cctagttccag	agtttgaggg	tcaaacacaa	acaaggttgg	gaaatccaga	agtcacggga	480
atagttgagc	agtcgtgtca	agaaaaacta	acagagtact	tagagcttca	tccagatggt	540
ctggattcaa	tc					

(2) INFORMATION FOR SEQ ID NO:1853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1853:

Arg	Ile	Arg	Glu	Leu	Ala	Phe	Leu	Asn	Pro	Glu	Leu	Thr	Ile	Ile	Leu
1			5					10			15				
Thr	Lys	Glu	Glu	Gly	His	Thr	Val	Gln	Arg	Asn	Glu	Tyr	Cys	Tyr	Ala
			20				25				30				
Gly	Gly	Leu	Val	Glu	Tyr	Val	Lys	Trp	Leu	Asn	Thr	Asp	Lys	Lys	Pro
		35				40					45				
Leu	His	Asp	Pro	Ile	Ala	Phe	Arg	Lys	Glu	Leu	Asp	Gly	Ile	Thr	Val
		50				55					60				
Asp	Val	Ser	Leu	Gln	Trp	Ser	Ser	Asp	Ser	Tyr	Ser	Asp	Thr	Val	Leu
65				70						75				80	
Gly	Tyr	Ala	Asn	Ser	Ile	Arg	Thr	Ile	Asp	Gly	Gly	Thr	His	Ile	Asp
				85					90				95		
Gly	Leu	Lys	Ala	Ser	Leu	Thr	Arg	Thr	Ile	Asn	Asn	Leu	Ala	Lys	Lys
			100				105					110			
Ser	Lys	Xaa	Leu	Arg	Ile	Arg	Ile	Leu	Pro						
			115				120								

(2) INFORMATION FOR SEQ ID NO:1854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1854:

actaccgag	ttcaactcac	actcgtgcac	ccatccgggt	cactggctca	ctgacaccgc	60
gccccaatca	cgcgcgcgc	accgcgcgatg	atggcgcgcg	cggcgatctc	cggtccacgc	120
ggccacctcg	tcgtctcctc	cccccgcttc	aggcagccgc	tcacgctccc	ttctcgacgc	180
ggtcgcccaa	tcgccgcgcg	cgccctcgcc	gtggcccgcg	cgggggctgc	ggtcgccgcc	240
gtgtccagcc	ccgctgtgtc	ggccgtcgcg	gggaaggatg	ccaaacaggc	tcctaaggat	300
ttccttcata	tcaatgattt	tgacaaggat	acaataatga	atatccttaa	tcgacgcgatc	360
gaggttaagg	cagcgataaa	gtctggagac	aggagcttcc	aaccattcaa	tgggaaatca	420
agggcgatga	tttttgccaa	gccatcaatg	aggaccgctg	tttcatttga	ggcgggatcc	480
ttcttacttg	gtggcgatgc	tatttatattg	ggctcc			

(2) INFORMATION FOR SEQ ID NO:1855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1855:

Tyr	Pro	Ser	Ser	Leu	His	Thr	Arg	Ala	Pro	Ile	Arg	Val	Thr	Gly	Ser
1				5				10					15		
Leu	Thr	Pro	Arg	Pro	Asn	His	Ala	Arg	Ala	Thr	Arg	Asp	Asp	Gly	Gly
				20				25					30		
Gly	Gly	Asp	Leu	Arg	Leu	Gln	Arg	Pro	Pro	Arg	Arg	Leu	Leu	Pro	Pro
				35				40					45		
Leu	Gln	Ala	Ala	Ala	His	Ala	Pro	Phe	Ser	Gln	Arg	Ser	Pro	Asn	Arg
				50				55					60		
Arg	Arg	Arg	Leu	Gly	Arg	Gly	Pro	Arg	Arg	Gly	Arg	Gly	Arg	Arg	Arg
				65				70					75		
Val	Gln	Pro	Arg	Cys	Val	Gly	Arg	Arg	Gly	Glu	Gly	Cys	Gln	Thr	Gly
				85				90					95		

Ser

(2) INFORMATION FOR SEQ ID NO:1856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1856:

Met	Met	Ala	Ala	Ala	Ala	Ile	Ser	Gly	Ser	Ser	Gly	His	Leu	Val	Val
1								5					10		
Ser	Ser	Pro	Arg	Phe	Arg	Gln	Pro	Leu	Thr	Leu	Pro	Ser	Arg	Ser	Gly
				20				25					30		
Arg	Pro	Ile	Ala	Ala	Ala	Ala	Ser	Ala	Val	Ala	Arg	Gly	Gly	Val	Ala
				35				40					45		
Val	Ala	Ala	Val	Ser	Ser	Pro	Ala	Val	Ser	Ala	Val	Ala	Gly	Lys	Asp
				50				55					60		
Ala	Lys	Gln	Ala	Pro	Lys	Asp	Phe	Leu	His	Ile	Asn	Asp	Phe	Asp	Lys

65	70	75	80
Asp Thr Ile Met Asn Ile Leu Asn Arg Ala Ile Glu Val Lys Ala Ala			
	85	90	95
Ile Lys Ser Gly Asp Arg Ser Phe Gln Pro Phe Asn Gly Lys Ser Met			
	100	105	110
Ala Met Ile Phe Ala Lys Pro Ser Met Arg Thr Arg Val Ser Phe Glu			
	115	120	125
Ala Gly Phe Phe Leu Leu Gly Gly His Ala Ile Tyr Leu Gly			
	130	135	140

(2) INFORMATION FOR SEQ ID NO:1857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1857:

Met Ala Ala Ala Ala Ile Ser Gly Ser Ser Gly His Leu Val Val Ser			
1	5	10	15
Ser Pro Arg Phe Arg Gln Pro Leu Thr Leu Pro Ser Arg Ser Gly Arg			
	20	25	30
Pro Ile Ala Ala Ala Ala Ser Ala Val Ala Arg Gly Gly Val Ala Val			
	35	40	45
Ala Ala Val Ser Ser Pro Ala Val Ser Ala Val Ala Gly Lys Asp Ala			
	50	55	60
Lys Gln Ala Pro Lys Asp Phe Leu His Ile Asn Asp Phe Asp Lys Asp			
	65	70	75
Thr Ile Met Asn Ile Leu Asn Arg Ala Ile Glu Val Lys Ala Ala Ile			
	85	90	95
Lys Ser Gly Asp Arg Ser Phe Gln Pro Phe Asn Gly Lys Ser Met Ala			
	100	105	110
Met Ile Phe Ala Lys Pro Ser Met Arg Thr Arg Val Ser Phe Glu Ala			
	115	120	125
Gly Phe Phe Leu Leu Gly Gly His Ala Ile Tyr Leu Gly			
	130	135	140

(2) INFORMATION FOR SEQ ID NO:1858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..577
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1858:

aacctctcgc	ctctctctcc	cacggtccgc	ccatttcgto	ccccgctcac	caactcaaac	60
ccctctcgcg	ctcaaacctc	aaccttagcc	ctagcccgct	cccgccggac	cgacgatgcc	120
gaagaggtgc	gcggggcgcc	ggacgaagag	gagttccgcg	ccgaggtgga	ggagcgccctc	180
atacaacgag	agtcacaagt	ctggaaagaag	aacacaccct	tcctctacga	ccctgcctac	240
accacgcgcg	tcgaatggcc	ctccccttacc	gtgcagtgcc	tcctccgaccg	caccgagccg	300
ccgggggaagg	accactccgt	ccagaagatg	atccttgagg	cgacacacct	tgacaacgag	360
cccaactacc	tcactgctgc	gcaggtccag	ctgcccctcg	acgacgcgca	ggcgacgcgc	420
cgcyactacg	acgatgacca	cgccgacatc	ggtggttttg	gcgcmgscct	cggsaargtg	480
caaatgtgtc	agcagataaa	tcattgatga	gaggtcaatc	gagctcgcta	tatgccccaa	540
aattcattta	taattgctac	taagacagtt	agcgcgag			

(2) INFORMATION FOR SEQ ID NO:1859:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1501490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1859:

```
Asn Pro Pro Ala Pro Pro Pro Thr Val Pro Pro Phe Arg Pro Pro Leu
1      5      10      15
Thr Asn Ser Asn Pro Leu Arg Ser Gln Thr Leu Thr Leu Ala Leu Ala
20
Arg Ser Arg Arg Thr Asp Asp Ala Glu Val Gly Gly Ala Ala Asp
35      40      45
Glu Glu Glu Phe Arg Ala Glu Val Glu Glu Arg Leu Ile Asn Glu Glu
50      55      60
Tyr Lys Ile Trp Lys Lys Asn Thr Pro Phe Leu Tyr Asp Leu Val Ile
65      70      75      80
Thr His Ala Leu Glu Trp Pro Ser Leu Thr Val Gln Trp Leu Pro Asp
85      90      95
Arg Thr Glu Pro Pro Gly Lys Asp His Ser Val Gln Lys Met Ile Leu
100      105      110
Gly Thr His Thr Ser Asp Asn Glu Pro Asn Tyr Leu Met Leu Ala Gln
115      120      125
Val Gln Leu Pro Leu Asp Asp Ala Glu Ala Asp Ala Arg Xaa Tyr Asp
130      135      140
Asp Asp His Ala Asp Ile Gly Gly Phe Gly Xaa Xaa Ser Xaa Xaa Val
145      150      155      160
Gln Ile Val Gln Gln Ile Asn His Asp Gly Glu Val Asn Arg Ala Arg
165      170      175
Tyr Met Pro Gln Asn Ser Phe Ile Ile Ala Thr Lys Thr Val Ser Ala
180      185      190
```

(2) INFORMATION FOR SEQ ID NO:1860:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1501491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1860:

```
Pro Ser Cys Ser Ser Ser His Gly Pro Ala Ile Ser Ser Pro Ala His
1      5      10      15
Gln Leu Lys Pro Pro Pro Leu Ser Asn Pro Asn Pro Ser Pro Ser Pro
20      25      30
Leu Pro Ala Asp Arg Arg Cys Arg Arg Gly Arg Arg Gly Gly Gly Arg
35      40      45
Arg Gly Val Pro Arg Arg Gly Gly Ala Pro His Gln Arg Gly Val
50      55      60
Gln Asp Leu Glu Glu Glu His Thr Leu Pro Leu Arg Pro Arg His His
65      70      75      80
Pro Arg Ala Arg Met Ala Leu Pro Tyr Arg Ala Val Ala Pro Arg Pro
```

85 90 95
His Arg Ala Ala Gly Glu Gly Pro Leu Arg Pro Glu Asp Asp Pro Trp
100 105 110
His Ala His Leu
115

(2) INFORMATION FOR SEQ ID NO:1861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..967
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1861:

aaaaactct	ctgtctctct	aggttttttg	attttagccg	ccgccgtgc	tcattctcaca	60
tcctcgcaga	agacgcctgc	tcctcgccga	tcgatacgat	ggcgcgtcttc	tcgcagctcc	120
acaccgcgca	cggcctcaag	tcctctcgagg	ctcacctcgc	cggcaaaacc	tatgtgtctg	180
gtgactccat	tactaaggat	gacattaaagg	tcttcgccgc	ggtgccgtcg	aagcctggcg	240
ctgagtttcc	taatgccgcc	cgtcggttag	agaccgtctc	tgcgggtgta	gcctcaagat	300
tcctctggtaa	ggctgttggt	gtaaaatctgc	ctgcggggatc	agctcctgcg	cgagctgctc	360
ctgcgggatga	ggctgaggat	gatgatgacc	ttgatctttt	ttggtgatgaa	actgaggagg	420
acaagaaggc	agctgatgag	cgtgccccgc	ctgcgaaggc	ctcttctaaa	aagaagaagaa	480
gtggtaaatc	tcctgtcctt	atggatgtca	aaccatggga	cgatgagact	gatatgaaga	540
agctggagga	ggctgtccgc	agtgctccaga	tggagggtct	gacttgggga	gcatacaaac	600
ttgtgcctgt	tggataccgc	atcaagaaga	tgactatcat	gttgacaatt	gtcgacgac	660
ttgtgtccat	cgacactcta	attgaggacc	accttaacga	agagcccatc	aatgagtaag	720
tcacagattg	cgacattgtg	gctttcaaca	agatctagag	ttcagtttct	gagattgggc	780
aacggcagcg	gctcagctcg	tcaagtttgt	gctgggatgc	cagtttatcc	cttctagtct	840
attacagaaa	tgttgttcgg	agctgagctc	attataaaca	tcttggtctg	agtttatgtt	900
tgagtggtgc	cagttttttt	caatatacat	ttatcttaaa	aacagcggtg	ctgatgtttt	960
ttgtct						

(2) INFORMATION FOR SEQ ID NO:1862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..251
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1862:

Lys	Thr	Leu	Cys	Leu	Ser	Arg	Phe	Phe	Asp	Phe	Ser	Arg	Arg	Arg	Cys
1			5						10				15		
Ser	Ser	His	Ile	Pro	Arg	Glu	Asp	Ala	Cys	Ser	Ser	Pro	Ile	Asp	Thr
			20				25						30		
Met	Ala	Val	Phe	Ser	Asp	Leu	His	Thr	Ala	Asp	Gly	Leu	Lys	Ser	Leu
			35				40					45			
Glu	Ala	His	Leu	Ala	Gly	Lys	Thr	Tyr	Val	Ser	Gly	Asp	Ser	Ile	Thr
			50				55					60			
Lys	Asp	Asp	Ile	Lys	Val	Phe	Ala	Ala	Val	Pro	Ser	Lys	Pro	Gly	Ala
			65				70				75			80	
Glu	Phe	Pro	Asn	Ala	Ala	Arg	Trp	Tyr	Glu	Thr	Val	Ser	Ala	Ala	Val
			85				90					95			
Ala	Ser	Arg	Phe	Pro	Gly	Lys	Ala	Val	Gly	Val	Asn	Leu	Pro	Ala	Gly
			100				105					110			
Ser	Ala	Pro	Ala	Ala	Ala	Pro	Ala	Asp	Glu	Ala	Glu	Asp	Asp	Asp	

115	120	125
Asp Leu Asp Leu Phe Gly Asp Glu Thr Glu Glu Asp Lys Lys Ala Ala		
130	135	140
Asp Glu Arg Ala Ala Ala Ala Lys Ala Ser Ser Lys Lys Lys Glu Ser		
145	150	155
Gly Lys Ser Ser Val Leu Met Asp Val Lys Pro Trp Asp Asp Glu Thr		
	160	165
Asp Met Lys Lys Leu Glu Glu Ala Val Arg Ser Val Gln Met Glu Gly		
	170	175
	180	185
Leu Thr Trp Gly Ala Ser Lys Leu Val Pro Val Gly Tyr Gly Ile Lys		
	190	195
Lys Met Thr Ile Met Leu Thr Ile Val Asp Asp Leu Val Ser Ile Asp		
	200	205
Thr Leu Ile Glu Asp His Leu Thr Gln Glu Pro Ile Asn Glu Tyr Val		
225	230	235
Gln Ser Cys Asp Ile Val Ala Phe Asn Lys Ile		240
	245	250

(2) INFORMATION FOR SEQ ID NO:1863:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1501517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1863:

Met Ala Val Phe Ser Asp Leu His Thr Ala Asp Gly Leu Lys Ser Leu		
1	5	10
Glu Ala His Leu Ala Gly Lys Thr Tyr Val Ser Gly Asp Ser Ile Thr		15
	20	25
Lys Asp Asp Ile Lys Val Phe Ala Ala Val Pro Ser Lys Pro Gly Ala		30
	35	40
Glu Phe Pro Asn Ala Ala Arg Trp Tyr Glu Thr Val Ser Ala Ala Val		45
	50	55
Ala Ser Arg Phe Pro Gly Lys Ala Val Gly Val Asn Leu Pro Ala Gly		60
65	70	75
Ser Ala Pro Ala Ala Ala Pro Ala Asp Glu Ala Glu Asp Asp Asp		80
	85	90
Asp Leu Asp Leu Phe Gly Asp Glu Thr Glu Glu Asp Lys Lys Ala Ala		95
	100	105
Asp Glu Arg Ala Ala Ala Ala Lys Ala Ser Ser Lys Lys Lys Glu Ser		110
	115	120
Gly Lys Ser Ser Val Leu Met Asp Val Lys Pro Trp Asp Asp Glu Thr		125
	130	135
Asp Met Lys Lys Leu Glu Glu Ala Val Arg Ser Val Gln Met Glu Gly		140
145	150	155
Leu Thr Trp Gly Ala Ser Lys Leu Val Pro Val Gly Tyr Gly Ile Lys		160
	165	170
Lys Met Thr Ile Met Leu Thr Ile Val Asp Asp Leu Val Ser Ile Asp		175
	180	185
Thr Leu Ile Glu Asp His Leu Thr Gln Glu Pro Ile Asn Glu Tyr Val		190
	195	200
Gln Ser Cys Asp Ile Val Ala Phe Asn Lys Ile		205
	210	215

(2) INFORMATION FOR SEQ ID NO:1864:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 584 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..584
(D) OTHER INFORMATION: / Ceres Seq. ID 1501543
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1864:
agctgacaac cagacgcgcc agggtttcag gcttccacga atctccccgc cgccctcaat 60
tcctcccgcc gccgcgcctt cctccctcgc cttcggtcct cggttagtta accatccagg 120
ttctgtcaag atgtctgata gccatgagac tgacaggaac attgagattt ggaaaaattaa 180
gaaactgata aaggcattgg aatcagccag aggcgaatggc acaagcatga tctctctaat 240
catgctctca cgtgatcagg ttgctcgagt ggctaagatg ttagggtgatg aatatgggtac 300
tgcttcgaac atcaagagta gagttaatcg tcaatctgtg ttggctgcga tcacctcagg 360
tcagcagagg ttgaagctct acaacaaagt gcctcctaac ggattgggtc tgtacactgg 420
aactattggt actgaagcag gaaaggaaaa gaaagttaac attgattttg agccattcaa 480
gcctatcaat gtgtcaactct acctttgtga caacaagttc cacactgagg ctttaaatga 540
gctcttgtaa tctgatgaca agtttgggtt catgtttatg gatg
(2) INFORMATION FOR SEQ ID NO:1865:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 194 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..194
(D) OTHER INFORMATION: / Ceres Seq. ID 1501544
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1865:
Ala Asp Asn Gln Thr Arg Gln Gly Phe Arg Leu Pro Arg Ile Ser Pro
1 5 10 15
Pro Pro Ser Ile Pro Leu Gly Ala Ala Ala Ser Ser Pro Arg Phe Gly
20 25 30
Pro Arg Leu Val Asn His Pro Gly Ser Val Lys Met Ser Asp Ser His
35 40 45
Glu Thr Asp Arg Asn Ile Glu Ile Trp Lys Ile Lys Lys Leu Ile Lys
50 55 60
Ala Leu Glu Ser Ala Arg Gly Asn Gly Thr Ser Met Ile Ser Leu Ile
65 70 75 80
Met Pro Pro Arg Asp Gln Val Ala Arg Val Ala Lys Met Leu Gly Asp
85 90 95
Glu Tyr Gly Thr Ala Ser Asn Ile Lys Ser Arg Val Asn Arg Gln Ser
100 105 110
Val Leu Ala Ala Ile Thr Ser Ala Gln Gln Arg Leu Lys Leu Tyr Asn
115 120 125
Lys Val Pro Pro Asn Gly Leu Val Leu Tyr Thr Gly Thr Ile Val Thr
130 135 140
Glu Asp Gly Lys Glu Lys Lys Val Thr Ile Asp Phe Glu Pro Phe Lys
145 150 155 160
Pro Ile Asn Val Ser Leu Tyr Leu Cys Asp Asn Lys Phe His Thr Glu
165 170 175
Ala Leu Asn Glu Leu Leu Glu Ser Asp Asp Lys Phe Gly Phe Ile Val
180 185 190
Met Asp

(2) INFORMATION FOR SEQ ID NO:1866:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..151
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501545
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1866:
Met Ser Asp Ser His Glu Thr Asp Arg Asn Ile Glu Ile Trp Lys Ile
1 5 10 15
Lys Lys Leu Ile Lys Ala Leu Glu Ser Ala Arg Gly Asn Gly Thr Ser
 20 25 30
Met Ile Ser Leu Ile Met Pro Pro Arg Asp Gln Val Ala Arg Val Ala
 35 40 45
Lys Met Leu Gly Asp Glu Tyr Gly Thr Ala Ser Asn Ile Lys Ser Arg
 50 55 60
Val Asn Arg Gln Ser Val Leu Ala Ala Ile Thr Ser Ala Gln Gln Arg
65 70 75 80
Leu Lys Leu Tyr Asn Lys Val Pro Pro Asn Gly Leu Val Leu Tyr Thr
 85 90 95
Gly Thr Ile Val Thr Glu Asp Gly Lys Glu Lys Lys Val Thr Ile Asp
 100 105 110
Phe Glu Pro Phe Lys Pro Ile Asn Val Ser Leu Tyr Leu Cys Asp Asn
 115 120 125
Lys Phe His Thr Glu Ala Leu Asn Glu Leu Leu Glu Ser Asp Asp Lys
 130 135 140
Phe Gly Phe Ile Val Met Asp
145 150
(2) INFORMATION FOR SEQ ID NO:1867:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..119
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501546
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1867:
Met Ile Ser Leu Ile Met Pro Pro Arg Asp Gln Val Ala Arg Val Ala
1 5 10 15
Lys Met Leu Gly Asp Glu Tyr Gly Thr Ala Ser Asn Ile Lys Ser Arg
 20 25 30
Val Asn Arg Gln Ser Val Leu Ala Ala Ile Thr Ser Ala Gln Gln Arg
 35 40 45
Leu Lys Leu Tyr Asn Lys Val Pro Pro Asn Gly Leu Val Leu Tyr Thr
 50 55 60
Gly Thr Ile Val Thr Glu Asp Gly Lys Glu Lys Lys Val Thr Ile Asp
65 70 75 80
Phe Glu Pro Phe Lys Pro Ile Asn Val Ser Leu Tyr Leu Cys Asp Asn
 85 90 95
Lys Phe His Thr Glu Ala Leu Asn Glu Leu Leu Glu Ser Asp Asp Lys
 100 105 110
Phe Gly Phe Ile Val Met Asp
115
(2) INFORMATION FOR SEQ ID NO:1868:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1030 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1030

(D) OTHER INFORMATION: / Ceres Seq. ID 1501547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1868:

aaaaggaacc	ctagccatga	gcgcgcgcctc	caagaagctc	ttccaggccg	ccagggtccct	60
cgctctctcc	gcttctaacc	gctccgtcct	cgccgcgcgag	ggccgcaccg	ccgcgctcgc	120
cacgctcacc	aacttttgca	ggaagaccct	ccccaccgcc	tacttatcct	accacaagca	180
gggatccccc	catgcgcgct	cggggtgggg	agccatcgcc	gccgcagtc	caagctgmgt	240
ttacatgctc	caggaccagg	aggctcatgc	tgacagatg	gagcgccact	tcattgccat	300
caagctgat	ggtgtccaaa	gagccctgat	ttctgagatt	atgagccgat	ttgagagaaa	360
aggctataag	cttgttgcca	tcaagctgat	tgttccatcc	aaagaatttg	ctgagaagca	420
ctaccatgat	ctcaaggaaa	ggcctttctt	cagtggggtg	tgtgattttc	tcagctctgg	480
ccctgtgctt	gcaatgggtt	gggaaggaga	gggtgtcatc	aagtatggga	gaaaactaat	540
tggtgccaca	gacccacaga	aatctgaacc	aggaaccatc	aggggtgatc	ttgccattgt	600
tggtggaaga	aacatcattc	atggaagtga	tggccacagag	acagcggaag	atgagatcgc	660
tttatgtgtt	gaaccacaag	agctggtctc	ttacaccagc	aatgcggaga	agtggatcta	720
tggggtgaat	taacgagaga	gtcaatctgt	tttttttctt	tcctttgatc	tcggttttca	780
cataattgcc	gcagacacct	ggcacaaagg	tgtaataaag	tcgctaccgt	caactctgag	840
ttgattgtg	accttcaggt	gtagtaaggc	acaaggaaag	atggaaagga	aggaatatata	900
ccgtgaaata	tagagcgtgc	actgagtagt	cgcgatgttc	aaatcaacct	atatatcacc	960
gtcactggag	tcattgtaac	caagatgggt	atgcagatgt	ttctttggat	ctattttctt	1020
agatatcccc						

(2) INFORMATION FOR SEQ ID NO:1869:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..243

(D) OTHER INFORMATION: / Ceres Seq. ID 1501548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1869:

Lys	Gly	Thr	Leu	Ala	Met	Ser	Ala	Ala	Ser	Lys	Lys	Leu	Phe	Gln	Ala	7
1					5				10					15		
Ala	Arg	Ser	Leu	Val	Leu	Ser	Ala	Ser	Asn	Arg	Ser	Val	Leu	Ala	Ala	21
			20					25				30				
Glu	Gly	Arg	Thr	Ala	Ala	Leu	Ala	Thr	Leu	Thr	Asn	Phe	Gly	Arg	Lys	27
			35					40				45				
Thr	Leu	Pro	Thr	Ala	Tyr	Leu	Ser	Tyr	His	Lys	Gln	Gly	Ser	His	Lys	33
			50					55				60				
Ala	Ala	Ser	Gly	Trp	Gly	Ala	Ile	Ala	Ala	Ala	Val	Pro	Ala	Xaa	Val	39
			65			70				75						
Tyr	Met	Leu	Gln	Asp	Gln	Glu	Ala	His	Ala	Ala	Glu	Met	Glu	Arg	Thr	45
			85					90						95		
Phe	Ile	Ala	Ile	Lys	Pro	Asp	Gly	Val	Gln	Arg	Gly	Leu	Ile	Ser	Glu	51
			100					105					110			
Ile	Met	Ser	Arg	Phe	Glu	Arg	Lys	Gly	Tyr	Lys	Leu	Val	Ala	Ile	Lys	57
			115					120				125				
Leu	Ile	Val	Pro	Ser	Lys	Glu	Phe	Ala	Glu	Lys	His	Tyr	His	Asp	Leu	63
			130					135				140				
Lys	Glu	Arg	Pro	Phe	Phe	Ser	Gly	Leu	Cys	Asp	Phe	Leu	Ser	Ser	Gly	69
			145					150				155				
Pro	Val	Leu	Ala	Met	Val	Trp	Glu	Gly	Glu	Gly	Val	Ile	Lys	Tyr	Gly	75
			165					170					175			
Arg	Lys	Leu	Ile	Gly	Ala	Thr	Asp	Pro	Gln	Lys	Ser	Glu	Pro	Gly	Thr	81
			180					185					190			
Ile	Arg	Gly	Asp	Leu	Ala	Ile	Val	Val	Gly	Arg	Asn	Ile	His	Gly		87

195	200	205
Ser Asp Gly Pro Glu Thr Ala Lys Asp Glu Ile Ala Leu Trp Phe Glu		
210	215	220
Pro Lys Glu Leu Val Ser Tyr Thr Ser Asn Ala Glu Lys Trp Ile Tyr		
225	230	235
Gly Val Asn		240

(2) INFORMATION FOR SEQ ID NO:1870:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..238

(D) OTHER INFORMATION: / Ceres Seq. ID 1501549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1870:

Met Ser Ala Ala Ser Lys Lys Leu Phe Gln Ala Ala Arg Ser Leu Val		
1	5	10
Leu Ser Ala Ser Asn Arg Ser Val Leu Ala Ala Glu Gly Arg Thr Ala		
	20	25
Ala Leu Ala Thr Leu Thr Asn Phe Gly Arg Lys Thr Leu Pro Thr Ala		
	35	40
Tyr Leu Ser Tyr His Lys Gln Gly Ser His His Ala Ala Ser Gly Trp		
	50	55
Gly Ala Ile Ala Ala Val Pro Ala Xaa Val Tyr Met Leu Gln Asp		
	65	70
Gln Glu Ala His Ala Ala Glu Met Glu Arg Thr Phe Ile Ala Ile Lys		
	85	90
Pro Asp Gly Val Gln Arg Gly Leu Ile Ser Glu Ile Met Ser Arg Phe		
	100	105
Glu Arg Lys Gly Tyr Lys Leu Val Ala Ile Lys Leu Ile Val Pro Ser		
	115	120
Lys Glu Phe Ala Glu Lys His Tyr His Asp Leu Lys Glu Arg Pro Phe		
	130	135
Phe Ser Gly Leu Cys Asp Phe Leu Ser Ser Gly Pro Val Leu Ala Met		
	145	150
Val Trp Glu Gly Glu Gly Val Ile Lys Tyr Gly Arg Lys Leu Ile Gly		
	165	170
Ala Thr Asp Pro Gln Lys Ser Glu Pro Gly Thr Ile Arg Gly Asp Leu		
	180	185
Ala Ile Val Val Gly Arg Asn Ile Ile His Gly Ser Asp Gly Pro Glu		
	195	200
Thr Ala Lys Asp Glu Ile Ala Leu Trp Phe Glu Pro Lys Glu Leu Val		
	210	215
Ser Tyr Thr Ser Asn Ala Glu Lys Trp Ile Tyr Gly Val Asn		
	225	230
		235

(2) INFORMATION FOR SEQ ID NO:1871:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1501550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1871:

```

Met Leu Gln Asp Gln Glu Ala His Ala Ala Glu Met Glu Arg Thr Phe
1          5          10          15
Ile Ala Ile Lys Pro Asp Gly Val Gln Arg Gly Leu Ile Ser Glu Ile
20          25          30
Met Ser Arg Phe Glu Arg Lys Gly Tyr Lys Leu Val Ala Ile Lys Leu
35          40          45
Ile Val Pro Ser Lys Glu Phe Ala Glu Lys His Tyr His Asp Leu Lys
50          55          60
Glu Arg Pro Phe Phe Ser Gly Leu Cys Asp Phe Leu Ser Ser Gly Pro
65          70          75          80
Val Leu Ala Met Val Trp Glu Gly Glu Gly Val Ile Lys Tyr Gly Arg
85          90          95
Lys Leu Ile Gly Ala Thr Asp Pro Gln Lys Ser Glu Pro Gly Thr Ile
100          105          110
Arg Gly Asp Leu Ala Ile Val Val Gly Arg Asn Ile Ile His Gly Ser
115          120          125
Asp Gly Pro Glu Thr Ala Lys Asp Glu Ile Ala Leu Trp Phe Glu Pro
130          135          140
Lys Glu Leu Val Ser Tyr Thr Ser Asn Ala Glu Lys Trp Ile Tyr Gly
145          150          155          160
Val Asn

```

(2) INFORMATION FOR SEQ ID NO:1872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..563
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1872:

```

attggcgac aaatcagcaa caggcgccg gaacaaatgg ggctgtctgta gtcgggaggg      60
cttcttagtt taggggctct gggccargtc gacctgtgtt tttttttcca atagcggatt      120
arcccaacag agaacccttc acggccctgc tagagagagt ttaacaatca aaatagaaaa      180
cagaaacaaa attcatcaga gtgagagttc atcttctctt ccaagctgat tctgtctgtg      240
tagctactca cgtcaacaga aaatctcgcg ttcagctcct ctccagtcct tccgctccc      300
gcttactctc ctgactctgt cctctttcgt ttctttcttg tcggcgacgg ctggcggtcg      360
gggtgctcgc cgcgtctcac ctccaccgcc gacgagcatt cacaagtagt gttctcttcc      420
wggtagcgcc gtagagtgta cgaaaaagcc ttgacaatga gcagcatagg cacaggttat      480
gactgtctcg tcaccacatt ctctcccgat ggccgcgtct tccaggtcga gtagccacg      540
aargctgtcg acaacagcgg gac

```

(2) INFORMATION FOR SEQ ID NO:1873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1873:

```

Met Ser Ser Ile Gly Thr Gly Tyr Asp Leu Ser Val Thr Thr Phe Ser
1          5          10          15
Pro Asp Gly Arg Val Phe Gln Val Glu Tyr Ala Thr Xaa Ala Val Asp
20          25          30
Asn Ser Gly

```

35

(2) INFORMATION FOR SEQ ID NO:1874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..567
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1874:

agggc	aaaaag	aggaa	atttct	tttggg	ctgg	gtcta	ataaaa	cccta	atggg	ctgcg	ggcctc	60
gtaga	taaac	cagca	ctact	catccg	tcgc	cccac	ggaag	tttcg	gcggc	gcsgc	gtgct	120
cgatg	atcga	acca	aggcgt	gtctcc	gcctc	cggtc	accgc	tcact	ccacg	caaac	atgtc	180
gaggag	gaag	accag	gggagc	ccaag	gagga	gaacg	tcacc	cttgg	acccta	ctgtc	ccgtga	240
aggag	agat	gtctt	tttgt	tgcgt	cacat	ctttg	catcc	ttcaat	gaca	ctttc	atcatca	300
tatcact	gat	ttgtc	ttggga	gggaa	actct	ggttc	gggatc	accgg	tggtga	tgaag	gtgaa	360
ggctg	accgt	gacga	gtcgt	cacct	tacgc	tgctat	gctt	gctgc	tcaag	acgtc	gcaca	420
gcgctg	caag	gagct	ttggca	ttact	gcact	gcacatt	aag	cttcg	tgcca	ccggag	gcaca	480
caagac	caag	accccc	ggac	ctggg	tgccta	gtctg	ccctc	agggc	gcttg	ctcgt	ttctgg	540
gatga	aaatc	ggacg	cattg	aggac	gt							

(2) INFORMATION FOR SEQ ID NO:1875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1875:

Met	Gly	Cys	Gly	Leu	Val	Asp	Lys	Pro	Ala	Leu	Leu	Ile	Arg	Arg	Pro
1			5					10					15		
Thr	Glu	Val	Ser	Ala	Ala	Xaa	Arg	Ala	Arg	Asp	Leu	Asn	Gln	Gly	Val
			20					25					30		
Ser	Pro	Leu	Arg	Ser	Pro	Val	Thr	Pro	Arg	Lys	His	Val	Glu	Glu	Glu
			35					40					45		
Asp	Gln	Gly	Ala	Gln	Gly	Gly	Glu	Arg	His	Pro	Trp	Thr	His	Cys	Pro
			50					55					60		

(2) INFORMATION FOR SEQ ID NO:1876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1876:

Met	Ser	Arg	Arg	Lys	Thr	Arg	Glu	Pro	Lys	Glu	Glu	Asn	Val	Thr	Leu
1				5				10					15		
Gly	Pro	Thr	Val	Arg	Glu	Gly	Glu	Tyr	Val	Phe	Xaa	Val	Ala	His	Ile
			20					25					30		

Phe Ala Ser Phe Asn Asp Thr Phe Ile His Ile Thr Asp Leu Ser Gly
35 40 45
Arg Glu Thr Leu Val Arg Ile Thr Gly Gly Met Lys Val Lys Ala Asp
50 55 60
Arg Asp Glu Ser Ser Pro Tyr Ala Ala Met Leu Ala Ala Gln Asp Val
65 70 75 80
Ala Gln Arg Cys Lys Glu Leu Gly Ile Thr Ala Leu His Ile Lys Leu
85 90 95
Arg Ala Thr Gly Gly Asn Lys Thr Lys Thr Pro Gly Pro Gly Ala Gln
100 105 110
Ser Ala Leu Arg Ala Leu Ala Arg Ser Gly Met Lys Ile Gly Arg Ile
115 120 125
Glu Asp
130

(2) INFORMATION FOR SEQ ID NO:1877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1877:

Met Lys Val Lys Ala Asp Arg Asp Glu Ser Ser Pro Tyr Ala Ala Met
1 5 10 15
Leu Ala Ala Gln Asp Val Ala Gln Arg Cys Lys Glu Leu Gly Ile Thr
20 25 30
Ala Leu His Ile Lys Leu Arg Ala Thr Gly Gly Asn Lys Thr Lys Thr
35 40 45
Pro Gly Pro Gly Ala Gln Ser Ala Leu Arg Ala Leu Ala Arg Ser Gly
50 55 60
Met Lys Ile Gly Arg Ile Glu Asp
65 70

(2) INFORMATION FOR SEQ ID NO:1878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..495
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1878:

gtcataaact aaatactcag acaaccatg ggcaccagca ggcgcasacg gcaaggacga 60
cacgcaggag ctgcttgacg cccacgggca gctgtgtgct catgccctgg gctacgtcaa 120
gtccatggcg ctaagtgcg ccttggaact gcgcacccc gacaccatcg accgctgogg 180
cgggagcgcc accctgggcg agctgctcgc cgccagcgag atccccgcgt ccaaccacga 240
ctactctcgg cgggtatcgc gcacgctgac agccatgcgc atcttcgcgg ccagccacga 300
ccccgccaa ggcgacgacg cgcccgccat ctccctaccg ctgaaccccg cgtcccggt 360
gctcgtcagc agcagcagca ggtcgacga cgccgcgggg cctcgaagga gaacactact 420
accgcagca tcctcccca catcgccacc ctggtccgcc ccaacacat etccctgctg 480
ttcagcatgg gcgag

(2) INFORMATION FOR SEQ ID NO:1879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..165
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501572
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1879:
Val Ile Asn Gln Ile Leu Arg Gln Pro Trp Gly Thr Ser Arg Arg Xaa
1 5 10 15
Arg Gln Gly Arg His Arg Gly Ala Ala Cys Ser Pro Pro Ala Ala Xaa
 20 25 30
Val Pro Cys Pro Gly Leu Arg Gln Val His Gly Ala Gln Val Arg Pro
 35 40 45
Gly Pro Ala His Pro Arg His His Arg Pro Leu Arg Arg Glu Arg His
 50 55 60
Pro Gly Arg Ala Ala Arg Arg Gln Arg Asp Pro Gly Val Gln Pro Arg
65 70 75 80
Leu Pro Pro Ala Gly His Ala His Ala Asp Ser His Ala His Leu Arg
 85 90 95
Gly Gln Pro Arg Pro Arg Gln Gly Arg Arg Gly Arg His Arg Leu
 100 105 110
Pro Ala Asp Pro Gly Val Pro Ala Ala Arg Gln Gln Gln Gln Arg
 115 120 125
Arg Arg Arg Arg Arg Ala Ser Lys Glu Asn Thr Thr Thr Pro Ser Ile
 130 135 140
Leu Pro Asn Ile Ala His Leu Val Arg Pro Asn Thr Ile Ser Leu Leu
145 150 155 160
Phe Ser Met Gly Glu
 165
(2) INFORMATION FOR SEQ ID NO:1880:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..164
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501573
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1880:
Ser Ser Ile Lys Tyr Ser Asp Asn His Gly Ala Pro Ala Gly Ala Xaa
1 5 10 15
Gly Lys Asp Asp Thr Glu Glu Leu Leu Ala Ala His Gln Leu Xaa
 20 25 30
Cys His Ala Leu Gly Tyr Val Lys Ser Met Ala Leu Lys Cys Ala Leu
 35 40 45
Asp Leu Arg Ile Pro Asp Thr Ile Asp Arg Cys Gly Gly Ser Ala Thr
 50 55 60
Leu Gly Glu Leu Leu Ala Ala Ser Glu Ile Pro Ala Ser Asn His Asp
65 70 75 80
Tyr Leu Arg Arg Val Met Arg Thr Leu Thr Ala Met Arg Ile Phe Ala
 85 90 95
Ala Ser His Asp Pro Ala Lys Ala Asp Asp Ala Ala Ala Ile Ser Tyr
 100 105 110
Gln Leu Thr Pro Ala Ser Arg Leu Leu Val Ser Ser Ser Ser Val
 115 120 125
Asp Asp Ala Ala Gly Pro Arg Arg Arg Thr Leu Leu Pro Arg Ala Ser
130 135 140
Ser Pro Thr Ser Pro Thr Trp Ser Ala Pro Thr Pro Ser Pro Cys Cys

145
Ser Ala Trp Ala

150

155

160

(2) INFORMATION FOR SEQ ID NO:1881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1501574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1881:

```
Met Ala Leu Lys Cys Ala Leu Asp Leu Arg Ile Pro Asp Thr Ile Asp
1          5          10          15
Arg Cys Gly Gly Ser Ala Thr Leu Gly Glu Leu Leu Ala Ala Ser Glu
          20          25          30
Ile Pro Ala Ser Asn His Asp Tyr Leu Arg Arg Val Met Arg Thr Leu
          35          40          45
Thr Ala Met Arg Ile Phe Ala Ala Ser His Asp Pro Ala Lys Ala Asp
          50          55          60
Asp Ala Ala Ala Ile Ser Tyr Gln Leu Thr Pro Ala Ser Arg Leu Leu
          65          70          75          80
Val Ser Ser Ser Ser Ser Val Asp Asp Ala Ala Gly Pro Arg Arg Arg
          85          90          95
Thr Leu Leu Pro Arg Ala Ser Ser Pro Thr Ser Pro Thr Trp Ser Ala
          100          105          110
Pro Thr Pro Ser Pro Cys Cys Ser Ala Trp Ala
          115          120
```

(2) INFORMATION FOR SEQ ID NO:1882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..500

(D) OTHER INFORMATION: / Ceres Seq. ID 1501582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1882:

```
atcttaaacag ccaggaagct ggcgtcttgc ttgtccttgt tcttttccca cccggctacc 60
cccgctgctgc ccgcgcgttt ccccgctgggt tcagagctcg agtcggctag ctaggccgcc 120
tggtctaactc cctgccttc tataagtaca ggttcattgt gtgctgtgct cccagctcca 180
tcactgacac aagagagcac gctactactc atcactcgcc aacgtgcaga gatcagggag 240
gcggcacact ccatccactg accgctcatg gcgaaggtcc acctctactg cgccgcggcc 300
tgcgcgctgc tcctcgcgct cgccgccccg gccctcgccg gcgaccocga catgctgcag 360
gacgtctgcc cggtcgacta cgctcccccg gtgaagctga acgggttcgc gtgcaaggcg 420
aacctttcgg cggacgactt ctctctgcac gggctgagga accccggcaa caccaacaac 480
ccggcgggct ccgtgtgac
```

(2) INFORMATION FOR SEQ ID NO:1883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1501583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1883:

Met Ala Lys Val His Leu Tyr Val Ala Ala Cys Ala Val Val Leu
1 5 10 15
Ala Leu Ala Ala Pro Ala Leu Ala Gly Asp Pro Asp Met Leu Gln Asp
20 25 30
Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu Asn Gly Phe Ala
35 40 45
Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Phe Asp Gly Leu Arg
50 55 60
Asn Pro Gly Asn Thr Asn Asn Pro Ala Gly Ser Val Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:1884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1501584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1884:

Met Leu Gln Asp Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu
1 5 10 15
Asn Gly Phe Ala Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Phe
20 25 30
Asp Gly Leu Arg Asn Pro Gly Asn Thr Asn Asn Pro Ala Gly Ser Val
35 40 45
Val

(2) INFORMATION FOR SEQ ID NO:1885:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 515 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..515

(D) OTHER INFORMATION: / Ceres Seq. ID 1501589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1885:

agtggacagg tggcatcttc tgcgctcgca acacctcgcc gcccaaacgt aaccgtccca 60
acaaactcct ctccctcccc ttcccagcag aagtaccagc gccggccatg gacatgcagt 120
tcttcccaga caggcgcaact tgcgcctgcg gascgctggc acggcatgta ccttcacggc 180
gaggaagacg ggggtgagat caccctgcgc cgccgcgcgt ggacgctgaa cgaggcgtgg 240
gtrgtgaacc acctcgagcg caacggcgctc aactacgtcc tcttccacag cgccgcctac 300
ggcgcgttac tcgcacatcgt aagcatggaa gcgactccgc cgccgtcttc gggccaaggt 360
caaggcgccc gccgcacctg cctcgccgtc cagcgccctt acgacgccc agggcagaaac 420
gacgtctcgt ggcagttccg cttcgcgacg acgggtccga cgatgtgtgc atgcgcaaat 480
ggcgtgacgg caactggcac aactacggcg acgag

(2) INFORMATION FOR SEQ ID NO:1886:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1501590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1886:

Ser	Gly	Gln	Val	Ala	Ser	Ser	Ala	Leu	Ala	Thr	Pro	Arg	Arg	Pro	Asn	
1				5					10					15		
Val	Thr	Val	Pro	Thr	Asn	Ser	Ser	Pro	Ser	Pro	Ser	Gln	Gln	Lys	Tyr	
			20					25					30			
Gln	Arg	Arg	Pro	Trp	Thr	Cys	Ser	Ser	Ser	Pro	Thr	Gly	Ala	Leu	Ala	
			35				40					45				
Pro	Ala	Xaa	Arg	Trp	His	Gly	Met	Tyr	Leu	His	Ala	Glu	Glu	Asp	Gly	
			50			55					60					
Val	Arg	Ile	Thr	Leu	Arg	Arg	Arg	Arg	Gly	Thr	Leu	Asn	Glu	Ala	Trp	
65				70					75					80		
Xaa	Val	His	His	Leu	Glu	Arg	Asn	Gly	Val	Asn	Tyr	Val	Leu	Leu	His	
				85				90					95			
Ser	Ala	Ala	Tyr	Gly	Arg	Tyr	Leu	Ala	Ile	Val	Ser	Met	Glu	Ala	Thr	
			100					105					110			
Pro	Ala	Pro	Ser	Ser	Gly	Gln	Gly	Gln	Gly	Ala	Arg	Arg	Thr	Cys	Leu	
			115				120					125				
Ala	Val	Gln	Arg	Leu	Tyr	Asp	Ala	Pro	Gly	Gln	Asn	Asp	Val	Leu	Trp	
			130				135				140					
Gln	Phe	Arg	Phe	Ala	Thr	Thr	Gly	Pro	Thr	Met	Ser	Ser	Cys	Ala	Ile	
145				150					155					160		
Ala	Cys	Thr	Ala	Pro	Gly	Thr	Thr	Thr	Ala	Thr						
				165					170							

(2) INFORMATION FOR SEQ ID NO:1887:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1501591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1887:

Trp	Thr	Gly	Gly	Ile	Phe	Cys	Ala	Arg	Asn	Thr	Ser	Ala	Pro	Lys	Arg	
1				5					10					15		
Asn	Arg	Pro	Asn	Lys	Leu	Leu	Ser	Leu	Pro	Phe	Pro	Ala	Glu	Val	Pro	
			20					25					30			
Ala	Pro	Ala	Met	Asp	Met	Gln	Phe	Phe	Pro	Asp	Arg	Arg	Thr	Cys	Ala	
			35				40					45				
Cys	Gly	Xaa	Leu	Ala	Arg	His	Val	Pro	Ser	Arg	Arg	Gly	Arg	Arg	Gly	
			50			55					60					
Glu	Asp	His	Pro	Ala	Pro	Ala	Pro	Trp	Asp	Ala	Glu	Arg	Gly	Val	Gly	
65				70					75					80		
Xaa	Ala	Pro	Pro	Arg	Ala	Gln	Arg	Arg	Gln	Leu	Arg	Pro	Pro	Pro	Gln	
				85				90					95			
Arg	Arg	Leu	Arg	Pro	Leu	Pro	Arg	His	Arg	Lys	His	Gly	Ser	Asp	Ser	
			100					105					110			
Gly	Ala	Val	Phe	Gly	Pro	Arg	Ser	Arg	Arg	Pro	Pro	His	Leu	Pro	Arg	
			115				120					125				
Arg	Pro	Ala	Pro	Leu	Arg	Arg	Pro	Arg	Ala	Glu	Arg	Arg	Pro	Val	Ala	
			130				135				140					
Val	Pro	Leu	Arg	Asp	Asp	Gly	Ser	Asp	Asp	Val	Val	Met	Arg	Asn	Arg	
145				150					155					160		
Val	Tyr	Gly	Thr	Trp	His	Asn	Tyr	Gly	Asp	Glu						
				165					170							

(2) INFORMATION FOR SEQ ID NO:1888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1888:

Met Asp Met Gln Phe Phe Pro Asp Arg Arg Thr Cys Ala Cys Gly Xaa
1 5 10 15
Leu Ala Arg His Val Pro Ser Arg Arg Gly Arg Arg Gly Glu Asp His
20 25 30
Pro Ala Pro Ala Pro Trp Asp Ala Glu Arg Gly Val Gly Xaa Ala Pro
35 40 45
Pro Arg Ala Gln Arg Arg Gln Leu Arg Pro Pro Pro Gln Arg Arg Leu
50 55 60
Arg Pro Leu Pro Arg His Arg Lys His Gly Ser Asp Ser Gly Ala Val
65 70 75 80
Phe Gly Pro Arg Ser Arg Arg Pro Pro His Leu Pro Arg Arg Pro Ala
85 90 95
Pro Leu Arg Arg Pro Arg Ala Glu Arg Arg Pro Val Ala Val Pro Leu
100 105 110
Arg Asp Asp Gly Ser Asp Asp Val Val Met Arg Asn Arg Val Tyr Gly
115 120 125
Thr Trp His Asn Tyr Gly Asp Glu
130 135

(2) INFORMATION FOR SEQ ID NO:1889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..452
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1889:

atcacaaagca atcgatcaag ctagcatggc ggtgaagggtg tgggtgttcg ccgtggcact 60
gatgatgtgc gctggtgttag ggcttggagc tgacgacgac ggccggcagac cttattagcc 120
gctgtcgtct garctcgccc aactaccgcg gcgccctggc aaaggccatc ctcttcttcg 180
argggcgagcg gtcggggcgcg ctgccggcaa accagagagt cagtggtgcg ggggactcgg 240
cgctcaccca cgcccaaccc gaaaactgta acttgacggg tggctactac gacgccggag 300
acaacgtcaa gttcgggttc ccgatggcgt tcagcgtcac ctcctgarc tggagrcgcg 360
tcgagtaccg cbacgaggtg gcggcgcgcg gtcagctccg cmacctccgg tccgccatcc 420
agtkgggcgc cgaattccct ctcctdccc ac

(2) INFORMATION FOR SEQ ID NO:1890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1890:
Ser Gln Ala Ile Asp Gln Ala Ser Met Ala Val Lys Val Trp Val Phe
1 5 10 15
Ala Val Ala Leu Met Met Cys Ala Gly Val Gly Leu Gly Ala Asp Asp
 20 25 30
Asp Gly Gly Xaa Pro Tyr
 35

(2) INFORMATION FOR SEQ ID NO:1891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1891:

Met Ala Val Lys Val Trp Val Phe Ala Val Ala Leu Met Met Cys Ala
1 5 10 15
Gly Val Gly Leu Gly Ala Asp Asp Asp Gly Gly Xaa Pro Tyr
 20 25 30

(2) INFORMATION FOR SEQ ID NO:1892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1892:

Met Ala Phe Ser Val Thr Leu Leu Xaa Trp Ser Xaa Val Glu Tyr Arg
1 5 10 15
Xaa Glu Val Ala Ala Ala Gly Gln Leu Arg Xaa Leu Arg Ser Ala Ile
 20 25 30
Gln Xaa Gly Ala Asp Phe Leu Leu Arg Xaa His
 35 40

(2) INFORMATION FOR SEQ ID NO:1893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..501
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1893:

aaactctggtg	aatatacttta	caccgggaag	aaggcggaag	ccgtcgcgct	ctcggcrgcg	60
gcggcgccgg	cggcagcggc	gatgcttgcg	ttcgagcagc	aggtgttggc	ggatctgggtg	120
gaagatccga	acggaggtct	ggtggtgtct	tccctgggtc	tccctctcgc	ttccctagcc	180
gctaccctcc	tctccatct	ccaccagacc	cccggcaacg	cggtctggagg	aggatgtctc	240
ctcgtctctc	ccggcaccga	taccctcaag	gcccgatcc	ggcgccgcct	ccaagacaag	300
ctgcaggttc	acgacgtgcc	ccctgacctc	gccgcgcasa	gcgcgenmam	cctttacgcc	360
tctgggctgc	tctcttctct	tctccccgcg	cmctcgcmgc	cgacctctct	amctccccgm	420
tctctccctc	cccggtccaa	gcctactctc	tctctcgcg	cccacmgctc	camcgatacc	480

(2) INFORMATION FOR SEQ ID NO:1894:

```
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
```

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..167
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1501625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1894:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1895:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..107
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1501626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1895:

Thr	Ala	Gly	Ile	Tyr	Leu	His	Arg	Glu	Glu	Gly	Glu	Gly	Arg	Arg	Ala
1			5						10					15	
Leu	Gly	Xaa	Gly	Gly	Gly	Gly	Gly	Ser	Gly	Asp	Ala	Cys	Val	Arg	Ala
			20					25					30		
Ala	Gly	Val	Gly	Gly	Ser	Gly	Gly	Arg	Ser	Glu	Arg	Arg	Ser	Gly	Gly
		35					40					45			
Ala	Leu	Leu	Gly	Ser	Pro	Ser	Arg	Phe	Pro	Ser	Arg	Tyr	Pro	Pro	Pro
50						55					60				
Pro	Ser	Pro	Pro	Asp	Pro	Arg	Gln	Arg	Gly	Trp	Arg	Arg	Met	Ser	Pro
65				70						75					80
Arg	Pro	Leu	Arg	His	Arg	Tyr	Pro	Gln	Gly	Pro	Asp	Pro	Ala	Pro	Pro
				85					90					95	
Pro	Arg	Gln	Ala	Ala	Gly	Ser	Arg	Arg	Ala	Pro					
			100					105							

(2) INFORMATION FOR SEQ ID NO:1896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1896:

Met	Leu	Ala	Phe	Glu	Gln	Gln	Val	Leu	Ala	Asp	Leu	Val	Glu	Asp	Pro
1															
				5				10					15		
Asn	Gly	Gly	Leu	Val	Val	Leu	Ser	Ser	Gly	Leu	Pro	Leu	Ala	Ser	Leu
				20				25					30		
Ala	Ala	Thr	Leu	Leu	Leu	His	Leu	His	Gln	Thr	Pro	Gly	Asn	Ala	Ala
				35				40				45			
Gly	Gly	Gly	Cys	Leu	Leu	Val	Leu	Ser	Ala	Thr	Asp	Thr	Leu	Lys	Ala
				50				55				60			
Arg	Ile	Arg	Arg	Arg	Leu	Gln	Asp	Lys	Leu	Gln	Val	His	Asp	Val	Pro
				65				70				75			80
Pro	Asp	Leu	Ala	Ala	Xaa	Ser	Ala	Xaa	Xaa	Leu	Tyr	Ala	Ser	Gly	Leu
				85				90					95		
Leu	Ser	Ser	Ser	Leu	Pro	Ala	Xaa	Ser	Xaa	Pro	Thr	Ser	Ser	Xaa	Pro
				100				105					110		
Xaa	Ser	Ser	Pro	Pro	Ala	Ser	Lys	Pro	Tyr	Ser	Ser	Ser	Pro	Pro	His
				115				120					125		
Xaa	Ser	Xaa	Asp	Thr	Ser	Ser	Asp	Ala	Phe	Ile	Cys				
				130				135							140

(2) INFORMATION FOR SEQ ID NO:1897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..427

- (D) OTHER INFORMATION: / Ceres Seq. ID 1501632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1897:

aaactctgct	gcattctctt	ccactctcca	gtctccacta	gcactcagtcg	ccgctgccta	60
tcctcgagca	ccatttccat	caacagcatc	cgcctctggc	aagctagcga	casaactcat	120
ggcactccgc	gcgctcgaca	acacgatgcc	cgcmgccgtc	gaggagcgcc	ccaagaaggt	180
ggctaagggtg	ggcgtccccc	cmgcmgccgc	caaggccgcm	gcctccccc	ggagtggcgg	240
caagaagaag	aaggggaacg	acgagaactc	ggcgccaagg	gccacggccg	cggcgccgga	300
gcaggcmgtg	gagtagcatct	cgtcggagga	gctggaggcg	cgggccaacc	ctaaggccaa	360
ggccgcgggg	ctggtcgcgg	gccttgactc	caaggactgg	gtcaggacct	gcraggcgct	420
caacgac						

(2) INFORMATION FOR SEQ ID NO:1898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..142

- (D) OTHER INFORMATION: / Ceres Seq. ID 1501633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1898:
Asn Ser Ala Ala Ser Ser Ser Thr Leu Gln Ser Pro Leu Ala Ser Val
1 5 10 15
Ala Ala Ala Tyr Pro Arg Ala Pro Phe Pro Ser Thr Ala Ser Ala Ser
20 25 30
Gly Lys Leu Ala Thr Xaa Leu Met Ala Leu Arg Ala Leu Asp Asn Thr
35 40 45
Met Pro Xaa Ala Val Glu Glu Arg Pro Lys Lys Val Ala Lys Val Gly
50 55 60
Val Pro Xaa Xaa Ala Ala Lys Ala Xaa Ala Ser Pro Gly Ser Gly Gly
65 70 75 80
Lys Lys Lys Lys Gly Asn Asp Glu Asn Ser Ala Pro Arg Ala Thr Ala
85 90 95
Ala Ala Ala Glu Gln Xaa Val Glu Tyr Ile Ser Ser Glu Glu Leu Glu
100 105 110
Ala Ala Ala Asn Pro Lys Ala Lys Ala Ala Gly Leu Val Ala Gly Leu
115 120 125
Asp Ser Lys Asp Trp Val Arg Thr Cys Xaa Ala Leu Asn Asp
130 135 140

(2) INFORMATION FOR SEQ ID NO:1899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1899:
Met Ala Leu Arg Ala Leu Asp Asn Thr Met Pro Xaa Ala Val Glu Glu
1 5 10 15
Arg Pro Lys Lys Val Ala Lys Val Gly Val Pro Xaa Xaa Ala Ala Lys
20 25 30
Ala Xaa Ala Ser Pro Gly Ser Gly Gly Lys Lys Lys Lys Gly Asn Asp
35 40 45
Glu Asn Ser Ala Pro Arg Ala Thr Ala Ala Ala Glu Gln Xaa Val
50 55 60
Glu Tyr Ile Ser Ser Glu Glu Leu Glu Ala Ala Asn Pro Lys Ala
65 70 75 80
Lys Ala Ala Gly Leu Val Ala Gly Leu Asp Ser Lys Asp Trp Val Arg
85 90 95
Thr Cys Xaa Ala Leu Asn Asp
100

(2) INFORMATION FOR SEQ ID NO:1900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1900:
Met Pro Xaa Ala Val Glu Glu Arg Pro Lys Lys Val Ala Lys Val Gly
1 5 10 15
Val Pro Xaa Xaa Ala Ala Lys Ala Xaa Ala Ser Pro Gly Ser Gly Gly
20 25 30

Lys Lys Lys Lys Gly Asn Asp Glu Asn Ser Ala Pro Arg Ala Thr Ala
35 40 45
Ala Ala Ala Glu Gln Xaa Val Glu Tyr Ile Ser Ser Glu Glu Glu
50 55 60
Ala Ala Ala Asn Pro Lys Ala Lys Ala Ala Gly Leu Val Ala Gly Leu
65 70 75 80
Asp Ser Lys Asp Trp Val Arg Thr Cys Xaa Ala Leu Asn Asp
85 90

(2) INFORMATION FOR SEQ ID NO:1901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..541
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1901:

ccggaacgcc	cgccccgtcc	gtccctctccc	catccacatc	catccccgtg	gctccctactg	60
ctcctcgatt	tgatcaccca	ttagggggagg	cggttttacca	gtgagcacgc	gcgagarata	120
ggataggagg	aaagggaagc	tagcggsttc	gctctcgccg	ggagatggcg	cargcggtkg	180
aggatgggta	ccggcagatg	cccatcatca	cgcgctccta	cctcamcgcc	gctgtcgctca	240
ccaccgtcgg	ctgcamcctc	gaatcatatt	cgccgatcat	cctgtacctt	aaccggaagc	300
tcgtgggtgca	gcactacgag	atttrgcgcc	tcgtcaccaa	sttsctctan	yttccgcgaaa	360
gatggatttg	gattttctat	tcacatgtw	ctttcttgca	cgatactgca	agcttctgga	420
ggaaaactca	tttagaggaa	gaactgctga	ctttttttac	atgcwcttgt	ttggtcttac	480
tgctcaact	ggcattggtt	ctgatcgagg	ggatgatacc	ttacatttct	gagacatttg	540

c

(2) INFORMATION FOR SEQ ID NO:1902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1902:

Met	Ala	Xaa	Ala	Xaa	Glu	Glu	Trp	Tyr	Arg	Gln	Met	Pro	Ile	Ile	Thr
1		5						10					15		
Arg	Ser	Tyr	Leu	Xaa	Ala	Ala	Val	Val	Thr	Thr	Val	Gly	Cys	Xaa	Leu
		20						25				30			
Glu	Ile	Ile	Ser	Pro	Tyr	His	Leu	Tyr	Leu	Asn	Pro	Lys	Leu	Val	Val
		35				40						45			
Gln	His	Tyr	Glu	Ile	Xaa	Arg	Leu	Val	Thr	Xaa	Xaa	Leu	Xaa	Xaa	Pro
		50				55				60					
Gln	Arg	Trp	Ile	Trp	Ile	Phe	Tyr	Ser	Thr	Cys	Xaa	Phe	Leu	His	Asp
65			70					75					80		
Thr	Ala	Ser	Phe	Trp	Arg	Lys	Thr	His	Leu	Glu	Glu	Glu	Leu	Leu	Thr
			85					90					95		
Phe	Phe	Thr	Cys	Xaa	Cys	Leu	Val	Leu	Leu	Ser					
			100					105							

(2) INFORMATION FOR SEQ ID NO:1903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..96
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501641
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1903:
Met Pro Ile Ile Thr Arg Ser Tyr Leu Xaa Ala Ala Val Val Thr Thr
1 5 10 15
Val Gly Cys Xaa Leu Glu Ile Ile Ser Pro Tyr His Leu Tyr Leu Asn
 20 25 30
Pro Lys Leu Val Val Gln His Tyr Glu Ile Xaa Arg Leu Val Thr Xaa
 35 40 45
Xaa Leu Xaa Xaa Pro Gln Arg Trp Ile Trp Ile Phe Tyr Ser Thr Cys
50 55 60
Xaa Phe Leu His Asp Thr Ala Ser Phe Trp Arg Lys Thr His Leu Glu
65 70 75 80
Glu Glu Leu Leu Thr Phe Phe Thr Cys Xaa Cys Leu Val Leu Leu Ser
 85 90 95

(2) INFORMATION FOR SEQ ID NO:1904:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..56
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501642
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1904:
Met Asp Leu Asp Phe Leu Phe His Met Xaa Phe Leu Ala Arg Tyr Cys
1 5 10 15
Lys Leu Leu Glu Glu Asn Ser Phe Arg Gly Arg Thr Ala Asp Phe Phe
 20 25 30
Tyr Met Xaa Leu Phe Gly Ala Thr Val Leu Thr Gly Ile Gly Ser Asp
 35 40 45
Arg Arg Asp Asp Thr Leu His Phe
50 55

(2) INFORMATION FOR SEQ ID NO:1905:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1144
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501643
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1905:
tttacaggca cagctaaagc aagagtcact gctaaggcaa caggagcaac aacaattagc 60
tgaacaatcc cagctgaggc aacaagagca agaaaaacta gccaaagagc aaaccctgat 120
tgettctctg gaggctgaaa agcaacagtt ggaagaccaa attactatgt tgacaagaa 180
agctacagag gacgctcttg agtttctgac acgcaaggca ttttcaatgc aagataggga 240
aaaacttgaa cagcagttgc atgacatggc tttgatgatt gagaggctag aggggagctg 300
tcaaaaactg ctaagtggaa ttgattctca atcgtcagaa atagagaaac tgtttgagga 360
gaactcagcc ttatctgctt cttatcaaga agccattgat gttactgtac aatgggaaaa 420
ccagaaaatt tcagggttaga gactgtctga agcaaaatga agagctccgt tctcacttgg 480

agaaaactaag	acttgaacaa	gttagcctgt	tgaagtaag	caatctcgct	acccaatcag	540
atgggcaaac	tgaaaacagt	atctcaaacc	caccacaaat	ggctcatcgag	aattattctc	600
taaarggwtc	agcttataaa	agwacagwgc	agatctgagg	ggttgtcggc	agagataatg	660
aaactttcag	ctgagcttaag	gaaagcagtc	catgcacaga	ataaccttgc	acgcttaatac	720
agacctgtat	taagagacat	tgagagcaat	ctgatgaaaa	tgaacaaga	aacttaatgcg	780
acgatccagt	gatacatgtt	gacatgttgt	gaaactcagt	cctctggcat	ggccgcatgg	840
gtccacagtt	actgattttc	gtcgtggatg	tatttatctc	atgccatctt	caagatgctg	900
gtgcaaaagc	gttcttttgc	tggccaccat	ttataagtag	agttcagtag	agatcgttgt	960
acttgatcaa	tactcatgta	tacccgatcc	ccagactggt	tcattctcgt	aattggaagc	1020
gatgttttga	tgccatgta	tcaagtggat	cataaacatc	caaacaacgc	cttaaaatag	1080
atcgtttcga	cattattatt	ttctgcttg	caatccaggc	tctaacaact	tctcggtctt	1140
gttt						

(2) INFORMATION FOR SEQ ID NO:1906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1501644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1906:

Leu	Gln	Ala	Gln	Leu	Lys	Gln	Glu	Ser	Leu	Leu	Arg	Gln	Gln	Glu	Gln
1			5				10				15				
Gln	Gln	Leu	Ala	Glu	Gln	Ser	Gln	Leu	Arg	Gln	Gln	Glu	Gln	Glu	Lys
			20				25					30			
Leu	Ala	Lys	Glu	Gln	Thr	Arg	Ile	Ala	Ser	Leu	Glu	Ala	Glu	Lys	Gln
			35				40					45			
Gln	Leu	Glu	Asp	Gln	Ile	Thr	Met	Leu	Thr	Lys	Lys	Ala	Thr	Glu	Asp
			50				55					60			
Ala	Ser	Glu	Phe	Ala	Ala	Arg	Lys	Ala	Phe	Ser	Met	Gln	Asp	Arg	Glu
			65				70					75			
Lys	Leu	Glu	Gln	Gln	Leu	His	Asp	Met	Ala	Leu	Met	Ile	Glu	Arg	Leu
							85					90			
Glu	Gly	Ser	Arg	Gln	Lys	Leu	Leu	Met	Glu	Ile	Asp	Ser	Gln	Ser	Ser
							100					105			
Glu	Ile	Glu	Lys	Leu	Phe	Glu	Glu	Asn	Ser	Ala	Leu	Ser	Ala	Ser	Tyr
							115					120			
Gln	Glu	Ala	Ile	Asp	Val	Thr	Val	Gln	Trp	Glu	Asn	Gln	Lys	Ile	Ser
							130					135			
Gly															
145															

(2) INFORMATION FOR SEQ ID NO:1907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1501645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1907:

Met	Leu	Thr	Lys	Lys	Ala	Thr	Glu	Asp	Ala	Ser	Glu	Phe	Ala	Ala	Arg
1							5				10				15
Lys	Ala	Phe	Ser	Met	Gln	Asp	Arg	Glu	Lys	Leu	Glu	Gln	Gln	Leu	His
							20				25			30	
Asp	Met	Ala	Leu	Met	Ile	Glu	Arg	Leu	Glu	Gly	Ser	Arg	Gln	Lys	Leu

35 40 45
Leu Met Glu Ile Asp Ser Gln Ser Ser Glu Ile Glu Lys Leu Phe Glu
50 55 60
Glu Asn Ser Ala Leu Ser Ala Ser Tyr Gln Glu Ala Ile Asp Val Thr
65 70 75 80
Val Gln Trp Glu Asn Gln Lys Ile Ser Gly
85 90

(2) INFORMATION FOR SEQ ID NO:1908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1908:

Met Leu Leu Tyr Asn Gly Lys Thr Arg Lys Phe Gln Val Arg Asp Cys
1 5 10 15
Leu Lys Gln Asn Glu Glu Leu Arg Ser His Leu Glu Lys Leu Arg Leu
20 25 30
Glu Gln Val Ser Leu Leu Lys Val Ser Asn Ile Ala Thr Gln Ser Asp
35 40 45
Gly Gln Thr Glu Asn Ser Ile Ser Asn Pro Pro Gln Met Val Ile Glu
50 55 60
Asn Ile Ser Leu Xaa Xaa Ser Ala Tyr Lys Xaa Thr Xaa Gln Ile
65 70 75

(2) INFORMATION FOR SEQ ID NO:1909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..597
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1909:

ttttttcgcc tataattact cttccccgtg cggcctcgcg aggtcggaacc cccaaggcga 60
ggcgacgaaa cctccgccag tcaccaactc gaacctcagt caggcgcgct gagggagggga 120
gagttcgagg accgagggcg cgctggggcga gatgaagctt aacgtcaaga ccctcaaggag 180
caccaaactc gagatcgagg cgagcccccga tgcgtcggtt caaatgctta tataccaagg 240
tgagaccact cagggtcaga gtacctaccg ggccgaccag caaatgctta tataccaagg 300
gaaaattctc aaggatgaga ccaactttgga aagcaacgga gttctganga acagcttctc 360
tgttataatg ttgtccaagg ctaaggcacc gtccagtgga gttctaccca ctactgtcgc 420
aaaagctcct gcaactctgg cccaacctgc tgcctctgtg cccctgtgct catcagttgc 480
aagaacacca acacaggctc ctgttgccac agctgaaacg gcacctccaa gtgcccaacc 540
tcaggctgct cagctgctac ggttgctgct actgatgatg ctgatgtgta cagtcag

(2) INFORMATION FOR SEQ ID NO:1910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1501690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1910:

Met Lys Leu Asn Val Lys Thr Leu Lys Gly Thr Asn Phe Glu Ile Glu
1 5 10 15
Ala Ser Pro Asp Ala Ser Val Ala Asp Val Lys Arg Ile Ile Glu Thr
20 25 30
Thr Gln Gly Gln Ser Thr Tyr Arg Ala Asp Gln Gln Met Leu Ile Tyr
35 40 45
Gln Gly Lys Ile Leu Lys Asp Glu Thr Thr Leu Glu Ser Asn Gly Val
50 55 60
Leu Xaa Asn Ser Phe Leu Val Ile Met Leu Ser Lys Ala Lys Ala Ser
65 70 75 80
Ser Ser Gly Ala Ser Thr Thr Thr Ala Ala Lys Ala Pro Ala Thr Leu
85 90 95
Ala Gln Pro Ala Ala Pro Val Pro Pro Ala Ala Ser Val Ala Arg Thr
100 105 110
Pro Thr Gln Ala Pro Val Ala Thr Ala Glu Thr Ala Pro Pro Ser Ala
115 120 125
Gln Pro Gln Ala Ala Gln Leu Arg Leu Leu Leu Met Met Leu
130 135 140
Met Cys Thr Val
145

(2) INFORMATION FOR SEQ ID NO:1911:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1501691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1911:

Met Leu Ile Tyr Gln Gly Lys Ile Leu Lys Asp Glu Thr Thr Leu Glu
1 5 10 15
Ser Asn Gly Val Leu Xaa Asn Ser Phe Leu Val Ile Met Leu Ser Lys
20 25 30
Ala Lys Ala Ser Ser Ser Gly Ala Ser Thr Thr Thr Ala Ala Lys Ala
35 40 45
Pro Ala Thr Leu Ala Gln Pro Ala Ala Pro Val Pro Pro Ala Ala Ser
50 55 60
Val Ala Arg Thr Pro Thr Gln Ala Pro Val Ala Thr Ala Glu Thr Ala
65 70 75 80
Pro Pro Ser Ala Gln Pro Gln Ala Ala Gln Leu Leu Arg Leu Leu Leu
85 90 95
Leu Met Met Leu Met Cys Thr Val
100

(2) INFORMATION FOR SEQ ID NO:1912:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1501692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1912:

Met Leu Ser Lys Ala Lys Ala Ser Ser Ser Gly Ala Ser Thr Thr Thr

1 5 10 15
Ala Ala Lys Ala Pro Ala Thr Leu Ala Gln Pro Ala Ala Pro Val Pro
20 25 30
Pro Ala Ala Ser Val Ala Arg Thr Pro Thr Gln Ala Pro Val Ala Thr
35 40 45
Ala Glu Thr Ala Pro Pro Ser Ala Gln Pro Gln Ala Ala Gln Leu Leu
50 55 60
Arg Leu Leu Leu Met Met Leu Met Cys Thr Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:1913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..272
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1913:

ccgcctcgatc gcgcgcccat caataaatca atcaattctc gacctcacta ctcgatctct 60
cgctctatca gtgtgactgt gtgagtgtcc gagcagcgtt gcacgcgcaa tggacgctct 120
gtcgtgact accctctctcgt tcccgcgtgg ggcgctctc ctcggttccg ggtccgggtc 180
cgcgccacgc ctgcmgcgcg ccttctctgt gttcggtgac tccctcgtgg acaacggcaa 240
caacaactac ctgatgacga cggcgcgcg cg

(2) INFORMATION FOR SEQ ID NO:1914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1914:

Ala Arg Ser Arg Pro His Gln Ser Ile Asn Gln Phe Ser Thr Ser Leu
1 5 10 15
Leu Asp Leu Ser Ser His Gln Cys Asp Cys Val Ser Val Arg Ala Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO:1915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1915:

Met Asp Ala Leu Leu Val Thr Thr Phe Leu Val Pro Val Ala Leu
1 5 10 15
Leu Leu Gly Ser Gly Ser Gly Ser Ala Ala Pro Leu Xaa Arg Ala Phe
20 25 30
Phe Val Phe Gly Asp Ser Leu Val Asp Asn Gly Asn Asn Asn Tyr Leu

35
Met Thr Thr Ala Arg Ala
50

40

45

(2) INFORMATION FOR SEQ ID NO:1916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..562
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1916:

gacgaccgca	ttctcttcc	ttctctcgc	agtctgcct	cgcccaaccc	agtcctcgc	60
gcgcgctctc	ttctctgcaa	ggaccgcag	ggaaggacct	gctgtttcaa	agtattgtgc	120
gagacaccta	cacgctgagc	ttcgccgaca	tgaagtttt	cgggataatc	tcagactgc	180
aattgagaga	acgttcttaa	ggatggatga	gatgatgaga	gacaggaggg	cagggaggga	240
attatctggg	tacgggtgtaa	tgacaattgg	aaagcatata	gaaaggctat	caacatgagt	300
ctatttctac	ctttctgtca	gaagccagct	tatcaggggc	cagtaatgga	tgatgtacc	360
gcgtgtgtgg	ttctcattag	agacaaccga	atcattgtgg	gaaatgctgg	tgattctcgt	420
tggtactctc	caaggaataa	tcaggcgatt	gatctatcca	ccgattttaa	accaaacctt	480
ccagacgaaa	gacaaagaat	agaagctgca	rgacatgtgg	taacttttag	cgagagagga	540
aatgtgcac	gtattgatga	tg				

(2) INFORMATION FOR SEQ ID NO:1917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1917:

Thr	Thr	Ala	Phe	Ser	Phe	Leu	Ser	Leu	Ala	Val	Ser	Pro	Arg	Pro	Thr
1			5						10				15		
Gln	Ser	Leu	Ala	Arg	Ala	Leu	Ser	Pro	Ala	Arg	Thr	Ala	Arg	Glu	Gly
			20					25				30			
Pro	Ala	Val	Ser	Lys	Tyr	Cys	Ala	Arg	His	Leu	His	Ala	Glu	Leu	Arg
			35				40					45			
Arg	His	Glu	Ser	Phe	Arg	Asp	Asn	Leu	Gln	Thr	Ala	Ile	Glu	Arg	Thr
			50				55				60				
Phe	Leu	Arg	Met	Asp	Glu	Met	Met	Arg	Asp	Arg	Arg	Ala	Gly	Arg	Glu
			65				70				75			80	
Leu	Ser	Gly	Tyr	Gly	Val	Met	Thr	Ile	Gly	Lys	His	Ile	Glu	Arg	Leu
				85					90					95	

Ser Thr

(2) INFORMATION FOR SEQ ID NO:1918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1501712
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1918:
Met Ser Leu Phe Leu Pro Phe Cys Gln Lys Pro Ala Tyr Gln Gly Pro
1 5 10 15
Val Met Asp Gly Cys Thr Ala Cys Val Val Leu Ile Arg Asp Asn Arg
20 25 30
Ile Ile Val Gly Asn Ala Gly Asp Ser Arg Cys Val Leu Ser Arg Asn
35 40 45
Asn Gln Ala Ile Asp Leu Ser Thr Asp Phe Lys Pro Asn Leu Pro Asp
50 55 60
Glu Arg Gln Arg Ile Glu Ala Ala Xaa His Val Val Thr Phe Ser Glu
65 70 75 80
Arg Gly Asn Val His Arg Ile Asp Asp
85

(2) INFORMATION FOR SEQ ID NO:1919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1501713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1919:

Met Asp Gly Cys Thr Ala Cys Val Val Leu Ile Arg Asp Asn Arg Ile
1 5 10 15
Ile Val Gly Asn Ala Gly Asp Ser Arg Cys Val Leu Ser Arg Asn Asn
20 25 30
Gln Ala Ile Asp Leu Ser Thr Asp Phe Lys Pro Asn Leu Pro Asp Glu
35 40 45
Arg Gln Arg Ile Glu Ala Ala Xaa His Val Val Thr Phe Ser Glu Arg
50 55 60
Gly Asn Val His Arg Ile Asp Asp
65 70

(2) INFORMATION FOR SEQ ID NO:1920:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..508

(D) OTHER INFORMATION: / Ceres Seq. ID 1501718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1920:

aaggcagcaaa ggccactaac actagtattac acatccacca taacgaccat ggctaccacc 60
tcagcttttg tagctcttgt cttgttagcc agcctccttg caggcaacgtt gtccagtgtat 120
gatatcgatc ccattccatc accttgtgtt gatcgggttc aagcctggca ggccgaatac 180
aaccgcacat atgcgacccc agaggaattc cagcaacgct tcattggtcta tagcgagaat 240
gtcaagtcca tcgagaccat gaaccagcct gggagctcat atgagctcgg tgagaaccga 300
ttcgctgacc tcaccgagga ggaattcaag gacacgtatc ttatgaagct tgacaacgtg 360
gcctcgtccc ctgaggccat ggcactgacc gtcgatacca tgaatatagc aggcacatct 420
ggcgcgagca acaccaacga ggctcccaat agtgtggact ggaggaccaa gggagcagtg 480
acgcgggtca agagccagca acattgtg

(2) INFORMATION FOR SEQ ID NO:1921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..169
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501719
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1921:
Lys Ala Ala Arg Pro Leu Thr Leu Val Ile Thr Ser Thr Ile Thr Thr
1 5 10 15
Met Ala Thr Thr Ser Ala Leu Leu Ala Leu Val Leu Leu Ala Ser Leu
 20 25 30
Leu Ala Gly Thr Val Phe Ser Asp Asp Ile Val Pro Ile His Ile Pro
 35 40 45
Leu Leu Asp Arg Phe Gln Ala Trp Gln Ala Glu Tyr Asn Arg Thr Tyr
 50 55 60
Ala Thr Pro Glu Glu Phe Gln Gln Arg Phe Met Val Tyr Ser Glu Asn
65 70 75 80
Val Lys Phe Ile Glu Thr Met Asn Gln Pro Gly Ser Ser Tyr Glu Leu
 85 90 95
Gly Glu Asn Arg Phe Ala Asp Leu Thr Glu Glu Phe Lys Asp Thr
 100 105 110
Tyr Leu Met Lys Leu Asp Asn Val Ala Ser Ser Pro Glu Ala Met Ala
 115 120 125
Leu Thr Val Asp Thr Met Asn Arg Ala Gly Thr Ser Gly Gly Ser Asn
 130 135 140
Thr Asn Glu Ala Pro Asn Ser Val Asp Trp Arg Thr Lys Gly Ala Val
145 150 155 160
Thr Pro Val Lys Ser Gln Gln His Cys
 165
(2) INFORMATION FOR SEQ ID NO:1922:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..153
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501720
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1922:
Met Ala Thr Thr Ser Ala Leu Leu Ala Leu Val Leu Leu Ala Ser Leu
1 5 10 15
Leu Ala Gly Thr Val Phe Ser Asp Asp Ile Val Pro Ile His Ile Pro
 20 25 30
Leu Leu Asp Arg Phe Gln Ala Trp Gln Ala Glu Tyr Asn Arg Thr Tyr
 35 40 45
Ala Thr Pro Glu Glu Phe Gln Gln Arg Phe Met Val Tyr Ser Glu Asn
50 55 60
Val Lys Phe Ile Glu Thr Met Asn Gln Pro Gly Ser Ser Tyr Glu Leu
65 70 75 80
Gly Glu Asn Arg Phe Ala Asp Leu Thr Glu Glu Glu Phe Lys Asp Thr
 85 90 95
Tyr Leu Met Lys Leu Asp Asn Val Ala Ser Ser Pro Glu Ala Met Ala
 100 105 110
Leu Thr Val Asp Thr Met Asn Arg Ala Gly Thr Ser Gly Gly Ser Asn
 115 120 125
Thr Asn Glu Ala Pro Asn Ser Val Asp Trp Arg Thr Lys Gly Ala Val
130 135 140
Thr Pro Val Lys Ser Gln Gln His Cys

145

150

(2) INFORMATION FOR SEQ ID NO:1923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1923:

Met	Val	Tyr	Ser	Glu	Asn	Val	Lys	Phe	Ile	Glu	Thr	Met	Asn	Gln	Pro	
1				5					10					15		
Gly	Ser	Ser	Tyr	Glu	Leu	Gly	Glu	Asn	Arg	Phe	Ala	Asp	Leu	Thr	Glu	
			20				25						30			
Glu	Glu	Phe	Lys	Asp	Thr	Tyr	Leu	Met	Lys	Leu	Asp	Asn	Val	Ala	Ser	
		35					40					45				
Ser	Pro	Glu	Ala	Met	Ala	Leu	Thr	Val	Asp	Thr	Met	Asn	Arg	Ala	Gly	
	50					55					60					
Thr	Ser	Gly	Gly	Ser	Asn	Thr	Asn	Glu	Ala	Pro	Asn	Ser	Val	Asp	Trp	
65				70					75					80		
Arg	Thr	Lys	Gly	Ala	Val	Thr	Pro	Val	Lys	Ser	Gln	Gln	His	Cys		
				85					90					95		

(2) INFORMATION FOR SEQ ID NO:1924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 911 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..911
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1924:

gagccgcgaca	tatgggcccc	gcttgagaag	taagggccac	atgtcgggtg	gaactctccc	60
ggagtgcgca	actaatcgac	cccgtagcgc	ggctccaccc	gaagcgcaag	aggaagagggt	120
ggccatacgc	aacaagcaaa	gcatancccc	aaatccccaa	tcgccaatcc	ccaatcccca	180
aaccttaggt	tatctcggcg	cggcagcgan	tggcggcgcg	gggcctgag	aaggggaatg	240
cgcgctcccc	gcgggaggtg	aaccgggtgc	tctacgtcgc	gaacctgcgc	tccaacatct	300
cgagcgagga	gatgtacgac	atcttcggca	agtacggcgc	gatccggcag	atccgctctg	360
gcaacgcca	ggacacgcgc	gggaacgctt	acgttgctta	csagacatc	tacgacgcca	420
agaacgcgct	cgaccacctc	tmcggttca	acgtcgccaa	ccgctacott	atcgtgctct	480
actaccagcc	cgccaagats	tccaagaagy	cggataatca	gaagaaggag	gacgagatcc	540
accaggctcc	aggagaagta	cggaaatcgg	tccaagacgc	ccggcccggg	ctccagcgac	600
tgagcgccca	gggtattgcc	tctgcagcct	cttgatatgat	gaagagcaat	caaaaggaac	660
aaattgggtt	cgctgtgctg	tgttacatcc	agcgctgccta	attactctgt	tgttattcag	720
gctccataac	aattgaatat	atatgtgctt	gtctaatacgc	cagcgataat	gtttagtctt	780
tacaaaacac	aagaggaatg	agtagtgtag	acctaacacc	tgtggctatg	cttgaattgt	840
tgatctatat	tctgttgtga	gactgagagt	agcatggtta	ggctgttaaa	tttgtgcttc	900
tattattggt	t					

(2) INFORMATION FOR SEQ ID NO:1925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..244
(D) OTHER INFORMATION: / Ceres Seq. ID 1501723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1925:

Thr	Pro	Thr	Tyr	Gly	Pro	Arg	Leu	Arg	Ser	Lys	Gly	His	Met	Ser	Val
1				5				10					15		
Gly	Thr	Leu	Pro	Glu	Ser	Ala	Thr	Asn	Arg	Pro	Arg	Ala	Pro	Ala	Pro
			20				25					30			
Pro	Glu	Ala	Gln	Glu	Glu	Glu	Val	Ala	Ile	Arg	Asn	Lys	Gln	Ser	Ile
		35					40				45				
Xaa	Pro	Asn	Pro	Gln	Ser	Pro	Ile	Pro	Asn	Pro	Gln	Thr	Leu	Gly	Tyr
	50					55					60				
Leu	Gly	Ala	Ala	Ala	Xaa	Gly	Gly	Gly	Gly	Pro	Glu	Glu	Gly	Glu	Cys
	65			70						75					80
Ala	Pro	Pro	Ala	Gly	Gly	Glu	Pro	Gly	Ala	Leu	Arg	Ala	Glu	Pro	Ala
			85						90				95		
Val	Gln	His	Leu	Glu	Arg	Gly	Asp	Val	Arg	His	Leu	Arg	Gln	Val	Arg
		100					105						110		
Arg	Asp	Pro	Ala	Asp	Pro	Ser	Gly	Gln	Arg	Gln	Gly	His	Ala	Arg	Asp
	115					120					125				
Arg	Leu	Arg	Cys	Leu	Xaa	Gly	His	Leu	Arg	Arg	Gln	Glu	Arg	Arg	Arg
	130				135						140				
Pro	Pro	Xaa	Arg	Leu	Gln	Arg	Arg	Gln	Pro	Leu	Pro	Tyr	Arg	Ala	Leu
	145			150						155					160
Leu	Pro	Ala	Arg	Gln	Asp	Xaa	Gln	Glu	Xaa	Gly	Tyr	Xaa	Glu	Glu	Gly
			165					170					175		
Gly	Arg	Asp	Pro	Pro	Gly	Ser	Arg	Arg	Ser	Thr	Glu	Ser	Gly	Pro	Arg
		180					185						190		
Arg	Pro	Ala	Arg	Ala	Pro	Ala	Thr	Glu	Arg	Pro	Gly	Tyr	Cys	Leu	Cys
	195						200					205			
Ser	Leu	Leu	Tyr	Asp	Glu	Glu	Gln	Ser	Lys	Gly	Thr	Asn	Trp	Leu	Arg
	210				215						220				
Cys	Ala	Val	Leu	His	Pro	Ala	Ser	Leu	Ile	Thr	Leu	Leu	Leu	Phe	Arg
	225				230					235					240
Leu	His	Asn	Asn												

(2) INFORMATION FOR SEQ ID NO:1926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..231
(D) OTHER INFORMATION: / Ceres Seq. ID 1501724

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1926:

Met	Ser	Val	Gly	Thr	Leu	Pro	Glu	Ser	Ala	Thr	Asn	Arg	Pro	Arg	Ala
1			5					10					15		
Pro	Ala	Pro	Pro	Glu	Ala	Gln	Glu	Glu	Val	Ala	Ile	Arg	Asn	Lys	
			20					25				30			
Gln	Ser	Ile	Xaa	Pro	Asn	Pro	Gln	Ser	Pro	Ile	Pro	Asn	Pro	Gln	Thr
		35					40					45			
Leu	Gly	Tyr	Leu	Gly	Ala	Ala	Ala	Xaa	Gly	Gly	Gly	Gly	Pro	Glu	Glu
	50				55						60				
Gly	Glu	Cys	Ala	Pro	Pro	Ala	Gly	Gly	Glu	Pro	Gly	Ala	Leu	Arg	Ala
	65			70					75				80		
Glu	Pro	Ala	Val	Gln	His	Leu	Glu	Arg	Gly	Asp	Val	Arg	His	Leu	Arg
			85					90					95		
Gln	Val	Arg	Arg	Asp	Pro	Ala	Asp	Pro	Ser	Gly	Gln	Arg	Gln	Gly	His

100 105 110
Ala Arg Asp Arg Leu Arg Cys Leu Xaa Gly His Leu Arg Arg Gln Glu
115 120 125
Arg Arg Arg Pro Pro Xaa Arg Leu Gln Arg Arg Gln Pro Leu Pro Tyr
130 135 140
Arg Ala Leu Leu Pro Ala Arg Gln Asp Xaa Gln Glu Xaa Gly Tyr Xaa
145 150 155 160
Glu Glu Gly Gly Arg Asp Pro Pro Gly Ser Arg Arg Ser Thr Glu Ser
165 170 175
Gly Pro Arg Arg Pro Ala Arg Ala Pro Ala Thr Glu Arg Pro Gly Tyr
180 185 190
Cys Leu Cys Ser Leu Leu Tyr Asp Glu Glu Gln Ser Lys Gly Thr Asn
195 200 205
Trp Leu Arg Cys Ala Val Leu His Pro Ala Ser Leu Ile Thr Leu Leu
210 215 220
Leu Phe Arg Leu His Asn Asn
225 230

(2) INFORMATION FOR SEQ ID NO:1927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..129
(D) OTHER INFORMATION: / Ceres Seq. ID 1501725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1927:

Met Tyr Asp Ile Phe Gly Lys Tyr Gly Ala Ile Arg Gln Ile Arg Leu
1 5 10 15
Gly Asn Ala Lys Asp Thr Arg Gly Thr Ala Tyr Val Val Tyr Xaa Asp
20 25 30
Ile Tyr Asp Ala Lys Asn Ala Val Asp His Leu Xaa Gly Phe Asn Val
35 40 45
Ala Asn Arg Tyr Leu Ile Val Leu Tyr Tyr Gln Pro Ala Lys Xaa Ser
50 55 60
Lys Lys Xaa Asp Ile Xaa Lys Lys Glu Asp Glu Ile His Gln Ala Pro
65 70 75 80
Gly Glu Val Arg Asn Arg Val Gln Asp Ala Arg Pro Gly Leu Gln Arg
85 90 95
Leu Ser Gly Gln Gly Ile Ala Ser Ala Ala Ser Cys Met Met Lys Ser
100 105 110
Asn Gln Lys Glu Gln Ile Gly Cys Ala Val Leu Cys Tyr Ile Gln Arg
115 120 125
Arg

(2) INFORMATION FOR SEQ ID NO:1928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 916 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..916
(D) OTHER INFORMATION: / Ceres Seq. ID 1501730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1928:

atccattgtca tgacgatact gcaggctcca attgtcagct gaactgtgtt tgcattctgt
ccagctatag ctcaatttgt tctacttgtc gacatagact caagcttgct tattagtacy

60
120

tccaagaacg	acgtacatgg	cttcagctgc	tgcggctagc	gctgttaag	aggccttggt	180
cgctgctgcc	gtgtgcatgg	tgtgtgtgct	ccactctctg	gcgggacatc	agccgcceaa	240
gtcgcgcgct	ccaccgcatt	gccattacac	ggggcagcag	ccaccgcctt	gcgcggtgcc	300
agcgtcggtg	tactcgccgc	cgccaccacc	accagtacca	gcgcccatgc	cgctgcgcgtc	360
gccgcgcgca	ccgcccagtc	aagcgcccat	gcgcgcgcgc	ccgcgcgcac	caacgcccgc	420
acctgcgcga	acgcccacgc	cgctgcgcgc	gccgcmacc	gtcaataact	gcagctacat	480
gtactgcgcg	atgcaatgta	gcccggtctg	ccaagccaaa	ccamgaagcc	ggcatcgcca	540
agtgcgaaa	cgacctcgcc	accaaactac	aacgggtgct	acgacagctg	caccagccat	600
gtctgccccg	gcgactcctg	cgccggcagt	ggctgcggct	tcggccactg	ccccgcgcag	660
aacgccaacg	cgaccagctg	ctgccaatcc	tgcggcaacg	ttctgtaccg	cgaggagcac	720
cgctgcgcga	attactacga	cagggtctgt	gagtagctga	tgatcgactg	ccaggacacc	780
tgctacaaga	actgactacta	ggcgcgctag	agagctcttg	attggtcttg	tcattctcagt	840
tagtctgaat	gtttctgtat	gttcatgacg	tttctacgat	tgatcaataa	aaacaaggtg	900
atgagcattg	agctcc					

(2) INFORMATION FOR SEQ ID NO:1929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..208
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1929:

Met	Ala	Ser	Ala	Ala	Ala	Ser	Ala	Val	Lys	Glu	Ala	Leu	Val	Val
1			5				10				15			
Val	Ala	Val	Cys	Ile	Val	Leu	Leu	His	Ser	Ser	Ala	Gly	His	Gln
			20				25				30			
Pro	Pro	Lys	Ser	Pro	Pro	Pro	Pro	His	Cys	His	Tyr	Thr	Gly	Gln
			35				40				45			
Pro	Pro	Pro	Ser	Pro	Val	Pro	Ala	Ser	Leu	Tyr	Ser	Pro	Pro	Pro
			50				55				60			
Pro	Pro	Val	Pro	Ala	Pro	Met	Pro	Ser	Pro	Ser	Pro	Pro	Pro	Pro
			65				70				75			
Val	Gln	Ala	Pro	Met	Pro	Pro	Pro	Pro	Pro	Ala	Pro	Thr	Pro	Thr
			85				90				95			
Ala	Pro	Thr	Pro	Xaa	Pro	Ser	Pro	Ser	Pro	Xaa	Pro	Val	Asn	Asn
			100				105				110			
Ser	Tyr	Met	Tyr	Cys	Ala	Met	Gln	Cys	Ser	Pro	Val	Cys	Gln	Ala
			115				120				125			
Pro	Xaa	Arg	Arg	His	Arg	Gln	Val	Arg	Lys	Arg	Pro	Arg	His	Gln
			130				135				140			
Thr	Thr	Gly	Ala	Thr	Thr	Ala	Ala	Pro	Ala	Met	Ser	Ala	Pro	Ala
			145				150				155			
Pro	Ala	Pro	Ala	Val	Ala	Ala	Ala	Ser	Ala	Thr	Ala	Pro	Ala	Thr
			165				170				175			
Pro	Thr	Arg	Pro	Ala	Ala	Ala	Asn	Pro	Ala	Ala	Thr	Phe	Cys	Thr
			180				185				190			
Arg	Ser	Ser	Ala	Ala	Gly	Ile	Thr	Thr	Thr	Gly	Leu	Trp	Ser	Thr
			195				200				205			

(2) INFORMATION FOR SEQ ID NO:1930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1501732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1930:

Met	Pro	Ser	Pro	Ser	Pro	Pro	Pro	Pro	Pro	Val	Gln	Ala	Pro	Met	Pro
1				5						10				15	
Pro	Pro	Pro	Pro	Pro	Ala	Pro	Thr	Pro	Thr	Pro	Ala	Pro	Thr	Pro	Xaa
				20					25					30	
Ser	Pro	Ser	Pro	Xaa	Pro	Val	Asn	Asn	Cys	Ser	Tyr	Met	Tyr	Cys	Ala
				35				40					45		
Met	Gln	Cys	Ser	Pro	Val	Cys	Gln	Ala	Lys	Pro	Xaa	Arg	Arg	His	Arg
							55					60			
Gln	Val	Arg	Lys	Arg	Pro	Arg	His	Gln	Thr	Thr	Gly	Ala	Thr	Thr	
							70				75				80
Ala	Ala	Pro	Ala	Met	Ser	Ala	Pro	Ala	Thr	Pro	Ala	Pro	Ala	Val	Ala
							85							95	
Ala	Ala	Ser	Ala	Thr	Ala	Pro	Ala	Thr	Thr	Pro	Thr	Arg	Pro	Ala	Ala
							100							110	
Ala	Asn	Pro	Ala	Ala	Thr	Phe	Cys	Thr	Ala	Arg	Ser	Ser	Ala	Ala	Gly
							115						125		
Ile	Thr	Thr	Thr	Gly	Leu	Trp	Ser	Thr	Ala						

(2) INFORMATION FOR SEQ ID NO:1931:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1501733

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1931:

Met	Pro	Pro	Pro	Pro	Pro	Ala	Pro	Thr	Pro	Thr	Pro	Ala	Pro	Thr	Pro
1					5					10				15	
Xaa	Pro	Ser	Pro	Ser	Pro	Xaa	Pro	Val	Asn	Asn	Cys	Ser	Tyr	Met	Trp
					20					25				30	
Cys	Ala	Met	Gln	Cys	Ser	Pro	Val	Cys	Gln	Ala	Lys	Pro	Xaa	Arg	Arg
							40					45			
His	Arg	Gln	Val	Arg	Lys	Arg	Pro	Arg	His	Gln	Thr	Thr	Thr	Gly	Ala
							55				60				
Thr	Thr	Ala	Ala	Pro	Ala	Met	Ser	Ala	Pro	Ala	Thr	Pro	Ala	Pro	Ala
							70				75				80
Val	Ala	Ala	Ala	Ser	Ala	Thr	Ala	Pro	Ala	Thr	Thr	Pro	Thr	Arg	Pro
							85				90				95
Ala	Ala	Ala	Asn	Pro	Ala	Ala	Thr	Phe	Cys	Thr	Ala	Arg	Ser	Ser	Ala
							100							110	
Ala	Gly	Ile	Thr	Thr	Thr	Gly	Leu	Trp	Ser	Thr	Ala				
							115								

(2) INFORMATION FOR SEQ ID NO:1932:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..493

(D) OTHER INFORMATION: / Ceres Seq. ID 1501737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1932:

attctgttcg gttccttcg aaaaacacac aggaacacac acgcacacac	60
cgaatggcca cggcgggtgct cgcgcgcgcca ttctctgcgc cgctcctccc	120
ggggcgctccg ggacctctctc ttggttcggt ccccgagagc gttaggtctc	180
cgcgcggtgt cttccgaact ccccaagccc gtgcctctca cctcctcccc	240
gacagccccc acgaggaacc accggtccta ccgctctccc aggagcttgc	300
attcttccac ccaagctcct cgctcagctc ccgagcgacc ttgctctega	360
gctgcgtttg atctctccaa cgggcagatt ctgcagcagt gtggccaaga	420
ctgctctcta acctggcaaa agcatgggag tttagctgata cgtcaacatc	480
gccaaagcgc tgc	

(2) INFORMATION FOR SEQ ID NO:1933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1933:

Ile	Leu	Phe	Gly	Ser	Phe	Arg	Lys	His	Asn	Arg	Lys	Thr	His	Ala	Gln
1				5					10					15	
Asn	Cys	Arg	Phe	Arg	Met	Ala	Thr	Ala	Val	Leu	Arg	Arg	Pro	Phe	Leu
								20						30	
Ala	Ala	Leu	Leu	Pro	Ala	Ala	Gly	Gly	Ala	Ser	Gly	Thr	Ser	Ser	Trp
								35						45	
Phe	Arg	Pro	Arg	Arg	Arg	Arg	Ser	Ser	Pro	Ser	Val	Arg	Ala	Val	Ser
								50						60	
Ser	Asp	Ser	Pro	Lys	Pro	Val	Ala	Ser	Thr	Ser	Ser	Pro	Thr	Gly	Gly
								65						80	
Asp	Ser	Pro	Asp	Glu	Glu	Pro	Pro	Val	Leu	Pro	Leu	Leu	Gln	Glu	Leu
								85						95	
Ala	Asp	Cys	Leu	Ile	Leu	Pro	Pro	Lys	Leu	Leu	Ala	Gln	Leu	Pro	Ser
								100						110	
Asp	Leu	Arg	Leu	Asp	Leu	Asn	Asp	Ala	Ala	Phe	Asp	Leu	Ser	Asn	Gly
								115						125	
Pro	Val	Leu	Asp	Glu	Cys	Gly	Gln	Glu	Val	Gly	Asp	Leu	Leu	Leu	Asn
								130						140	
Leu	Ala	Lys	Ala	Trp	Glu	Leu	Ala	Asp	Thr	Ser	Thr	Ser	Asn	Ser	Ile
								145						155	
Ala	Lys	Gln	Leu												

(2) INFORMATION FOR SEQ ID NO:1934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1934:

Phe	Cys	Ser	Val	Pro	Ser	Glu	Asn	Thr	Thr	Gly	Lys	His	Thr	His	Lys
1				5					10					15	
Thr	Ala	Val	Ser	Glu	Trp	Pro	Arg	Pro	Cys	Ser	Ala	Ala	His	Ser	Ser
								20						30	

Pro Arg Ser Ser Pro Pro Pro Glu Gly Arg Pro Gly Pro Pro Leu Gly
35 40 45
Ser Val Pro Gly Asp Val Gly Pro Leu Leu Pro Cys Ala Arg Cys Leu
50 55 60
Pro Thr Pro Pro Ser Pro Ser Pro Pro Pro Pro Pro Ala Val
65 70 75 80
Thr Ala Pro Thr Arg Asn His Arg Ser Tyr Arg Ser Ser Arg Ser Leu
85 90 95
Arg Ile Ala

(2) INFORMATION FOR SEQ ID NO:1935:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1501740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1935:

Met Ala Thr Ala Val Leu Arg Arg Pro Phe Leu Ala Ala Leu Leu Pro
1 5 10 15
Ala Ala Gly Gly Ala Ser Gly Thr Ser Ser Trp Phe Arg Pro Arg Arg
20 25 30
Arg Arg Ser Ser Pro Ser Val Arg Ala Val Ser Ser Asp Ser Pro Lys
35 40 45
Pro Val Ala Ser Thr Ser Ser Pro Thr Gly Gly Asp Ser Pro Asp Glu
50 55 60
Glu Pro Pro Val Leu Pro Leu Leu Gln Glu Leu Ala Asp Cys Leu Ile
65 70 75 80
Leu Pro Pro Lys Leu Leu Ala Gln Leu Pro Ser Asp Leu Arg Leu Asp
85 90 95
Leu Asn Asp Ala Ala Phe Asp Leu Ser Asn Gly Pro Val Leu Asp Glu
100 105 110
Cys Gly Gln Glu Val Gly Asp Leu Leu Leu Asn Leu Ala Lys Ala Trp
115 120 125
Glu Leu Ala Asp Thr Ser Thr Ser Asn Ser Ile Ala Lys Gln Leu
130 135 140

(2) INFORMATION FOR SEQ ID NO:1936:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..363

(D) OTHER INFORMATION: / Ceres Seq. ID 1501741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1936:

acaaacttc cctgtcacga gactacgaga ccacgccttc cgtgggatca atcggctagg 60
gtttccggaga tgttcggccg cgcccgcaag aagagcgaca acaccoggta ctacgagatc 120
ctgggggttt ccaaggacgc gtcacaggat gacctcaaga aggcctaccg caaggccgcc 180
atcaagaacc accccgacaa gggcgggcac cccgagaagt tcaaggagct atgtatgctg 240
tatgcatgtg gtgaagcaag tgctcgtcgg tgtgtagtgt tgcctctctt gatccattgt 300
ctgtgctctg tactgtagtg atcagcgtca aaataaagaa atgcctgtcc ttgtttagaa 360
ttg

(2) INFORMATION FOR SEQ ID NO:1937:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..105
(D) OTHER INFORMATION: / Ceres Seq. ID 1501742
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1937:
Thr Asn Phe Pro Cys His Glu Ser Thr Arg Pro Arg Leu Pro Trp Asp
1 5 10 15
Gln Ser Ala Arg Val Ser Glu Met Phe Gly Arg Ala Pro Lys Lys Ser
20 25 30
Asp Asn Thr Arg Tyr Tyr Glu Ile Leu Gly Val Ser Lys Asp Ala Ser
35 40 45
Gln Asp Asp Leu Lys Lys Ala Tyr Arg Lys Ala Ala Ile Lys Asn His
50 55 60
Pro Asp Lys Gly Gly Asp Pro Glu Lys Phe Lys Glu Leu Cys Met Leu
65 70 75 80
Tyr Ala Cys Gly Glu Ala Ser Ala Arg Arg Cys Val Val Phe Ala Leu
85 90 95
Leu Ile His Cys Leu Cys Ser Val Leu
100 105
(2) INFORMATION FOR SEQ ID NO:1938:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..91
(D) OTHER INFORMATION: / Ceres Seq. ID 1501743
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1938:
Gln Thr Ser Pro Val Thr Arg Val Arg Asp His Ala Phe Arg Gly Ile
1 5 10 15
Asn Arg Leu Gly Phe Arg Arg Cys Ser Ala Ala Arg Arg Arg Ala
20 25 30
Thr Thr Pro Gly Thr Thr Arg Ser Trp Gly Phe Pro Arg Thr Arg His
35 40 45
Arg Met Thr Ser Arg Arg Pro Thr Ala Arg Pro Pro Ser Arg Thr Thr
50 55 60
Pro Thr Arg Ala Ala Thr Pro Arg Ser Ser Arg Ser Tyr Val Cys Cys
65 70 75 80
Met His Val Val Lys Gln Val Leu Val Gly Val
85 90
(2) INFORMATION FOR SEQ ID NO:1939:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..82
(D) OTHER INFORMATION: / Ceres Seq. ID 1501744
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1939:
Met Phe Gly Arg Ala Pro Lys Lys Ser Asp Asn Thr Arg Tyr Tyr Glu

1	5	10	15												
Ile	Leu	Gly	Val	Ser	Lys	Asp	Ala	Ser	Gln	Asp	Asp	Leu	Lys	Lys	Ala
	20							25					30		
Tyr	Arg	Lys	Ala	Ala	Ile	Lys	Asn	His	Pro	Asp	Lys	Gly	Gly	Asp	Pro
	35							40					45		
Glu	Lys	Phe	Lys	Glu	Leu	Cys	Met	Leu	Tyr	Ala	Cys	Gly	Glu	Ala	Ser
	50					55					60				
Ala	Arg	Arg	Cys	Val	Val	Phe	Ala	Leu	Leu	Ile	His	Cys	Leu	Cys	Ser
	65				70					75				80	
Val	Leu														

(2) INFORMATION FOR SEQ ID NO:1940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..483
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1940:

ctcgttttac	ccgcaccgcg	cgcagcccg	aacgccgaga	agacgcgaga	kgaagggagg	60
aggtgagcca	ccgaagcgga	gacgtgagta	gtcgaccaac	cccgtcggtc	cggcgactcc	120
ggctggcgcg	cggcgtgcta	gacgctacc	gaccatggtg	gtggaggaga	tcgccgaggg	180
ggtgaaaaac	ctcaccgtta	ccggagatgc	ggcggttca	ggcgagaggg	ggcagaggag	240
ggcgcgcgcg	ggcacagcaa	ccgcattccag	gtgtccaaca	ccaagaagcc	cctcttcttc	300
tagctcaacc	tcgcgaagag	tatatgcaac	agcacgacga	tgtagagcta	tccgctcttg	360
ggatggccat	agcaacagtt	gtgaccgttg	cagaaattct	gaagaacaat	ggatttgccg	420
ttgaaaagaa	aattaggacc	tctactgttg	aaataaacga	cgaatcaaga	ggcgctccat	480
tcc						

(2) INFORMATION FOR SEQ ID NO:1941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1941:

Arg	Phe	Thr	Arg	Thr	Arg	Arg	Ser	Pro	Gln	Arg	Arg	Glu	Asp	Ala	Arg
1		5						10				15			
Xaa	Arg	Glu	Glu	Val	Ser	His	Arg	Ser	Gly	Asp	Val	Ser	Ser	Arg	Pro
		20					25					30			
Thr	Pro	Ser	Val	Arg	Arg	Leu	Arg	Leu	Arg	Arg	Gly	Val	Leu	Asp	Arg
		35				40					45				
Tyr	Arg	Pro	Trp	Trp	Trp	Arg	Arg	Ser	Pro	Arg	Gly				
	50				55					60					

(2) INFORMATION FOR SEQ ID NO:1942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1501757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1942:

Met Val Val Glu Glu Ile Ala Glu Gly Val Lys Asn Leu Thr Val Thr
1 5 10 15
Gly Asp Ala Ala Ala Ser Gly Gly Glu Gly Gln Arg Arg Gly Gly Gly
20 25 30
Gly Thr Ala Thr Ala Ser Arg Cys Pro Thr Pro Arg Ser Pro Ser Ser
35 40 45
Ser Thr Ser Thr Ser Pro Arg Val Tyr Ala Thr Ala Arg Arg Cys Arg
50 55 60
Ala Ile Arg Ser Trp Asp Gly His Ser Asn Ser Cys Asp Arg Gly Arg
65 70 75 80
Asn Ser Glu Glu Gln Trp Ile Cys Arg
85

(2) INFORMATION FOR SEQ ID NO:1943:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1501758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1943:

Met Arg Arg Leu Gln Ala Glu Arg Gly Arg Gly Ala Ala Ala Ala
1 5 10 15
Gln Gln Pro His Pro Gly Val Gln His Gln Glu Ala Pro Leu Leu Leu
20 25 30
Arg Gln Pro Arg Gln Glu Tyr Met Gln Gln His Asp Asp Val Glu Leu
35 40 45
Ser Ala Leu Gly Met Ala Ile Ala Thr Val Val Thr Val Ala Glu Ile
50 55 60
Leu Lys Asn Asn Gly Phe Ala Val Glu Lys Lys Ile Arg Thr Ser Thr
65 70 75 80
Val Glu Ile Asn Asp Glu Ser Arg Gly Arg Pro Phe
85 90

(2) INFORMATION FOR SEQ ID NO:1944:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..576

(D) OTHER INFORMATION: / Ceres Seq. ID 1501763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1944:

aagattgggt	ccaacaccag	ccgcgcgcat	gtcgaagcga	ggcargggag	gttcggcggg	60
gaacaagtgc	cgcatgtcgc	tgggtctgcc	agtgcccgcg	acggtgaact	gcgcggacaa	120
caccggcgcc	aagaacctct	acatcatctc	cgtaaggggc	atcaagggcc	gcctcaatcg	180
ctcctcgctc	gctgcggtg	gcgacatggt	catggccacc	gtcaagaagg	ggaagcccca	240
ctcagggaag	aaggtgatgc	ccgcgcgtcat	cgctccgccag	cgcaagccgt	ggcgcccgaa	300
ggacgggggt	tacatgtact	togaagataa	tgtctggagt	atttgtgaat	ccaagggtga	360
gatgaagggt	tccgctatca	ctggacacct	cgccaaggag	tgtgctgata	tttggcgctg	420
gattgctagc	gcagcacaacg	ccattgtttg	agagcttggt	ggaatatgtt	cagactctta	480
tatgatcatc	ttattatcag	ttgctagact	gcaattgggc	ttatgtttgt	tcactcaatt	540
ttgtagtaaa	cagaatttgg	tataccaagg	ggatct			

(2) INFORMATION FOR SEQ ID NO:1945:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1501764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1945:

Arg Leu Gly Pro Thr Pro Ala Ala Ala Met Ser Lys Arg Gly Xaa Gly
1 5 10 15
Gly Ser Ala Gly Asn Lys Phe Arg Met Ser Leu Gly Leu Pro Val Ala
20 25 30
Ala Thr Val Asn Cys Ala Asp Asn Thr Gly Ala Lys Asn Leu Tyr Ile
35 40 45
Ile Ser Val Lys Gly Ile Lys Gly Arg Leu Asn Arg Leu Pro Ser Ala
50 55 60
Cys Val Gly Asp Met Val Met Ala Thr Val Lys Lys Gly Lys Pro Asp
65 70 75 80
Leu Arg Lys Lys Val Met Pro Ala Val Ile Val Arg Gln Arg Lys Pro
85 90 95
Trp Arg Arg Lys Asp Gly Val Tyr Met Tyr Phe Glu Asp Asn Ala Gly
100 105 110
Val Ile Val Asn Pro Lys Gly Glu Met Lys Gly Ser Ala Ile Thr Gly
115 120 125
Pro Ile Gly Lys Glu Cys Ala Asp Leu Trp Pro Arg Ile Ala Ser Ala
130 135 140
Ala Asn Ala Ile Val
145

(2) INFORMATION FOR SEQ ID NO:1946:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1501765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1946:

Met Ser Lys Arg Gly Xaa Gly Gly Ser Ala Gly Asn Lys Phe Arg Met
1 5 10 15
Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn Thr
20 25 30
Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly Arg
35 40 45
Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala Thr
50 55 60
Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala Val
65 70 75 80
Ile Val Arg Gln Arg Lys Pro Trp Arg Arg Lys Asp Gly Val Tyr Met
85 90 95
Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu Met
100 105 110
Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala Asp Leu
115 120 125
Trp Pro Arg Ile Ala Ser Ala Ala Asn Ala Ile Val

130 135 140

(2) INFORMATION FOR SEQ ID NO:1947:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1501766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1947:

Met	Ser	Leu	Gly	Leu	Pro	Val	Ala	Ala	Thr	Val	Asn	Cys	Ala	Asp	Asn	
1			5						10					15		
Thr	Gly	Ala	Lys	Asn	Leu	Tyr	Ile	Ile	Ser	Val	Lys	Gly	Ile	Lys	Gly	
			20					25					30			
Arg	Leu	Asn	Arg	Leu	Pro	Ser	Ala	Cys	Val	Gly	Asp	Met	Val	Met	Ala	
		35					40					45				
Thr	Val	Lys	Lys	Gly	Lys	Pro	Asp	Leu	Arg	Lys	Lys	Val	Met	Pro	Ala	
		50				55					60					
Val	Ile	Val	Arg	Gln	Arg	Lys	Pro	Trp	Arg	Arg	Lys	Asp	Gly	Val	Tyr	
65				70					75					80		
Met	Tyr	Phe	Glu	Asp	Asn	Ala	Gly	Val	Ile	Val	Asn	Pro	Lys	Gly	Glu	
				85					90					95		
Met	Lys	Gly	Ser	Ala	Ile	Thr	Gly	Pro	Ile	Gly	Lys	Glu	Cys	Ala	Asp	
			100				105						110			
Leu	Trp	Pro	Arg	Ile	Ala	Ser	Ala	Ala	Asn	Ala	Ile	Val				
		115				120					125					

(2) INFORMATION FOR SEQ ID NO:1948:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 554 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..554

(D) OTHER INFORMATION: / Ceres Seq. ID 1501771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1948:

attattctat	caagtggtgtg	tgctttttatt	ttatgtgctg	gagctgcact	agtgctttat	60
ttcaagcttc	gaaacacat	ccatttaact	gaagcgtcac	ttgtgccaac	aaaacctaca	120
ggctcctgttt	ctgcaatggt	tgggaaacagg	ctagaaagca	gacctatttc	ggcatcacca	180
tccttcagct	caagtttggt	ggcatataaa	ggatctgccca	aaacatttaa	cctggttgag	240
atggagagag	ctacactagg	attgatgag	tcacagaatta	ttggtgaggg	tggttttggg	300
cgtgtctatg	aaggtattct	tgaggatgga	gaacgggttg	ctatcaagg	tttaaaagcg	360
gacgatcaac	aaggtaccgc	ggagtttttg	gctgargtcg	agatgcttag	cogattgcat	420
cataggaact	tggttaagct	gataggtata	tgacacagagg	ggcatagccg	atggttgggt	480
tatgagcttg	ttccgaatgg	cagtggtgga	atctcacttg	catggatcag	ataaagggag	540
ctgctcagtt	tgat					

(2) INFORMATION FOR SEQ ID NO:1949:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1501772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1949:

Ile Ile Leu Ser Ser Val Cys Ala Phe Ile Leu Cys Ala Gly Ala Ala
1 5 10 15
Leu Val Leu Tyr Phe Lys Leu Arg Asn His Ile His Leu Thr Glu Ala
20 25 30
Ser Leu Val Pro Thr Lys Pro Thr Gly Pro Val Ser Ala Met Val Gly
35 40 45
Asn Arg Leu Glu Ser Arg Pro Ile Ser Ala Ser Pro Ser Phe Ser Ser
50 55 60
Ser Leu Val Ala Tyr Lys Gly Ser Ala Lys Thr Phe Asn Leu Val Glu
65 70 75 80
Met Glu Arg Ala Thr Leu Gly Phe Asp Glu Ser Arg Ile Ile Gly Glu
85 90 95
Gly Gly Phe Gly Arg Val Tyr Glu Gly Ile Leu Glu Asp Gly Glu Arg
100 105 110
Val Ala Ile Lys Val Leu Lys Arg Asp Gln Gln Gly Thr Arg Glu
115 120 125
Phe Leu Ala Xaa Val Glu Met Leu Ser Arg Leu His His Arg Asn Leu
130 135 140
Val Lys Leu Ile Gly Ile Cys Thr Glu Gly His Ser Arg Cys Leu Val
145 150 155 160
Tyr Glu Leu Val Pro Asn Gly Ser Val Gly Ile Ser Leu Ala Trp Ile
165 170 175

Arg

(2) INFORMATION FOR SEQ ID NO:1950:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1501773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1950:

Met Val Gly Asn Arg Leu Glu Ser Arg Pro Ile Ser Ala Ser Pro Ser
1 5 10 15
Phe Ser Ser Ser Ser Leu Val Ala Tyr Lys Gly Ser Ala Lys Thr Phe Asn
20 25 30
Leu Val Glu Met Glu Arg Ala Thr Leu Gly Phe Asp Glu Ser Arg Ile
35 40 45
Ile Gly Glu Gly Gly Phe Gly Arg Val Tyr Glu Gly Ile Leu Glu Asp
50 55 60
Gly Glu Arg Val Ala Ile Lys Val Leu Lys Arg Asp Asp Gln Gln Gly
65 70 75 80
Thr Arg Glu Phe Leu Ala Xaa Val Glu Met Leu Ser Arg Leu His His
85 90 95
Arg Asn Leu Val Lys Leu Ile Gly Ile Cys Thr Glu Gly His Ser Arg
100 105 110
Cys Leu Val Tyr Glu Leu Val Pro Asn Gly Ser Val Gly Ile Ser Leu
115 120 125
Ala Trp Ile Arg
130

(2) INFORMATION FOR SEQ ID NO:1951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..97
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501774
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1951:
Met Glu Arg Ala Thr Leu Gly Phe Asp Glu Ser Arg Ile Ile Gly Glu
1 5 10 15
Gly Gly Phe Gly Arg Val Tyr Glu Gly Ile Leu Glu Asp Gly Glu Arg
 20 25 30
Val Ala Ile Lys Val Leu Lys Arg Asp Gln Gln Gly Thr Arg Glu
 35 40 45
Phe Leu Ala Xaa Val Glu Met Leu Ser Arg Leu His His Arg Asn Leu
 50 55 60
Val Lys Leu Ile Gly Ile Cys Thr Glu Gly His Ser Arg Cys Leu Val
65 70 75 80
Tyr Glu Leu Val Pro Asn Gly Ser Val Gly Ile Ser Leu Ala Trp Ile
 85 90 95
Arg

(2) INFORMATION FOR SEQ ID NO:1952:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 420 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..420
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501786
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1952:
aaaaaacctcg caagcgaccc cagtaatggc gaccaaggcg ctatccgtct cctcgctcac 60
ctccacggcc ttgcctctct ttctcttgcc gcggcccgcg aggccttcac cttcgctccc 120
cctctctcgc cttctcggcc ctgcgccccc gcctccact ctctccgcgc cgctccccc 180
cgacgaggac ggcgtcgaca ccgtggagca gctctccac ccamgcccgc ctgagacctc 240
agcccccgcc ggatcccgcg gcgcgatcga mcgcctcatg aagctccagc gcmgcgccga 300
cgggamgccg tgcccggggg ccggaggagg tggttccctt acctggagcg gttccggccc 360
gcggccgcn gn ggcgcggast gtccagcggg gaggtcatag aggtgctgga gccgcacatc 420

(2) INFORMATION FOR SEQ ID NO:1953:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..77
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501787
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1953:
Lys Asn Leu Ala Ser Asp Pro Ser Asn Gly Asp Gln Gly Ala Ile Arg
1 5 10 15
Leu Leu Ala His Leu His Gly Leu Cys Leu Leu Phe Leu Ala Ala
 20 25 30
Pro Gln Ala Phe Thr Phe Ala Ser Pro Pro Pro Ser Arg Pro Ser
 35 40 45
Pro Pro Arg Leu His Ser Leu Arg Arg Arg Ser Arg Arg Gly Arg
50 55 60

Arg Arg His Arg Gly Ala Ala Pro Pro Pro Xaa Pro Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:1954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1501788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1954:

Lys Thr Ser Gln Ala Thr Pro Val Met Ala Thr Lys Ala Leu Ser Val
1 5 10 15
Ser Ser Leu Thr Ser Thr Ala Phe Ala Ser Phe Ser Leu Pro Arg Pro
20 25 30
Arg Arg Pro Ser Pro Ser Pro Pro Leu Arg Leu Leu Gly Pro Arg
35 40 45
Pro Arg Ala Ser Thr Leu Ser Ala Ala Pro Gly Asp Glu Asp Gly
50 55 60
Val Asp Thr Val Glu Gln Leu Leu His Pro Xaa Pro Pro Glu Thr Ser
65 70 75 80
Ala Pro Ala Gly Ser Arg Gly Arg Ile Xaa Arg Leu Met Lys Leu Gln
85 90 95
Arg Xaa Ala Asp Gly Xaa Pro Cys Pro Gly Ala Gly Gly Gly Ser
100 105 110
Leu Thr Trp Thr Arg Ser Gly Pro Arg Pro Xaa Gly Ala Xaa Cys Pro
115 120 125
Ala Gly Arg Ser
130

(2) INFORMATION FOR SEQ ID NO:1955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1501789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1955:

Met Ala Thr Lys Ala Leu Ser Val Ser Ser Leu Thr Ser Thr Ala Phe
1 5 10 15
Ala Ser Phe Ser Leu Pro Arg Pro Arg Arg Pro Ser Pro Ser Pro Pro
20 25 30
Leu Leu Arg Leu Leu Gly Pro Arg Pro Arg Ala Ser Thr Leu Ser Ala
35 40 45
Ala Ala Pro Gly Asp Glu Asp Gly Val Asp Thr Val Glu Gln Leu Leu
50 55 60
His Pro Xaa Pro Pro Glu Thr Ser Ala Pro Ala Gly Ser Arg Gly Arg
65 70 75 80
Ile Xaa Arg Leu Met Lys Leu Gln Arg Xaa Ala Asp Gly Xaa Pro Cys
85 90 95
Pro Gly Ala Gly Gly Gly Gly Ser Leu Thr Trp Thr Arg Ser Gly Pro
100 105 110
Arg Pro Xaa Gly Ala Xaa Cys Pro Ala Gly Arg Ser
115 120
(2) INFORMATION FOR SEQ ID NO:1956:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 493 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..493

(D) OTHER INFORMATION: / Ceres Seq. ID 1501794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1956:

aacctaaacc	tgtctcgc	tcgcctccgc	cagtcagccc	cctcaacccc	ggcggccaaa	60
agtgcagcca	ccgaagcggc	ggccatggcg	gactaaagcg	gctgtcagag	agccgggacc	120
tgacgcggat	cgagccatcg	gcgcgcactc	ccacatccgg	gggctagggc	tggactctc	180
catggaggcg	cgcgacgcct	cggaggcgcat	ggtcgggcag	ctgccgcgcg	gcgcggcgcg	240
ggngctcata	ctccagctca	tccgccaggg	caagatcgcc	ggcgcgcgcg	ttctcctcgc	300
gggccagccc	ggtaaccggca	agaccgcgct	cggcatgggc	atcgccaagt	cgctcggcgc	360
ggagacgccc	ttcgctctcg	tgcgagcctc	ggagctcttc	tcgctcgamc	tctccaagac	420
ggaggcgctc	acgcaggcct	tccgcgcgcg	catcgggtgc	gcatacaagg	ggagacggaa	480
atcatcgagg	gcg					

(2) INFORMATION FOR SEQ ID NO:1957:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..54

(D) OTHER INFORMATION: / Ceres Seq. ID 1501795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1957:

Pro	Lys	Pro	Arg	Leu	Ala	Ser	Pro	Pro	Pro	Val	Ser	Pro	Leu	Asn	Pro
1			5					10					15		
Gly	Gly	Gln	Lys	Ser	Thr	His	Arg	Ser	Gly	Gly	His	Gly	Gly	Leu	Lys
			20					25					30		
Arg	Leu	Ser	Glu	Ser	Arg	Asp	Leu	Thr	Arg	Ile	Glu	Pro	Ser	Ala	Arg
			35				40					45			
Thr	Pro	Thr	Ser	Gly	Gly										
			50												

(2) INFORMATION FOR SEQ ID NO:1958:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1501796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1958:

Met	Glu	Ala	Arg	Asp	Ala	Ser	Glu	Gly	Met	Val	Gly	Gln	Leu	Pro	Ala
1				5					10				15		
Arg	Xaa	Xaa	Arg	Xaa	Leu	Ile	Leu	Gln	Leu	Ile	Arg	Gln	Gly	Lys	Ile
			20					25					30		
Ala	Gly	Arg	Ala	Val	Leu	Leu	Ala	Gly	Gln	Pro	Gly	Thr	Gly	Lys	Thr
			35				40					45			
Ala	Leu	Ala	Met	Gly	Ile	Ala	Lys	Ser	Leu	Gly	Ala	Glu	Thr	Pro	Phe
			50			55				60					
Ala	Ser	Val	Ala	Ala	Ser	Glu	Leu	Phe	Ser	Leu	Xaa	Leu	Ser	Lys	Xaa

(2) INFORMATION FOR SEQ ID NO:1959:

- | (X1) SEQUENCE DESCRIPTION: SEQ ID: 1 | | | | | | | | | | | | | | | |
|--------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Gly | Gln | Leu | Pro | Ala | Arg | Xaa | Xaa | Arg | Xaa | Leu | Ile | Leu | Gln |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Leu | Val | Ile | Arg | Gln | Gly | Lys | Ile | Ala | Gly | Arg | Ala | Val | Leu | Leu | Ala |
| | | | | 20 | | | | 25 | | | | | 30 | | |
| Gln | Pro | Gly | Thr | Gly | Lys | Thr | Ala | Leu | Ala | Met | Gly | Ile | Ala | Lys | Ser |
| | | | | 35 | | | 40 | | | | | 45 | | | |
| Leu | Gly | Ala | Glu | Thr | Pro | Phe | Ala | Ser | Val | Ala | Ala | Ser | Glu | Leu | Phe |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Ser | Leu | Xaa | Leu | Ser | Lys | Xaa | Glu | Ala | Leu | Thr | Gln | Ala | Phe | Arg | |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Ala | Ile | Gly | Cys | Ala | Ser | Arg | Arg | Arg | Arg | Lys | Ser | Ser | Arg | Ala | |
| | | | | 85 | | | | 90 | | | | | | 95 | |

- (2) INFORMATION FOR SEQ ID NO:1960:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- ```
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
```

- (A) NAME/KEY: -  
(B) LOCATION: 1..461

- (D) OTHER INFORMATION: / Ceres Seq. ID 1501804

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1960:

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:1 |             |             |             |            |             |     |
|----------------------------------------|-------------|-------------|-------------|------------|-------------|-----|
| atcccaaga                              | gcacgcagcg  | casactgaag  | caccacttcc  | tgcactcatc | gctagtctgt  | 60  |
| caacacgctc                             | tagtaaacatg | ccatcacaccg | taccacacaa  | tggctcccaa | ggttgcgctc  | 120 |
| ttccttgccc                             | tcggcctctt  | ctcttgtctg  | gcgcgcgaatg | ctgtcgcaac | ctactgtccc  | 180 |
| ggcccgactg                             | ttcccaacgcg | gcgcagctgt  | ccgcagccgct | cgctcgacag | ccacggggcgc | 240 |
| tgccgcatgt                             | acgcgctcaa  | aatcatgtgt  | ggcccaactg  | ctgtagcctc | ctcaaggctg  | 300 |
| gctgcgccca                             | gcacgagcaga | tgcctgccac  | ttctggaagg  | gctggtggac | ctcgcagcgc  | 360 |
| catctgtgct                             | ctgcaccgsc  | atcaggcaga  | acggctcgca  | tttcatcatc | aacgggcgatg | 420 |
| aacactgctt                             | ggaacacatc  | agcagcagag  | acagcccaat  | c          |             |     |

(2) INFORMATION FOR SEQ ID NO:1961:

- (2) INFORMATION FOR SEQ ID NO:1961:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 94 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- ```
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
```

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..94

- (D) OTHER INFORMATION: / Ceres Seq. ID 1501805

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1961:

Ile Pro Lys Ser Thr Gln Arg Xaa Leu Lys His His Phe Leu His Ser
1 5 10 15
Leu Leu Ala Ala His Thr Val Leu Val Thr Val His His Gln Ser Pro
20 25 30
Pro Met Ala Pro Lys Val Ala Leu Phe Leu Ala Leu Gly Leu Leu Phe
35 40 45
Ala Ala Ala Ala Asn Gly Cys Glu Pro Tyr Cys Pro Gly Pro Val Val
50 55 60
Pro Thr Pro Pro Val Val Pro Thr Pro Ser Ser His Ser His Gly Arg
65 70 75 80
Cys Pro Ile Asp Ala Leu Lys Ile Met Cys Ala Pro Thr Cys
85 90

(2) INFORMATION FOR SEQ ID NO:1962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1501806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1962:

Pro Lys Glu His Ala Ala Xaa Thr Glu Ala Pro Leu Pro Ala Leu Thr
1 5 10 15
Ala Ser Cys Ser His Arg Ala Ser Asn Ser Pro Ser Pro Val Thr Thr
20 25 30
Asn Gly Ser Gln Gly Cys Ala Leu Pro Cys Pro Arg Pro Ser Leu Arg
35 40 45
Cys Arg Arg Glu Trp Leu Arg Thr Leu Leu Ser Arg Pro Ser Arg Pro
50 55 60
Asn Ala Ala Ser Arg Ala Asp Ala Val Val Ala Gln Pro Arg Ala Leu
65 70 75 80
Pro Asp Arg Arg Ala Gln Asn His Val Cys Ala Asn Val Leu Gly Leu
85 90 95
Val Lys Val Gly Leu Pro Gln His Glu Gln Cys Cys Pro Leu Leu Glu
100 105 110
Gly Leu Val Asp Leu Asp Ala Ala Leu Cys Leu Cys Thr Xaa Ile Lys
115 120 125
Ala Asn Gly Val Asp Phe Tyr Ile Asn Gly His Asp His Cys Leu Glu
130 135 140
His Ile Ser Ser Arg Asp Ser Pro Ile
145 150

(2) INFORMATION FOR SEQ ID NO:1963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1501807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1963:

Met Ala Asn Pro Thr Val Pro Ala Gln Ser Ser Gln Arg Arg Gln
1 5 10 15
Ser Cys Arg Arg Arg Arg Arg Thr Ala Thr Gly Ala Ala Arg Ser Thr
20 25 30
Arg Ser Lys Ser Cys Val Arg Gln Arg Ala Arg Pro Arg Gln Gly Arg

35 40 45
Pro Ala Pro Ala Arg Ala Met Leu Pro Thr Ser Gly Gly Ala Gly Gly
50 55 60
Pro Arg Arg Arg Thr Val Pro Leu His Xaa His Gln Gly Gln Arg Arg
65 70 75 80
Arg Phe Leu His Gln Arg Ala
85

(2) INFORMATION FOR SEQ ID NO:1964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..446
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1964:

agacaaccat agaccgcaga ggtgtgaact gtaatttcag atttcagagc gcgcagaagc 60
cctcttgacc accgcgcgcg cgcgcgcgaa scaagccaaa ctgagtaagc agctatggag 120
ggatccgcgc cgcctccgcg ccgcacgcgc atctgcatca tcgggagcgc tcccgctgcg 180
cacacggcag ccactcacgc ggccgcgcgc gagctcaagc ctgtdctctt cgaggcctgg 240
atggccaaac acatcgccgc gggcgggcag ctaccacca ccaccgacgt cgagaatttc 300
cgggcttcc ccaacggcat catggggccc gacctcatgg acaactgcgc gcgcagttcc 360
ctgcgctttg gcaccaacat cctctccgag accgtcaccg ccgtcgactt ttgcgctgc 420
ccattccgag ttagtgcaga ctccac

(2) INFORMATION FOR SEQ ID NO:1965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1965:

Met Glu Gly Ser Ala Ala Ala Pro Leu Arg Thr Arg Ile Cys Ile Ile
1 5 10 15
Gly Ser Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala
20 25 30
Glu Leu Lys Pro Xaa Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala
35 40 45
Ala Gly Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly
50 55 60
Phe Pro Asn Gly Ile Met Gly Ala Asp Leu Met Asp Asn Cys Arg Ala
65 70 75 80
Gln Ser Leu Arg Phe Gly Thr Asn Ile Leu Ser Glu Thr Val Thr Ala
85 90 95
Val Asp Phe Ser Ala Cys Pro Phe Arg Val Ser Ala Asp Ser
100 105 110

(2) INFORMATION FOR SEQ ID NO:1966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1501812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1966:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1967:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 758 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..758

(D) OTHER INFORMATION: / Ceres Seq. ID 1501813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1967:

(X1) SEQUENCE DESCRIPTION						
aaatttcccaa	cgcgcgcagc	gcacacaccg	cggtcggatc	ggggggagaa	cggaaaggcca	60
acagcagcagc	gcgaattcca	cgcgaacaatc	caagattttcg	agccacagaca	cagcgcaaac	120
tcgatggcg	aggggtccaa	cgcggcagac	ccgctgttcc	agctctccag	cgatctcttc	180
cagcagctgg	agtcacatga	caatcaggaa	gaagttagac	tgccgcctaa	gattgaagca	240
tttagattga	aagtcactaa	gtgtaccagag	cagccgcgta	atmacttcag	cgagctagaa	300
matagctgca	gattgtggaca	aagctgttcac	cgcggcttga	ataaattgtc	acaaagatga	360
ttcatctctc	catgtgcctca	gatccagagac	tgaagtctct	tctgacgcag	acatctgata	420
tcctgagctc	ggtctcaaca	cgcctgtcca	atgagaggcg	ggggtttgtt	gggacagcta	480
cggaagcgac	ccagaaaagc	caggagaatt	ccagaagaat	ctcgtgtaat	ggcgctgtaa	540
tagtttttgt	tttgtggctt	taccagacct	tattctatgt	ctctcaaac	agttgttcca	600
tgccaaaaag	tttgtggcgt	aataaacact	aaaaaccact	gtctctcat	cggaatagta	660
atagctgcat	atagattctaa	atttactatt	tggtcgcccg	ttagttctat	ttgtaactaa	720
caggcgatga	atagaaaaga	accagaggag	tatgattt			

(2) INFORMATION FOR SEQ ID NO:1968:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1501814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1968:

Lys	Phe	Pro	Thr	Ala	Ala	Arg	Gln	His	Gln	Arg	Ser	Asp	Arg	Gly	Arg
1			5						10					15	
Asn	Gly	Arg	Ala	Thr	Ala	Glu	Arg	Glu	Phe	His	Arg	Gln	Ile	Gln	Asp
1			20					25					30		
Phe	Glu	His	Arg	His	Arg	Arg	Asn	Ser	Met	Ala	Glu	Gly	Ser	Lys	Pro
			35				40					45			
Asp	Val	Pro	Leu	Phe	Gln	Leu	Leu	Ser	Asp	Leu	Leu	Gln	Gln	Val	Glu
	50					55				60					
Ser	Met	Ser	Asn	Gln	Glu	Glu	Val	Glu	Leu	Arg	Ala	Lys	Ile	Glu	Ala
65				70						75				80	

Leu Gly Leu Glu Val Thr Lys Val Pro Glu Gln Pro Ala Asn Xaa Leu
85 90 95
Ser Glu Leu Glu Xaa Ser Cys Arg Val Gly Gln Ser Cys His Arg Gly
100 105 110
Leu Asn Lys Cys Arg Gln Arg
115

(2) INFORMATION FOR SEQ ID NO:1969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1969:

Ile Pro Asn Arg Arg Thr Ala Thr Pro Ala Val Gly Ser Gly Glu Lys
1 5 10 15
Arg Lys Gly Asn Ser Arg Ala Arg Ile Pro Pro Thr Asn Pro Arg Phe
20 25 30
Arg Ala Gln Thr Gln Ala Lys Leu Asp Gly Gly Val Gln Ala Gly
35 40 45
Arg Ala Ala Val Pro Ala Pro Gln Arg Ser Ser Pro Ala Gly Gly Val
50 55 60
Asn Glu Gln Ser Gly Arg Ser Arg Ala Ala Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:1970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1970:

Met Ala Glu Gly Ser Lys Pro Asp Val Pro Leu Phe Gln Leu Leu Ser
1 5 10 15
Asp Leu Leu Gln Gln Val Glu Ser Met Ser Asn Gln Glu Glu Val Glu
20 25 30
Leu Arg Ala Lys Ile Glu Ala Leu Gly Leu Glu Val Thr Lys Val Pro
35 40 45
Glu Gln Pro Ala Asn Xaa Leu Ser Glu Leu Glu Xaa Ser Cys Arg Val
50 55 60
Gly Gln Ser Cys His Arg Gly Leu Asn Lys Cys Arg Gln Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:1971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..607
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1971:
aaaacgcacac ggagataact agcgagcgag agcgtngaga tcgaggagaa gaaggcaagc 60
agcgagagaa agagagagag agatggatga ggagtagcac gtgacgtgtg tggggacggg 120
gctcaaggag tgcatacatca gcggcctcct ctcgctcgat ggccctcaagg tccttcacat 180
ggacaggaat gactactacg gaggagaaatc ttcgtccctg aatctaacca agctctggaa 240
taggttcaag ggcaacgaca gccctccgga gcacctgggc gtcacaaaga gtacaacgtc 300
gacatggtgc ccaagtccat gatggcaaac ggcgcgctgg tccgctgctt gatccgcacc 360
agcgtgacca agtatctcaa ctccaaggct gttgacggga gctttgtgta caacaatggc 420
aagatccaca aagtcgccgc aaccgacgtg gaggccctca agtcgaacct gatgggctcg 480
ttcgagaagc ggcgcgccgc gaagttcttc atatacgttc aggactacga ggaggacgac 540
cccaagtccc acgagggcct ggacctcaac aaggtcacca ccagggaagt catctccaaa 600
tacggat

(2) INFORMATION FOR SEQ ID NO:1972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1501825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1972:

Met Val Pro Lys Phe Met Met Ala Asn Gly Ala Leu Val Arg Val Leu
1 5 10 15
Ile Arg Thr Ser Val Thr Lys Tyr Leu Asn Phe Lys Ala Val Asp Gly
20 25 30
Ser Phe Val Tyr Asn Asn Gly Lys Ile His Lys Val Pro Ala Thr Asp
35 40 45
Val Glu Ala Leu Lys Ser Asn Leu Met Gly Leu Phe Glu Lys Arg Arg
50 55 60
Ala Arg Lys Phe Phe Ile Tyr Xaa Gln Asp Tyr Glu Glu Asp Asp Pro
65 70 75 80
Lys Ser His Glu Gly Leu Asp Leu Asn Lys Val Thr Thr Arg Glu Val
85 90 95
Ile Ser Lys Tyr Gly
100

(2) INFORMATION FOR SEQ ID NO:1973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1501826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1973:

Met Met Ala Asn Gly Ala Leu Val Arg Val Leu Ile Arg Thr Ser Val
1 5 10 15
Thr Lys Tyr Leu Asn Phe Lys Ala Val Asp Gly Ser Phe Val Tyr Asn
20 25 30
Asn Gly Lys Ile His Lys Val Pro Ala Thr Asp Val Glu Ala Leu Lys
35 40 45
Ser Asn Leu Met Gly Leu Phe Glu Lys Arg Arg Ala Arg Lys Phe Phe
50 55 60
Ile Tyr Xaa Gln Asp Tyr Glu Glu Asp Asp Pro Lys Ser His Glu Gly
65 70 75 80
Leu Asp Leu Asn Lys Val Thr Thr Arg Glu Val Ile Ser Lys Tyr Gly

85

90

95

(2) INFORMATION FOR SEQ ID NO:1974:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1501827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1974:

Met	Ala	Asn	Gly	Ala	Leu	Val	Arg	Val	Leu	Ile	Arg	Thr	Ser	Val	Thr	
1		5						10					15			
Lys	Tyr	Leu	Asn	Phe	Lys	Ala	Val	Asp	Gly	Ser	Phe	Val	Tyr	Asn	Asn	
		20						25				30				
Gly	Lys	Ile	His	Lys	Val	Pro	Ala	Thr	Asp	Val	Glu	Ala	Leu	Lys	Ser	
		35						40				45				
Asn	Leu	Met	Gly	Leu	Phe	Glu	Lys	Arg	Arg	Ala	Arg	Lys	Phe	Phe	Ile	
		50						55				60				
Tyr	Xaa	Gln	Asp	Tyr	Glu	Glu	Asp	Asp	Pro	Lys	Ser	His	Glu	Gly	Leu	
65								70				75			80	
Asp	Leu	Asn	Lys	Val	Thr	Thr	Arg	Glu	Val	Ile	Ser	Lys	Tyr	Gly		
								85				90			95	

(2) INFORMATION FOR SEQ ID NO:1975:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 526 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..526

(D) OTHER INFORMATION: / Ceres Seq. ID 1501828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1975:

tctgttcccc	tttccctcct	gcgcaccccg	tcttctcctc	ccccgcgtcaa	acccccagcac	60
aaaaagcaac	cgcccgcgcg	ctctctcgctc	ctctcccgaa	tcagccgctcg	cggtgcctaa	120
tccggcgcag	ccccctcccg	atccgcgggt	gcgcccgcca	gaggcgcgcc	tccgggcctc	180
ccccgatgta	tagcaacttc	aaggagcagg	cgatcgagta	cgtaaacgag	gcagtcacagg	240
aggacaatcg	cggsaaactac	gtcaaggcgt	tccctctcta	catgaacgcg	ctcgagtact	300
tcaaaaccca	cctcaagtac	gagaagaacc	ccaagatcaa	ggaggccatc	accgccaagt	360
tcaccgagta	ctccgcgcmg	gccgaggaga	tccggggcgt	cctcgatgag	ggcgccgcar	420
ggcctggggc	caacggtggc	gacgcagctg	tmgccacgcg	ccccaaagacc	caagggcaag	480
gatkgggcgcg	gargcaacgcg	arggatgac	tccgagcagt	ccaagc		

(2) INFORMATION FOR SEQ ID NO:1976:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..168

(D) OTHER INFORMATION: / Ceres Seq. ID 1501829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1976:

Cys Ser Pro Phe Pro Pro Ala His Pro Val Phe Ser Pro Arg Gln

1	5	10	15
Thr Pro Ala Gln Lys Ala Thr Ala Arg Leu Leu Ala Pro Leu Pro			
20	25	30	
Asn Gln Pro Ser Arg Cys Leu Ile Arg Pro Thr Pro Pro Ile Arg			
35	40	45	
Gly Cys Pro Pro Gln Arg Arg Ala Ser Gly Pro Pro Pro Met Tyr Ser			
50	55	60	
Asn Phe Lys Glu Gln Ala Ile Glu Tyr Val Lys Gln Ala Val Gln Glu			
65	70	75	80
Asp Asn Ala Xaa Asn Tyr Val Lys Ala Phe Pro Leu Tyr Met Asn Ala			
85	90	95	
Leu Glu Tyr Phe Lys Thr His Leu Lys Tyr Glu Lys Asn Pro Lys Ile			
100	105	110	
Lys Glu Ala Ile Thr Ala Lys Phe Thr Glu Tyr Leu Arg Xaa Ala Glu			
115	120	125	
Glu Ile Arg Ala Val Leu Asp Glu Gly Gly Ala Xaa Pro Gly Ala Asn			
130	135	140	
Gly Gly Asp Ala Ala Xaa Ala Thr Arg Pro Lys Thr Gln Gly Gln Gly			
145	150	155	160
Xaa Gly Arg Xaa Gln Arg Xaa Gly			
165			

(2) INFORMATION FOR SEQ ID NO:1977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1501830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1977:

Met Tyr Ser Asn Phe Lys Glu Gln Ala Ile Glu Tyr Val Lys Gln Ala	
1	5
Val Gln Glu Asp Asn Ala Xaa Asn Tyr Val Lys Ala Phe Pro Leu Tyr	10
20	25
Met Asn Ala Leu Glu Tyr Phe Lys Thr His Leu Lys Tyr Glu Lys Asn	30
35	40
Pro Lys Ile Lys Glu Ala Ile Thr Ala Lys Phe Thr Glu Tyr Leu Arg	45
50	55
Xaa Ala Glu Glu Ile Arg Ala Val Leu Asp Glu Gly Gly Ala Xaa Pro	60
65	70
Gly Ala Asn Gly Gly Asp Ala Ala Xaa Ala Thr Arg Pro Lys Thr Gln	75
85	90
Gly Gln Gly Xaa Gly Arg Xaa Gln Arg Xaa Gly	95
100	105

(2) INFORMATION FOR SEQ ID NO:1978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..534

(D) OTHER INFORMATION: / Ceres Seq. ID 1501850

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1978:

atTTTTTTta tatggagatt atttctggwt tatataaaaag gacacaaagt gggacgaata
gcagaagact tcccttcgtc tgcttccagc agaccagacc atggcgatct cccagatctc

60
120

(2) INFORMATION FOR SEQ ID NO:1979:

(2) INFORMATION FOR SEQ ID NO:1979:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1979:

(2) INFORMATION FOR SEQ ID NO:1980:

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1980:

Met	Glu	Ile	Ile	Ser	Xaa	Leu	Tyr	Lys	Arg	Thr	Gln	Val	Gly	Thr	Asn
1				5					10					15	
Ser	Arg	Arg	Leu	Pro	Phe	Val	Cys	Phe	Pro	Glu	Thr	Gln	Pro	Trp	Arg
			20					25					30		
Ser	Pro	Arg	Ser	His	Ala	Tyr	Ser	Trp	Pro	Ser	Phe	Ser	Trp	Xaa	Pro
			35				40					45			
Pro	Ser	Pro	Pro	Pro	Gln	Leu	Arg	Leu	Arg	Thr	Ala	Thr	Thr	Trp	Trp
			50			55					60				
Pro	Leu	Pro	Asn	Pro	Arg	Ser	Arg	Arg	Ser	Thr	Glu	Arg	Thr	Ala	Ala
65				70					75						80
Pro	Ser	Ser	Ser	Ser	Thr	Pro	Pro	Gly	Val	Val	Thr	Ala	Arg	Ser	Leu
			85						90					95	
Leu	Leu	Ser	Met	Lys	Asp	Leu	Val	Gln	Val	Leu	Arg	Lys	Leu	Asn	Leu
			100					105					110		

Ser

(2) INFORMATION FOR SEQ ID NO:1981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1981:

```
Met Ala Ile Ser Gln Ile Ser Arg Ile Phe Leu Ala Ile Leu Leu Leu
1          5          10          15
Xaa Ala Ala Phe Ala Ala Ala Pro Ala Ala Leu Ala Asp Gly Asp Asp
20          25          30
Val Val Ala Leu Thr Glu Ser Thr Phe Glu Lys Glu Val Gly Lys Asp
35          40          45
Arg Gly Ala Leu Val Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Lys
50          55          60
Lys Leu Ala Pro Glu Tyr Glu Arg Leu Gly Ala Ser Phe Lys Lys Ala
65          70          75
Lys Ser Val Leu Ile Xaa Lys Val Asp Cys Xaa Glu His Lys Xaa Leu
85          90          95
Cys Ser Lys Tyr Gly Val Ser Gly Tyr Pro Thr Ile Gln Trp Phe Pro
100         105         110
Lys Gly Ser Leu Glu Pro Lys Lys Tyr Glu Gly Gln Arg Thr Ala Glu
115         120         125
Ala Leu Ala Glu Phe Leu Asn Thr Glu Gly Gly Thr Asn Val Lys Leu
130         135         140
```

(2) INFORMATION FOR SEQ ID NO:1982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..569
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1982:

```
acagcctctc cgctccgct cctcgccgcg cgcgcgcgtc tctctctgta caggtaaagg 60
gaggaagagg gcgaatggt gaagcacaac aacgtcatcc ccaacgggca cttcaagaag 120
cactggcaga actatgtcaa gacatggttc aaccagcccg ccgcgaagca gaggcgcggc 180
atcgctcgtc aaaagaaggc tgtgaagata ttcccccgcc cgactgctgg tctctaacgc 240
cccattgttc aatgcacgac tttaaagtac aacatgaagt caagggtctg gagaggcttt 300
acccttgagg agctgaaggc tgggctcacc ggcgagygga ggcgcgcgcg ggactacctg 360
tgccgcgctc cgacacaagt aaagaggatg gaagagaagg ccacagatag arcggtcaaa 420
gcacaaaagg aaccocacac catccoccatc aactggatct tcgataggac cattcctgtc 480
attctacctt agtgttttatc tttttgatc tttgtttgtg tatctatgct gttattgtaa 540
gctaattcca tggacattga tagcgctcgt
```

(2) INFORMATION FOR SEQ ID NO:1983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..101
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501863
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1983:
Ser Leu Ser Ala Ser Ala Pro Arg Ala Ala Ala Ser Pro Pro Val
1 5 10 15
Gln Val Arg Arg Gly Arg Gly Arg Asn Gly Glu Ala Gln Gln Arg His
 20 25 30
Pro Gln Arg Ala Leu Gln Glu Ala Leu Ala Glu Leu Cys Gln Asp Met
 35 40 45
Val Gln Pro Ala Arg Pro Gln Ala Glu Ala Pro His Arg Ser Ser Lys
50 55 60
Glu Gly Cys Glu Asp Ile Pro Pro Pro Asp Cys Trp Ser Ser Thr Pro
65 70 75 80
His Cys Ser Met Pro Asp Phe Lys Val Gln His Glu Val Lys Gly Trp
 85 90 95
Glu Arg Leu Tyr Pro
 100
(2) INFORMATION FOR SEQ ID NO:1984:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..138
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501864
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1984:
Met Val Lys His Asn Asn Val Ile Pro Asn Gly His Phe Lys Lys His
1 5 10 15
Trp Gln Asn Tyr Val Lys Thr Trp Phe Asn Gln Pro Ala Arg Lys Gln
 20 25 30
Arg Arg Arg Ile Ala Arg Gln Lys Lys Ala Val Lys Ile Phe Pro Arg
 35 40 45
Pro Thr Ala Gly Pro Leu Arg Pro Ile Val Gln Cys Gln Thr Leu Lys
50 55 60
Tyr Asn Met Lys Ser Arg Ala Gly Arg Gly Phe Thr Leu Glu Glu Leu
65 70 75 80
Lys Ala Gly Leu Thr Gly Glu Gly Arg Arg Ala Arg Asp Tyr Leu Cys
 85 90 95
Ala Leu Pro His Lys Ile Lys Arg Met Glu Glu Lys Ala His Asp Arg
 100 105 110
Xaa Val Lys Ala Gln Lys Lys Pro Thr Pro Ile Pro Ile Asn Trp Ile
 115 120 125
Phe Asp Arg Thr Ile Pro Val Ile Leu Pro
130 135
(2) INFORMATION FOR SEQ ID NO:1985:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1501865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1985:

Met Lys Ser Arg Ala Gly Arg Gly Phe Thr Leu Glu Glu Leu Lys Ala
1 5 10 15
Gly Leu Thr Gly Glu Gly Arg Arg Ala Arg Asp Tyr Leu Cys Ala Leu
20 25 30
Pro His Lys Ile Lys Arg Met Glu Glu Lys Ala His Asp Arg Xaa Val
35 40 45
Lys Ala Gln Lys Lys Pro Thr Pro Ile Pro Ile Asn Trp Ile Phe Asp
50 55 60
Arg Thr Ile Pro Val Ile Leu Pro
65 70

(2) INFORMATION FOR SEQ ID NO:1986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..514

(D) OTHER INFORMATION: / Ceres Seq. ID 1501872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1986:

atcgcaactcg tagtcgtagc tcaagcatca rcvgcaggag ctctggggcag cgtgcgcacg 60
trgggtacct agctcgctct gctagcctac catggctgat caccacgggg gcgcgacggg 120
argtgscggg ggctacggcg acctccagcg cgggggcggc atgcacggcg aggcgcgacga 180
gcagcagaag caggcgcgcca tgaatgacggc gctcaaggcc gcgacggcgcg cgacctctct 240
gaaccactgc cggcgcgcgcg gcatatggcc cttaaaggcg gtggctgctg ctacgtacgc 300
tgccgtagag tctcggtgcg cgcgatagct ctagctagtc gtttatgtgt tgtgctttgt 360
gtgtgcacgc ttgtgtctgg ggcatgcag tgcagtgcag tactatatgc tgtatgcgtc 420
tctctttgat cggagaggcg gatgtacagc atgctcgata tgtctagttt ggaatgcatg 480
tttatgatga ggaataaaat gcagtgttca gggt

(2) INFORMATION FOR SEQ ID NO:1987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1501873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1987:

Arg Thr Arg Ser Arg Ser Ser Ser Ile Xaa Xaa Arg Ser Ser Gly Gln
1 5 10 15
Arg Ala His Xaa Gly Tyr Leu Ala Arg Ser Ala Ser Leu Pro Trp Leu
20 25 30
Ile Thr Thr Gly Ala Arg Arg Xaa Val Xaa Gly Ala Thr Ala Thr Ser
35 40 45
Ser Ala Gly Ala Ala Cys Thr Ala Arg Arg Ser Ser Ser Arg Ser Arg
50 55 60
Ala Pro
65

(2) INFORMATION FOR SEQ ID NO:1988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..78
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501874
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1988:
Met Ala Asp His His Arg Gly Ala Thr Gly Xaa Xaa Gly Gly Tyr Gly
1 5 10 15
Asp Leu Gln Arg Gly Gly Gly Met His Gly Glu Ala Gln Gln Gln
 20 25 30
Lys Gln Gly Ala Met Met Thr Ala Leu Lys Ala Ala Thr Ala Ala Thr
 35 40 45
Ser Leu Asn His Cys Arg Arg Gly Gly Ile Trp Pro Leu Lys Ala Val
50 55 60
Ala Ala Ala Thr Tyr Ala Ala Val Glu Ser Arg Ser Pro Arg
65 70 75
(2) INFORMATION FOR SEQ ID NO:1989:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..55
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501875
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1989:
Met His Gly Glu Ala Gln Gln Gln Gln Lys Gln Gly Ala Met Met Thr
1 5 10 15
Ala Leu Lys Ala Ala Thr Ala Ala Thr Ser Leu Asn His Cys Arg Arg
 20 25 30
Gly Gly Ile Trp Pro Leu Lys Ala Val Ala Ala Ala Thr Tyr Ala Ala
 35 40 45
Val Glu Ser Arg Ser Pro Arg
50 55
(2) INFORMATION FOR SEQ ID NO:1990:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 556 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..556
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501884
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1990:
aagggtgctgcg cctgcgcccgc accaaacgta ggagaccocat tcccccatct cctctctttt 60
ctttccaaga aaggtcttct ctctctgtgc tcagcgccga cgcttcccaa ttccttccaa 120
tcgattcttc gtctcgtctc cgtgtaatoc ccagcttgcc ctccctcgctc ttccctccca 180
aaacctctacg cctccctgac caagctccgg ggacgaatgg acggaggagc cggttccct 240
ggcacgcmgg tcccgcgctc gccggaggac gtttccggg actaccgcgc gcgccaggcc 300
ggcctaatac gggcgctcac caccgatgtt gagaagtctt acgtgatgtg cgaccagag 360
aaggataatt tatgtttata tggacttccc aatgagacat ggggaagtaa cttgcctgt 420
gaggagggtc ctctcgaact ccagagcca gctctcgaa ttaattttgc tegtgtggg 480
atgaatgaaa aagattggct atcaattgtt gcagtgcata gtgattctgt gctaattgtc 540
gttgcatttt attttg
(2) INFORMATION FOR SEQ ID NO:1991:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..109
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501885
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1991:
Gly Leu Arg Leu Arg Pro Thr Lys Arg Arg Arg Pro Ile His Pro Ser
1 5 10 15
Pro Leu Phe Ser Phe Gln Glu Lys Ser Ser Leu Leu Cys Leu Ser Ala
 20 25 30
Asp Ala Ser Gln Phe Leu Pro Ile Asp Ser Ser Ser Arg Pro Arg Val
 35 40 45
Ile Pro Ser Leu Pro Ser Ser Leu Phe Pro Pro Lys Thr Leu Arg Leu
 50 55 60
Pro Asp Gln Ala Pro Gly Thr Asn Gly Arg Arg Ser Arg Leu Pro Trp
65 70 75 80
His Xaa Gly Pro Ala Leu Ala Gly Gly Arg Phe Pro Gly Leu Pro Arg
 85 90 95
Ala Pro Gly Arg Pro Asn Gln Gly Ala His His Arg Cys
 100 105
(2) INFORMATION FOR SEQ ID NO:1992:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..113
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501886
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1992:
Met Asp Gly Gly Ala Gly Phe Pro Gly Thr Xaa Val Pro Arg Ser Pro
1 5 10 15
Glu Asp Val Phe Arg Asp Tyr Arg Ala Arg Gln Ala Gly Leu Ile Arg
 20 25 30
Ala Leu Thr Thr Asp Val Glu Lys Phe Tyr Val Met Cys Asp Pro Glu
 35 40 45
Lys Asp Asn Leu Cys Leu Tyr Gly Leu Pro Asn Glu Thr Trp Glu Val
 50 55 60
Asn Leu Pro Ala Glu Glu Val Pro Pro Glu Leu Pro Glu Pro Ala Leu
65 70 75 80
Gly Ile Asn Phe Ala Arg Asp Gly Met Asn Glu Lys Asp Trp Leu Ser
 85 90 95
Leu Val Ala Val His Ser Asp Ser Trp Leu Met Ser Val Ala Phe Tyr
 100 105 110
Phe
(2) INFORMATION FOR SEQ ID NO:1993:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1501887
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1993:
Met Cys Asp Pro Glu Lys Asp Asn Leu Cys Leu Tyr Gly Leu Pro Asn
1 5 10 15
Glu Thr Trp Glu Val Asn Leu Pro Ala Glu Glu Val Pro Pro Glu Leu
20 25 30
Pro Glu Pro Ala Leu Gly Ile Asn Phe Ala Arg Asp Gly Met Asn Glu
35 40 45
Lys Asp Trp Leu Ser Leu Val Ala Val His Ser Asp Ser Trp Leu Met
50 55 60
Ser Val Ala Phe Tyr Phe
65 70

(2) INFORMATION FOR SEQ ID NO:1994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..532

(D) OTHER INFORMATION: / Ceres Seq. ID 1501888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1994:

gagcctttcg gtttttctct gtcttcattgt gtgtttgta tagagacctt gccttgctcg 60
ggcagcacac ttgggacgcg agggaggaga gttggtgagc gaactggga tcagtgggtg 120
accgcagagt tcttgcttct tctctcttga ggargagggc tgcagcctgc aggggcccga 180
gagagcagga ggaggcggag acatgggtag ctgcgctaag ctggcgaggga gggcggtgga 240
gacggacgct ccggtcatgg tgaagatata agaactgctc cgargggcca atgatgtrat 300
gtcgcttggc caggagagttg ttactggca acctcccgag tcagctatgg ataagatgca 360
aaagatcacc agggaaaccaa tagtcagtaa atatgtttct ratgatgggc ttctcgagct 420
tcgagaagca ctctctgaaa agctaaacag agagaacaag cttaccaaat catctgcat 480
ggtoactgct ggtgcaaatc aggtctttgk gaacttggtc ctcactcttt gt

(2) INFORMATION FOR SEQ ID NO:1995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1501889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1995:

Met Gly Ser Phe Ala Lys Leu Ala Arg Arg Ala Val Glu Thr Asp Ala
1 5 10 15
Pro Val Met Val Lys Ile Gln Glu Leu Leu Arg Xaa Ala Lys Asp Xaa
20 25 30
Met Ser Leu Ala Gln Gly Val Val Tyr Trp Gln Pro Pro Glu Ser Ala
35 40 45
Met Asp Lys Ile Glu Lys Ile Ile Arg Glu Pro Ile Val Ser Lys Tyr
50 55 60
Gly Ser Xaa Asp Gly Leu Pro Glu Leu Arg Glu Ala Leu Leu Glu Lys
65 70 75 80
Leu Ser Arg Glu Asn Lys Leu Thr Lys Ser Ser Val Met Val Thr Ala
85 90 95
Gly Ala Asn Gln Ala Phe Xaa Asn Leu Val Leu Thr Leu Cys
100 105 110

(2) INFORMATION FOR SEQ ID NO:1996:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..92
(D) OTHER INFORMATION: / Ceres Seq. ID 1501890
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1996:
Met Val Lys Ile Gln Glu Leu Leu Arg Xaa Ala Lys Asp Xaa Met Ser
1 5 10 15
Leu Ala Gln Gly Val Val Tyr Trp Gln Pro Pro Glu Ser Ala Met Asp
20 25 30
Lys Ile Glu Lys Ile Ile Arg Glu Pro Ile Val Ser Lys Tyr Gly Ser
35 40 45
Xaa Asp Gly Leu Pro Glu Leu Arg Glu Ala Leu Leu Glu Lys Leu Ser
50 55 60
Arg Glu Asn Lys Leu Thr Lys Ser Ser Val Met Val Thr Ala Gly Ala
65 70 75 80
Asn Gln Ala Phe Xaa Asn Leu Val Leu Thr Leu Cys
85 90

(2) INFORMATION FOR SEQ ID NO:1997:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..78
(D) OTHER INFORMATION: / Ceres Seq. ID 1501891
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1997:
Met Ser Leu Ala Gln Gly Val Val Tyr Trp Gln Pro Glu Ser Ala
1 5 10 15
Met Asp Lys Ile Glu Lys Ile Ile Arg Glu Pro Ile Val Ser Lys Tyr
20 25 30
Gly Ser Xaa Asp Gly Leu Pro Glu Leu Arg Glu Ala Leu Leu Glu Lys
35 40 45
Leu Ser Arg Glu Asn Lys Leu Thr Lys Ser Ser Val Met Val Thr Ala
50 55 60
Gly Ala Asn Gln Ala Phe Xaa Asn Leu Val Leu Thr Leu Cys
65 70 75

(2) INFORMATION FOR SEQ ID NO:1998:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 569 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..569
(D) OTHER INFORMATION: / Ceres Seq. ID 1501895
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1998:
aggatcggag aacatcgcgc gcgactccat gctccaggag atcaagtctg cctaccagat 60
tcttgcccaac aagtaccatc ctgatatgaa taagagtccc gaagcagaag aaaagttcaa 120
ggagatcagt gctgcatacg agccaagctt ggatctgacc gctgtacttt gtgtgcgcgc 180
ttgaatctac gggtctcttc ttctctgttc atcccgtgga tctgtcccggt ggtggtccaa 240
gcattcgatt tctgctatta taacatocaa cgttggcggt gaagagcaag gggacagata 300

agcccaaaagg	cagcaagggg	aacgtcgaca	aggaccccaa	caagcctgac	tcccaacatt	360
ttttgtccgc	cggtgtctgta	gcggaagccc	aaaggcagca	aggggaacgt	cgacaaggac	420
cccaacaagg	ctgactccca	acattttttg	tccgcgggtg	ctgtarcggc	ggcgctggtg	480
arctcccca	tgtgtgggtc	tgggatgctc	ccaggcgccg	gggttcggcg	agacggggac	540
tgawctggtg	ctgggctctg	ggatgtctc				

(2) INFORMATION FOR SEQ ID NO:1999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1999:

Gly	Ser	Glu	Asn	Ile	Arg	Arg	Asp	Ser	Met	Leu	Gln	Glu	Ile	Lys	Ser	
1			5					10					15			
Ala	Tyr	Gln	Ile	Leu	Ala	His	Lys	Tyr	His	Pro	Asp	Met	Asn	Lys	Ser	
			20					25					30			
Pro	Glu	Ala	Glu	Glu	Lys	Phe	Lys	Glu	Ile	Ser	Ala	Ala	Tyr	Glu	Pro	
			35				40					45				
Ser	Leu	Asp	Leu	Thr	Ala	Val	Leu	Cys	Val	Ala	Ala					
			50				55				60					

(2) INFORMATION FOR SEQ ID NO:2000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2000:

Met	Leu	Gln	Glu	Ile	Lys	Ser	Ala	Tyr	Gln	Ile	Leu	Ala	His	Lys	Tyr	
1			5					10					15			
His	Pro	Asp	Met	Asn	Lys	Ser	Pro	Glu	Ala	Glu	Glu	Lys	Phe	Lys	Glu	
			20					25					30			
Ile	Ser	Ala	Ala	Tyr	Glu	Pro	Ser	Leu	Asp	Leu	Thr	Ala	Val	Leu	Cys	
			35				40					45				
Val	Ala	Ala														
			50													

(2) INFORMATION FOR SEQ ID NO:2001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2001:

Met	Asn	Lys	Ser	Pro	Glu	Ala	Glu	Glu	Lys	Phe	Lys	Glu	Ile	Ser	Ala	
1			5					10					15			
Ala	Tyr	Glu	Pro	Ser	Leu	Asp	Leu	Thr	Ala	Val	Leu	Cys	Val	Ala	Ala	
			20				25						30			

(2) INFORMATION FOR SEQ ID NO:2002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..432
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2002:

ccatccagtc	ctggagcctg	cggcgctgcs	cttgcatcgc	atctccgtcg	tgtctctcgc	60
ccacgggaatc	cgccaattc	cccacgcccgc	ccgtcgtcct	tttctataaa	attcactccg	120
ccaccaaatc	tcgaatcccc	atcgcgctgc	ttttccaccg	accccgcacg	cgacgcccgc	180
gccacccgcg	ctccctcccc	agtcgccact	ccccttcccc	ggcgcgggac	agagatccgg	240
ggcgccgcgc	gatggcgaaac	atcgacatgg	cgaagatcct	ggcggacctg	gaccgcggcg	300
ccacgcggcg	ncgacgcgcg	ggtgcccaag	accaagctcg	tatgcacgct	cggcccgggc	360
tccgcgaccg	tgcccatgct	cgagaagctg	ctccgcgcmg	gcatgaacgt	cgcgcgcttc	420
aactctcccc	ac					

(2) INFORMATION FOR SEQ ID NO:2003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2003:

Pro	Ser	Ser	Pro	Gly	Ala	Cys	Ala	Ala	Xaa	Leu	Ala	Ser	His	Leu	Arg
1				5					10					15	
Arg	Arg	Pro	Arg	Pro	Arg	Asn	Pro	Ser	Asn	Ser	Pro	Arg	Arg	Pro	Ser
				20				25						30	
Ser	Phe	Ser	Ile	Lys	Phe	Thr	Pro	Pro	Asn	Leu	Glu	Ser	Pro	Ser	
				35				40						45	
Arg	Cys	Phe	Ser	Thr	Asp	Pro	Asp	Ala	Asp	Ala	Thr	Ala	Ala		
				50				55						60	
Pro	Ser	Pro	Val	Pro	Thr	Pro	Leu	Pro	Gly	Pro	Arg	Thr	Glu	Ile	Arg
				65				70						75	
Gly	Ala	Ala	Arg	Trp	Arg	Thr	Ser	Thr	Trp	Arg	Arg	Ser	Trp	Arg	Thr
				85				90						95	
Trp	Thr	Ala	Ala	Pro	Ala	Ala	Xaa	Asp	Ala	Arg	Val	Pro	Lys	Thr	Lys
				100				105						110	
Leu	Val	Cys	Thr	Leu	Gly	Pro	Ala	Ser	Arg	Thr	Val	Pro	Met	Leu	Glu
				115				120						125	
Lys	Leu	Leu	Arg	Xaa	Gly	Met	Asn	Val	Ala	Arg	Phe	Asn	Phe	Ser	His
				130				135						140	

(2) INFORMATION FOR SEQ ID NO:2004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1501901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2004:

```
Ile Gln Ser Trp Ser Leu Arg Gly Cys Xaa Cys Ile Ala Ser Pro Ser
1          5          10          15
Ser Ser Ser Pro Thr Glu Ser Val Gln Phe Pro Thr Pro Pro Val Val
20          25          30
Leu Phe Tyr Lys Ile His Ser Ala Thr Lys Ser Arg Ile Pro Ile Ala
35          40          45
Leu Leu Phe His Arg Pro Arg Arg Arg Arg Arg His Arg Arg Ser
50          55          60
Leu Pro Ser Pro His Ser Pro Ser Arg Ala Ala Asp Arg Asp Pro Gly
65          70          75          80
Arg Arg Ala Met Ala Asn Ile Asp Met Ala Lys Ile Leu Ala Asp Leu
85          90          95
Asp Arg Gly Ala Ser Gly Xaa Arg Arg Ala Gly Ala Gln Asp Gln Ala
100         105         110
Arg Met His Ala Arg Pro Gly Leu Pro His Arg Ala His Ala Arg Glu
115         120         125
Ala Ala Pro Arg Xaa His Glu Arg Arg Ala Leu Gln Leu Leu Pro
130         135         140
```

(2) INFORMATION FOR SEQ ID NO:2005:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..429

(D) OTHER INFORMATION: / Ceres Seq. ID 1501902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2005:

```
aaagctctctg ttttccactg ctctgcgtct gcgtctcgtg ctgcgtctgc actgcttcgc 60
gtctccctcc cccgcctctcc gccccgggaa aaaaaaaagc aaaacacggc catggaaggc 120
tacgaccggc agttctacca gttcagcgac cagctgcgcc tgcagacggc cgccttctcg 180
ggcctctccc tcggcgactc catctggtec ccgcgcggcc ggcgcaacaa cagcaacgac 240
gtcctcttgc ccgcctcggc gtgcgccgcc gacgcccggc ccaagaccaa cgccgtctgc 300
ggcctcaagc tcaacgacgg agggccccgc ctcctcggt cggggaagct ggccttcggc 360
ggcgcgcgca ccaaggccga ccgtactaac aacaacaacc tctccaacac cgacaacaag 420
accgtgtac
```

(2) INFORMATION FOR SEQ ID NO:2006:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1501903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2006:

```
Lys Leu Leu Leu Phe His Cys Ser Ala Ser Ala Ser Ala Ser
1          5          10          15
Ala Leu Leu Arg Val Ser Leu Pro Pro Pro Pro Arg Glu Lys Lys
20          25          30
Lys Gln Asn Thr Ala Met Glu Gly Tyr Asp Arg Glu Phe Tyr Gln Phe
35          40          45
```

Ser Asp Gln Leu Arg Leu Gln Thr Ala Ala Phe Ser Gly Leu Ser Leu
50 55 60
Gly Asp Ser Ile Trp Ser Pro Ala Gly Arg Arg Asn Ser Asn Asp
65 70 75 80
Val Leu Phe Ala Ala Ser Ala Ser Pro Ala Asp Ala Ala Lys Thr
85 90 95
Asn Ala Val Val Gly Leu Lys Leu Asn Asp Gly Gly Pro Gly Leu Ile
100 105 110
Gly Ser Gly Lys Leu Ala Phe Gly Gly Gly Thr Lys Ala Asp Arg
115 120 125
Tyr Asn Asn Asn Asn Leu Ser Asn Thr Asp Asn Lys Thr Val Tyr
130 135 140

(2) INFORMATION FOR SEQ ID NO:2007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1501904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2007:

Ser Ser Cys Phe Ser Thr Ala Leu Arg Leu Arg Leu Arg Leu Arg Leu
1 5 10 15
His Cys Phe Ala Ser Pro Ser Pro Arg Leu Arg Pro Gly Lys Lys Lys
20 25 30
Ser Lys Thr Arg Pro Trp Lys Ala Thr Thr Ala Ser Ser Thr Ser Ser
35 40 45
Ala Thr Ser Cys Ala Cys Arg Arg Pro Pro Ser Arg Ala Ser Pro Ser
50 55 60
Ala Thr Pro Ser Gly Pro Pro Pro Ala Gly Ala Thr Thr Ala Thr Thr
65 70 75 80
Ser Ser Ser Pro Pro Arg Arg Arg Pro Pro Thr Pro Pro Pro Arg Pro
85 90 95
Thr Pro Ser Ser Ala Ser Ser Ser Thr Thr Glu Gly Pro Ala Ser Ser
100 105 110
Ala Pro Gly Ser Trp Pro Ser Ala Ala Ala Pro Arg Pro Thr Ala
115 120 125
Thr Thr Thr Thr Ser Pro Thr Pro Thr Thr Arg Pro Cys
130 135 140

(2) INFORMATION FOR SEQ ID NO:2008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1501905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2008:

Ala Pro Ala Phe Pro Leu Leu Cys Val Cys Val Cys Val Cys Val Cys
1 5 10 15
Thr Ala Ser Arg Leu Pro Pro Pro Ala Ser Ala Pro Gly Lys Lys Lys
20 25 30
Ala Lys His Gly His Gly Arg Leu Arg Pro Arg Val Leu Pro Val Gln
35 40 45
Arg Pro Ala Ala Pro Ala Asp Gly Arg Leu Leu Gly Pro Leu Pro Arg

50	55	60
Arg Leu His Leu Val Pro Arg Arg Pro Ala Gln Gln Gln Arg Arg		
65	70	75
Pro Leu Arg Arg Leu Gly Val Ala Arg Arg Arg Arg Gln Asp Gln		80
	85	90
Arg Arg Arg Arg Pro Gln Ala Gln Arg Arg Arg Ala Arg Pro His Arg		95
	100	105
Leu Arg Glu Ala Gly Leu Arg Arg Arg Arg His Gln Gly Arg Pro Leu		110
	115	120
Gln Gln Gln Gln Pro Leu Gln His Arg Gln Gln Asp Arg Val		125
	130	135
		140

(2) INFORMATION FOR SEQ ID NO:2009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..515

(D) OTHER INFORMATION: / Ceres Seq. ID 1501906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2009:

aaatatctct	gcacactatg	acctgagtaa	tgattctctt	gctctttttc	tgatccgac	60
gatgacttac	tccttggtga	ttttcaakgm	rraagatgag	agtttagaag	cagcgcasta	120
cgtaaaccttg	acaatctaata	taataaggct	aagtggtatc	cggggcatca	tgctcttgac	180
attggctgtg	gttggggctc	attggcaata	cgtttggtga	agagaactgg	ctgcaagtgc	240
acaggaatta	cattatcgga	ggagcaactg	aaatatggaa	agagaaaggt	gaaagaattt	300
ggattagagg	accgcataac	tctcctgctt	tgtgattacc	gtcaaatacc	gaacggccag	360
aaagtttgata	ggattathag	ttgtgggatg	cttgaacacg	ttggccatga	gtctacgaa	420
gatttctttg	ctctctgcga	gtatcatttg	gccgaacacg	gcctacttgt	cttcacgtcc	480
atcgcggtcc	caaggaact	gtacgacaaa	atgag			

(2) INFORMATION FOR SEQ ID NO:2010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..45

(D) OTHER INFORMATION: / Ceres Seq. ID 1501907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2010:

Asn Ile Ser Ala His Tyr Asp Leu Ser Asn Asp Phe Phe Ala Leu Phe		
1	5	10
Leu Asp Pro Thr Met Thr Tyr Ser Cys Gly Ile Phe Xaa Xaa Xaa Asp		15
	20	25
Glu Ser Leu Glu Ala Ala Xaa Tyr Val Asn Leu Thr Ile		30
	35	40
		45

(2) INFORMATION FOR SEQ ID NO:2011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..42

(D) OTHER INFORMATION: / Ceres Seq. ID 1501908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2011:
Met Leu Glu His Val Gly His Glu Phe Tyr Glu Asp Phe Phe Ala Ser
1 5 10 15
Cys Glu Tyr His Leu Ala Glu His Gly Leu Leu Val Leu Gln Ser Ile
20 25 30
Ala Val Pro Glu Glu Leu Tyr Asp Lys Met
35 40

(2) INFORMATION FOR SEQ ID NO:2012:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..35

(D) OTHER INFORMATION: / Ceres Seq. ID 1501909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2012:

Met Ser Ser Thr Lys Ile Ser Leu Pro Pro Ala Ser Ile Ile Trp Pro
1 5 10 15
Asn Thr Ala Tyr Leu Ser Ser Ser Pro Ser Arg Ser Gln Arg Asn Cys
20 25 30
Thr Thr Lys
35

(2) INFORMATION FOR SEQ ID NO:2013:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 549 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..549

(D) OTHER INFORMATION: / Ceres Seq. ID 1501922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2013:

acaacaagca gaagcagaag cagaagctag cagctagtag acgagcgacg agtagctagc 60
tagctagcta tctagagagc tcatcatatc gctgctcgct ctcattccacc attatagaga 120
agagcagatc gagctgcagc tggcagaggg cgagttgttg ctatagtagct cctgcttgct 180
aaatttgcat cgtatccgat ccattccatg aagaagtcgt cgatgatggc gcccatgacg 240
atcatggcga gaggttgcgc tgtgctgcgc ctctcgtcgg ctgccatggc ttccgcccga 300
ggagcagcgt ggctggacat gaatttctac ggcagcacgt gcccgcgcggt ggagggccatc 360
gtcaaggagg agatggtggc gatcctcaag gcggcgccga cgctggccgg cccgctgctc 420
cgctccatt tccacgactg ctctgcacgg ggctgcgacg cctccgtgct cctggactcg 480
actccacca gcaaggcgga gaaggacgcc accccgaacc tcaccctcgg gggcttcggg 540
tccgtgcag

(2) INFORMATION FOR SEQ ID NO:2014:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1501923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2014:

Met Lys Lys Ser Ser Met Met Ala Pro Met Thr Ile Met Ala Arg Val
1 5 10 15

Ala Ala Val Leu Val Leu Ser Ser Ala Ala Met Ala Ser Ala Ala Gly
20 25 30
Ala Ala Gly Leu Asp Met Asn Phe Tyr Gly Ser Thr Cys Pro Arg Val
35 40 45
Glu Ala Ile Val Lys Glu Glu Met Val Ala Ile Leu Lys Ala Ala Pro
50 55 60
Thr Leu Ala Gly Pro Leu Leu Arg Leu His Phe His Asp Cys Phe Val
65 70 75 80
Arg Gly Cys Asp Ala Ser Val Leu Leu Asp Ser Thr Pro Thr Ser Thr
85 90 95
Ala Glu Lys Asp Ala Thr Pro Asn Leu Thr Leu Arg Gly Phe Gly Ser
100 105 110
Val Gln

(2) INFORMATION FOR SEQ ID NO:2015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2015:

Met Met Ala Pro Met Thr Ile Met Ala Arg Val Ala Ala Val Leu Val
1 5 10 15
Leu Ser Ser Ala Ala Met Ala Ser Ala Ala Gly Ala Ala Gly Leu Asp
20 25 30
Met Asn Phe Tyr Gly Ser Thr Cys Pro Arg Val Glu Ala Ile Val Lys
35 40 45
Glu Glu Met Val Ala Ile Leu Lys Ala Ala Pro Thr Leu Ala Gly Pro
50 55 60
Leu Leu Arg Leu His Phe His Asp Cys Phe Val Arg Gly Cys Asp Ala
65 70 75 80
Ser Val Leu Leu Asp Ser Thr Pro Thr Ser Thr Ala Glu Lys Asp Ala
85 90 95
Thr Pro Asn Leu Thr Leu Arg Gly Phe Gly Ser Val Gln
100 105

(2) INFORMATION FOR SEQ ID NO:2016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2016:

Met Ala Pro Met Thr Ile Met Ala Arg Val Ala Ala Val Leu Val Leu
1 5 10 15
Ser Ser Ala Ala Met Ala Ser Ala Ala Gly Ala Ala Gly Leu Asp Met
20 25 30
Asn Phe Tyr Gly Ser Thr Cys Pro Arg Val Glu Ala Ile Val Lys Glu
35 40 45
Glu Met Val Ala Ile Leu Lys Ala Ala Pro Thr Leu Ala Gly Pro Leu
50 55 60
Leu Arg Leu His Phe His Asp Cys Phe Val Arg Gly Cys Asp Ala Ser

(2) INFORMATION FOR SEQ ID NO:2017:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2017:

(2) INFORMATION FOR SEQ ID NO:2018:

- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Lys | Leu | Thr | Met | Ile | Ala | Arg | Val | Thr | Asp | Gly | Leu | Pro | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ser | Glu | Gly | Leu | Asp | Asp | Ser | Arg | Asp | Leu | Lys | Asp | Ala | Asp | Phe | Tyr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Lys | Gln | Gln | Ala | Lys | Leu | Leu | Phe | Lys | Asn | Leu | Ser | Arg | Gly | Gln | His |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Glu | Ala | Ser | Arg | Met | Ser | Ile | Glu | Thr | Gly | Pro | Tyr | Leu | Phe | His | Tyr |
| | | | | | | 55 | | | | | 60 | | | | |
| Ile | Ile | Glu | Gly | Arg | Val | Cys | Tyr | Leu | Thr | Leu | Cys | Asp | Arg | Ser | Tyr |
| 65 | | | | 70 | | | | | | 75 | | | | 80 | |
| Pro | Lys | Lys | Leu | Ala | Phe | Gln | Tyr | Leu | Glu | Asp | Leu | Lys | Asn | Glu | Phe |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Glu | Lys | Val | Asn | Gly | Ser | Gln | Ile | Glu | Thr | Ala | Ala | Arg | Pro | Tyr | Xaa |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Phe | Ile | Lys | Phe | Asp | Ala | Phe | Ile | Gln | Lys | | | | | | |
| | | 115 | | | | | 120 | | | | | | | | |

- (2) INFORMATION FOR SEQ ID NO:2019:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..117
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501928
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2019:
Met Ile Ala Arg Val Thr Asp Gly Leu Pro Leu Ser Glu Gly Leu Asp
1 5 10 15
Asp Ser Arg Asp Leu Lys Asp Ala Asp Phe Tyr Lys Gln Gln Ala Lys
20 25 30
Leu Leu Phe Lys Asn Leu Ser Arg Gly Gln His Glu Ala Ser Arg Met
35 40 45
Ser Ile Glu Thr Gly Pro Tyr Leu Phe His Tyr Ile Ile Glu Gly Arg
50 55 60
Val Cys Tyr Leu Thr Leu Cys Asp Arg Ser Tyr Pro Lys Lys Leu Ala
65 70 75 80
Phe Gln Tyr Leu Glu Asp Leu Lys Asn Glu Phe Glu Lys Val Asn Gly
85 90 95
Ser Gln Ile Glu Thr Ala Ala Arg Pro Tyr Xaa Phe Ile Lys Phe Asp
100 105 110
Ala Phe Ile Gln Lys
115

(2) INFORMATION FOR SEQ ID NO:2020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2020:

Met Ser Ile Glu Thr Gly Pro Tyr Leu Phe His Tyr Ile Ile Glu Gly
1 5 10 15
Arg Val Cys Tyr Leu Thr Leu Cys Asp Arg Ser Tyr Pro Lys Lys Leu
20 25 30
Ala Phe Gln Tyr Leu Glu Asp Leu Lys Asn Glu Phe Glu Lys Val Asn
35 40 45
Gly Ser Gln Ile Glu Thr Ala Ala Arg Pro Tyr Xaa Phe Ile Lys Phe
50 55 60
Asp Ala Phe Ile Gln Lys
65 70

(2) INFORMATION FOR SEQ ID NO:2021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..493
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2021:

aagtctctttt	gtgtttttta	taggcttgag	agccttggaa	agcggggggg	ggaggaagcg	60
gaagaggagc	tctcttttgt	gttctagagg	ggagtoatgt	tccatggcgg	caggcctctt	120
tccctccggg	ggctctctca	ggcgcttgaa	gctgatatcc	accatgcocaa	caccctggcg	180
catgctatac	acagggcgta	trggggtgcc	tgcgagatg	naggctgtcc	tacagctcca	240
tggtccaatt	ctttctcaac	cttatccaat	ggatggactg	cgagtgtctc	ctgtcataca	300

cgctccctag ctaccttggc ctgctcgagg ttctcgtcta caaggtttat gtcatgaag 360
atgcctccat atccaccata gaaaggagg cgagcctgaa ggaattctac actatcatat 420
accctttctt gcaacaactg gaggacaact tgatggacaa ggaactgcaag gacaagggt 480
ggctgtgtgc tgc

(2) INFORMATION FOR SEQ ID NO:2022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1501931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2022:

Ser	Leu	Phe	Val	Phe	Phe	Ile	Gly	Leu	Arg	Ala	Trp	Asn	Ser	Gly	Gly	
1			5				10				15					
Trp	Arg	Lys	Arg	Lys	Arg	Ser	Phe	Val	Leu	Cys	Ser	Arg	Gly	Glu	Ser	
			20				25						30			
Cys	Ser	Met	Ala	Ala	Gly	Leu	Cys	Pro	Ser	Gly	Gly	Leu	Ser	Arg	Arg	
			35				40					45				
Leu	Lys	Leu	Ile	Ser	Thr	Met	Pro	Thr	Pro	Trp	Arg	Met	Leu	Tyr	Thr	
			50				55					60				
Gly	Arg	Xaa	Gly	Val	Pro	Ala	Gln	Met	Xaa	Ala	Val	Leu	Gln	Leu	His	
			65				70				75				80	
Gly	Ser	Asn	Leu	Ser	Gln	Pro	Tyr	Pro	Met	Asp	Gly	Leu	Gln	Leu	Leu	
			85						90					95		
Pro	Val	Ile	His	Ala	Pro											
			100													

(2) INFORMATION FOR SEQ ID NO:2023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1501932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2023:

Met	Phe	His	Gly	Gly	Arg	Pro	Leu	Ser	Leu	Arg	Gly	Ser	Leu	Lys	Ala	
1			5				10				15					
Leu	Glu	Ala	Asp	Ile	His	His	Ala	Asn	Thr	Leu	Ala	His	Ala	Ile	His	
			20				25					30				
Arg	Ala	Tyr	Xaa	Gly	Ala	Cys	Ala	Asp	Xaa	Gly	Cys	Pro	Thr	Ala	Pro	
			35				40					45				
Trp	Leu	Gln	Ser	Phe	Ser	Thr	Leu	Ser	Asn	Gly	Trp	Thr	Ala	Ala	Ala	
			50				55				60					
Pro	Cys	His	Thr	Arg	Ser	Leu	Ala	Thr	Leu	Ala	Cys	Ser	Arg	Phe	Ser	
			65				70				75				80	
Ser	Thr	Arg	Phe	Met	Ser	Met	Lys	Met	Pro	Pro	Tyr	Pro	Pro			
			85						90							

(2) INFORMATION FOR SEQ ID NO:2024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2024:

Met Ala Pro Ile Phe Leu Asn Leu Ile Gln Trp Met Asp Cys Ser Cys
1 5 10 15
Ser Leu Ser Tyr Thr Leu Pro Ser Tyr Leu Gly Leu Leu Glu Val Leu
20 25 30
Val Tyr Lys Val Tyr Val Asp Glu Asp Ala Ser Ile Ser Thr Ile Glu
35 40 45
Arg Arg Ala Ser Leu Lys Glu Phe Tyr Thr Ile Ile Tyr Pro Phe Leu
50 55 60
Gln Gln Leu Glu Asp Asn Leu Met Asp Lys Asp Cys Lys Asp Lys Gly
65 70 75 80
Trp Ser Ala Ala

(2) INFORMATION FOR SEQ ID NO:2025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..586
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2025:

ccgcgcgtcaaa acgtcatccg aatccgcgcc gcgaccagcg aagaaggtag gaagcatccg 60
gaacggagacg gcgcctctctg cctcgcctttc ctcccatggc gccgccccctc gccgccctct 120
catcgctcgtc gccctattc tctccttcat cgtcccgccc catccgcgcg tgcacgcac 180
ctcctccttc tatctccttc cagacgcggg gacgctcgcc caecggcgcg cgggcagctg 240
agtcctctgt cagtaacgctt ctccgaggtgc gcggaactcac cgcctcgtg aaggagactg 300
ggcagcagat cctcgccggc gtcgacctca ccatacccgga gggcgagatt catcgatta 360
tgggaaaaaa cggtccggc aagagcacc tcacgaaagt tctcgtaggc catctcatt 420
atgaggtaac tgggtgtacc attctcttca aggtgagga cctggttgac atggagccag 480
aggacagatc tctagcaggc ctttcatga gtttccaagc acctattgag attccctgga 540
gtcagcaatt ttgattttct gtcctggct gtgaatgctc gcagag

(2) INFORMATION FOR SEQ ID NO:2026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2026:

Pro Pro Ser Asn Val Ile Arg Ile Arg Ala Ala Thr Ser Glu Glu Gly
1 5 10 15
Arg Lys His Pro Glu Arg Arg Arg Ala Ser Cys Leu Ala Phe Leu Pro
20 25 30
Trp Arg Arg Pro Ser Pro Pro Ser His Arg Arg Arg Pro Tyr Ser Leu
35 40 45
Leu His Arg Pro Ala Pro Ser Ala Ala Ala Thr His Leu Leu Leu Leu
50 55 60
Ser Pro Ser Arg Arg Gly Asp Ala Arg Pro Arg Arg Arg Gln Leu
65 70 75 80

Ser Pro Leu Ser Val Arg Phe Ser Arg Cys Ala Asp Ser Pro His Pro
85 90 95

(2) INFORMATION FOR SEQ ID NO:2027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2027:

Arg Arg Gln Thr Ser Ser Glu Ser Ala Pro Arg Pro Ala Lys Lys Val
1 5 10 15
Gly Ser Ile Arg Asn Gly Asp Ala Pro Pro Ala Ser Leu Ser Ser His
20 25 30
Gly Ala Ala Pro Arg Arg Arg Leu Ile Val Val Ala Pro Ile Leu Ser
35 40 45
Phe Ile Val Pro Pro His Pro Pro Leu Pro Arg Thr Ser Ser Phe Tyr
50 55 60
Leu Leu Pro Asp Ala Gly Thr Leu Ala His Gly Gly Gly Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:2028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2028:

Met Ala Pro Pro Leu Ala Ala Val Ser Ser Ser Ser Pro Leu Phe Ser
1 5 10 15
Pro Ser Ser Ser Arg Pro Ile Arg Arg Cys His Ala Pro Pro Pro Ser
20 25 30
Ile Ser Phe Gln Thr Arg Gly Arg Ser Pro Thr Ala Ala Ala Ala
35 40 45
Glu Ser Ser Val Ser Thr Leu Leu Glu Val Arg Gly Leu Thr Ala Ser
50 55 60
Val Lys Glu Thr Gly Gln Gln Ile Leu Ala Gly Val Asp Leu Thr Ile
65 70 75 80
Arg Glu Gly Glu Ile His Ala Ile Met Gly Lys Asn Gly Ser Gly Lys
85 90 95
Ser Thr Leu Thr Lys Val Leu Val Gly His Pro His Tyr Glu Val Thr
100 105 110
Gly Gly Thr Ile Leu Phe Lys Gly Glu Asp Leu Val Asp Met Glu Pro
115 120 125
Glu Asp Arg Ser Leu Ala Gly Leu Phe Met Ser Phe Gln Ala Pro Ile
130 135 140
Glu Ile Pro Trp Ser Gln Gln Phe
145 150

(2) INFORMATION FOR SEQ ID NO:2029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..657
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501976
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2029:
agtgcgggca cgcgcgctgt tgcagaagtt gcctcttttt tacgtcttgt ttctcctcca 60
ccccggcgac gcgaatggag aagggcagtg gaggcagcaa tcctccgcgc ccaccgctcc 120
acatggagda ctttccaaactg gaggggaaga agcccgctcaa gaaccccttt gtgcccacgc 180
gogcactggt tactgctgga gttctgactg ctggtctgat cagtttccga tatgggaact 240
ctcagctggg tcagaanaact atgagggcac gtgtagtgtc tcaaggcgct acagtcgctc 300
tgatgattgg cagtgccttac tactatggcg atcaaatcaa gctgttcaa aaagggtcga 360
gccccatgat ttcccatgaa tattgtctgt tttggtgtat ggaggaatgc cttgtatacg 420
cataaatttc aactggactc tgcgtccccc ttttaacatc attttggcct gacacgtggt 480
agctaacaag aaatcgctgt tggtcgcgat ggcaggattg aaaataaata attttgtttg 540
ttgatttttg tcaggatttg ttgggttgat taattaggct atatgcata attgttatat 600
ctttgtacaa acacgcgttc tgtgtctgc aatcagcggc tgaagtgacc attttgc
(2) INFORMATION FOR SEQ ID NO:2030:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..125
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501977
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2030:
Val Pro Ala Pro Pro Leu Leu Gln Lys Leu Pro Leu Phe Tyr Val Leu
1 5 10 15
Phe Leu Leu His Pro Gly Asp Ala Asn Gly Glu Gly Gln Trp Arg Gln
20 25 30
Gln Ser Ser Ala Ala Thr Ala Pro His Gly Gly Leu Pro Thr Gly Gly
35 40 45
Glu Glu Ala Arg Gln Glu Pro Leu Cys Ala His Arg Arg Thr Gly Tyr
50 55 60
Cys Trp Ser Ser Asp Cys Trp Ser Asp Gln Phe Pro Ile Trp Glu Leu
65 70 75 80
Ser Ala Gly Ser Glu Thr Asp Glu Gly Thr Cys Ser Cys Ser Arg Arg
85 90 95
Tyr Ser Arg Ser Asp Asp Trp Gln Cys Leu Leu Leu Trp Arg Ser Asn
100 105 110
Gln Ala Val Gln Glu Arg Val Glu Pro Met Ile Phe Pro
115 120 125
(2) INFORMATION FOR SEQ ID NO:2031:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..121
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501978
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2031:
Cys Arg His Arg Arg Cys Cys Arg Ser Cys Leu Phe Thr Ser Cys

1		5		10		15
Phe	Ser	Ser	Thr	Pro	Ala	Thr
		20		25		30
Asn	Pro	Pro	Pro	Pro	Leu	His
		35		40		45
Lys	Lys	Pro	Val	Lys	Asn	Pro
		50		55		60
Ala	Gly	Val	Leu	Thr	Ala	Gly
		65		70		75
Gln	Leu	Gly	Gln	Lys	Leu	Met
		85		90		95
Thr	Val	Ala	Leu	Met	Ile	Gly
		100		105		110
Lys	Leu	Phe	Lys	Lys	Gly	Ser
		115		120		

(2) INFORMATION FOR SEQ ID NO:2032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1501979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2032:

Met	Glu	Lys	Gly	Ser	Gly	Gly	Ser	Asn	Pro	Pro	Pro	Pro	Leu	His
1		5		10		15								
Met	Glu	Asp	Phe	Gln	Leu	Glu								
		20		25		30								
Val	Pro	Ile	Gly	Ala	Leu	Val								
		35		40		45								
Ile	Ser	Phe	Arg	Tyr	Gly	Asn								
		50		55		60								
Ala	Arg	Val	Val	Ala	Gln	Gly								
		65		70		75								
Ala	Tyr	Tyr	Tyr	Gly	Asp	Gln								
		85		90		95								

(2) INFORMATION FOR SEQ ID NO:2033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478

(D) OTHER INFORMATION: / Ceres Seq. ID 1502003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2033:

atgcgcctcg	cgccgccttc	gacagtcctc	cgctttccat	ttgcttcggc	tcattctcaga	60
tcaagctagc	gcacctgaca	cccaccacct	ccttccacaga	tcacacacc	cagccatggc	120
caccgccttt	gaetccccga	ectctctccc	cgccgcgcgc	ccttccacg	acgacctttt	180
cctccatttc	gaaggctcgg	cccccgccgc	cgccgcaggg	ttcccgccct	ccccggagcc	240
ctacgcgccc	tcccccttcg	gcattgcccc	ctccaaaggc	gacctccacg	acgacctttt	300
cgccgacctt	gctgactcca	acgggtgggc	catcctttcg	cgccccaccg	agatggggcg	360
cgaggaggga	ttctgtctcc	gcgagtggtg	ccgacaaaat	gctattcacc	ttgagggaaa	420
agagaagaag	gagaaggagc	tgaggagcca	aatcatcgtt	gatgctgaag	agtttaag	

(2) INFORMATION FOR SEQ ID NO:2034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2034:

Cys Ala Ser Arg Pro Leu Arg Gln Ser Leu Ala Phe His Leu Leu Arg
1 5 10 15
Leu Ile Ser Asp Gln Ala Ser Ala Pro Asp Thr His His Leu Pro Pro
20 25 30
Arg Ser Thr Thr Pro Ala Met Ala Thr Ala Phe Asp Ser Pro Thr Ser
35 40 45
Ser Pro Ala Ala Pro Phe His Asp Asp Pro Phe Leu His Phe Asp
50 55 60
Gly Ser Ala Pro Ala Ala Asp Gly Phe Pro Ala Ser Pro Asp Ala
65 70 75 80
Tyr Ala Pro Ser Pro Phe Gly Met Pro His Ser Asn Gly Asp Leu His
85 90 95
Asp Asp Pro Phe Ala Ala Pro Ala Asp Ser Asn Gly Gly Pro Ile Leu
100 105 110
Pro Pro Pro Thr Glu Met Gly Arg Glu Glu Gly Phe Leu Leu Arg Glu
115 120 125
Trp Cys Arg Gln Asn Ala Ile His Leu Glu Glu Lys Glu Lys Lys Glu
130 135 140
Lys Glu Leu Arg Ser Gln Ile Ile Val Asp Ala Glu Glu Phe Lys
145 150 155

(2) INFORMATION FOR SEQ ID NO:2035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2035:

Ala Pro Arg Gly Arg Phe Asp Ser Pro Ser Arg Ser Ile Cys Phe Gly
1 5 10 15
Ser Ser Gln Ile Lys Leu Ala His Leu Thr Pro Thr Thr Ser Leu Pro
20 25 30
Asp Pro Pro Pro Gln Pro Trp Pro Pro Pro Leu Thr Pro Arg Pro Pro
35 40 45
Pro Pro Pro Pro Arg Pro Ser Thr Thr Thr Leu Ser Ser Ile Ser Thr
50 55 60
Ala Arg Pro Pro Pro Pro Thr Ala Ser Arg Pro Pro Arg Thr Pro
65 70 75 80
Thr Arg Pro Pro Pro Ser Ala Cys Pro Thr Pro Thr Ala Thr Ser Thr
85 90 95
Thr Thr Leu Ser Pro His Leu Leu Thr Pro Thr Val Gly Pro Ser Phe
100 105 110
Arg Arg Pro Pro Arg Trp Ala Ala Arg Arg Asp Ser Cys Ser Ala Ser
115 120 125
Gly Ala Asp Lys Met Leu Phe Thr Leu Arg Lys Lys Arg Arg Arg Arg

130 135 140
Arg Ser
145
(2) INFORMATION FOR SEQ ID NO:2036:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..121
(D) OTHER INFORMATION: / Ceres Seq. ID 1502006
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2036:
Met Ala Thr Ala Phe Asp Ser Pro Thr Ser Ser Pro Ala Ala Pro
1 5 10 15
Phe His Asp Asp Pro Phe Leu His Phe Asp Gly Ser Ala Pro Ala Ala
20 25 30
Ala Asp Gly Phe Pro Ala Ser Pro Asp Ala Tyr Ala Pro Ser Pro Phe
35 40 45
Gly Met Pro His Ser Asn Gly Asp Leu His Asp Asp Pro Phe Ala Ala
50 55 60
Pro Ala Asp Ser Asn Gly Gly Pro Ile Leu Pro Pro Pro Thr Glu Met
65 70 75 80
Gly Arg Glu Glu Gly Phe Leu Leu Arg Glu Trp Cys Arg Gln Asn Ala
85 90 95
Ile His Leu Glu Glu Lys Glu Lys Lys Glu Lys Glu Leu Arg Ser Gln
100 105 110
Ile Ile Val Asp Ala Glu Glu Phe Lys
115 120

(2) INFORMATION FOR SEQ ID NO:2037:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 713 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..713
(D) OTHER INFORMATION: / Ceres Seq. ID 1502011
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2037:
acccaaaggta ccttgcaatc acaacgaaca gaagctctcg atctcaccga caccgaggaa 60
gaagagatca atggcgctcg agcagggagtg cgtgatcgcg tgccacagca aggctgagtt 120
cgacgcccac atgaccaagg ccacgaagaag cggcaagctg ttggctcatcg acttcactgc 180
cgctcgagca gtactgcagg gacacccgtca tgaccatctg gcattaccac ggcgggtgccc 240
aggctggcgc cgtcgtggac gacgattacc ggggtgttcg cgtgcagcga ctgatggtga 300
tcgacagctc cacgttcaag tactccccgc gcaccaaccc gcaggccacc gtcgatgatgc 360
tcggaaggta tatgggtgtg aaaattcagg ccgagagatg gaggaaatga tcgagatttc 420
aagtatcacg atgggtctagg gactaagcct ctgctgtgta taatgaacat caatcaaacac 480
atctgtaact gggtaaactgc tctagcctct agagttagtt ttatttttct ctagatattt 540
tttaatctcc tctagacata ctctagcttt ccgcatgttg ttggttccat tccaccacac 600
ccctagatgc attgttcagc atttcgcggg aataatgaga attatgctga aaaggcatga 660
tcgctctctc tgctattct acagaaaatt aaataaagaa ccgccatttc atc

(2) INFORMATION FOR SEQ ID NO:2038:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..61
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502012
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2038:
Pro Lys Val Pro Cys Asn His Asn Glu Gln Lys Leu Ser Ile Ser Pro
1 5 10 15
Thr Pro Arg Lys Lys Arg Ser Met Ala Ser Glu Gln Gly Val Val Ile
 20 25 30
Ala Cys His Ser Lys Ala Glu Phe Asp Ala His Met Thr Lys Ala Gln
 35 40 45
Glu Ala Gly Lys Leu Val Val Ile Asp Phe Thr Ala Ala
50 55 60
(2) INFORMATION FOR SEQ ID NO:2039:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..66
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502013
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2039:
Met Thr Ile Trp His Tyr His Gly Gly Cys Gln Val Gly Ala Val Val
1 5 10 15
Asp Asp Asp Thr Arg Val Phe Gly Val Gln Arg Leu Met Val Ile Asp
 20 25 30
Ser Ser Thr Phe Lys Tyr Ser Pro Gly Thr Asn Pro Gln Ala Thr Val
 35 40 45
Met Met Leu Gly Arg Tyr Met Gly Val Lys Ile Gln Ala Glu Arg Trp
50 55 60
Arg Lys
65
(2) INFORMATION FOR SEQ ID NO:2040:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..46
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502014
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2040:
Met Leu Leu Val Pro Phe His His Thr Pro Arg Cys Ile Val Gln His
1 5 10 15
Phe Ala Gly Ile Met Arg Ile Met Leu Lys Arg His Asp Arg Ser Ser
 20 25 30
Cys Leu Phe Tyr Arg Lys Leu Asn Lys Glu Pro Pro Phe His
 35 40 45
(2) INFORMATION FOR SEQ ID NO:2041:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 567 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..567

(D) OTHER INFORMATION: / Ceres Seq. ID 1502015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2041:

ctcgc	caaac	cacgt	ttcaa	aaaaa	agaga	ggaag	caaaa	gttc	cttctt	ccct	cgaaaa	60
aaaaa	atcag	tctcg	cccatg	gagag	cagcg	ttgg	cataga	gaag	gccgca	gcgg	tggcgg	120
ttggt	gcagg	tgtgg	gcggg	ggagg	tggag	ggtac	ggcts	cgcg	gggtgg	gagac	gcgcga	180
agcgc	gagga	gtscg	cccatc	ccggc	gacgc	tgcct	gtgcc	cgcg	gcgcgc	agga	aagccc	240
tgccg	gacct	cgga	aagcgg	cgcag	cccyg	ccca	agaacg	gtact	ttcca	gcgc	ccggag	300
ctggag	gcgc	tcttc	gcgc	gcgc	gcgc	cgcc	agccct	tctg	cgcg	ctg	actgg	360
gacttg	atatt	tttgg	ggagg	gagtt	gtaga	tagct	ttgcc	gtct	cgctct	gtt	gtactct	420
ttctag	tggg	ggtgt	tttagt	ggcc	scgggt	gtatt	aggga	ggc	agtag	gg	gttttag	480
gagtag	tagg	tagtg	aggtg	gtg	gactctt	aatc	ataag	catact	gttt	gg	ttaagct	540
atg	aaatc	tct	tata	ttgt	tct	ggc						

(2) INFORMATION FOR SEQ ID NO:2042:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1502016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2042:

Ser	Gln	Thr	His	Val	Ser	Lys	Lys	Arg	Glu	Glu	Ser	Lys	Val	Pro	Ser	
1				5				10					15			
Ser	Leu	Glu	Lys	Lys	Asn	Gln	Ser	Arg	His	Gly	Glu	Gln	Arg	Trp	His	
				20				25					30			
Arg	Glu	Gly	Arg	Ser	Gly	Gly	Gly	Trp	Cys	Arg	Cys	Gly	Arg	Gly	Arg	
				35			40					45				
Trp	Arg	Val	Arg	Xaa	Arg	Arg	Val	Gly	Asp	Ala	Glu	Ala	Arg	Gly	Xaa	
				50			55				60					
Pro	His	Pro	Gly	Asp	Ala	Ala	Val	Pro	Arg	Gly	Ala	Glu	Glu	Gly	Arg	
				65			70			75				80		
Ala	Gly	Leu	Arg	Glu	Glu	Ala	Gln	Pro	Xaa	Pro	Arg	Thr	Ala	Thr	Ser	
				85			90					95				
Ser	Arg	Arg	Thr	Trp	Arg	Arg	Ser	Ser	Arg	Ser	Arg	Arg	Ala	Ala	Arg	
				100			105					110				
Pro	Ser	Ala	Arg	Asp	Leu	Xaa	Arg	Thr								
				115			120									

(2) INFORMATION FOR SEQ ID NO:2043:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1502017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2043:

Arg	Lys	Pro	Thr	Phe	Gln	Lys	Lys	Glu	Arg	Lys	Ala	Lys	Phe	Leu	Leu	
1				5				10					15			
Pro	Ser	Lys	Lys	Lys	Ile	Ser	Leu	Ala	Met	Glu	Ser	Ser	Val	Gly	Ile	
				20			25					30				
Glu	Lys	Ala	Ala	Ala	Val	Ala	Val	Gly	Ala	Gly	Val	Gly	Gly	Gly	Gly	
				35			40					45				

Gly	Gly	Tyr	Gly	Xaa	Gly	Gly	Trp	Glu	Thr	Pro	Lys	Arg	Glu	Glu	Xaa
50					55					60					
Arg	Ile	Pro	Ala	Thr	Leu	Pro	Cys	Pro	Ala	Ala	Pro	Arg	Lys	Ala	Val
65					70				75					80	
Pro	Asp	Phe	Gly	Lys	Arg	Arg	Ser	Xaa	Ala	Gln	Glu	Arg	Leu	Leu	Pro
			85						90					95	
Ala	Ala	Gly	Pro	Gly	Gly	Ala	Leu	Arg	Ala	Ala	Pro	Pro	Gly		
			100				105				110				
Leu	Leu	Arg	Val	Thr	Trp	Xaa	Gly	Leu	Asp	Phe	Leu	Gly	Arg	Glu	Leu
			115				120							125	

(2) INFORMATION FOR SEQ ID NO:2044:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..103

- (D) OTHER INFORMATION: / Ceres Seq. ID 1502018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2044:

Met	Glu	Ser	Ser	Val	Gly	Ile	Glu	Lys	Ala	Ala	Ala	Val	Ala	Val	Gly
1				5				10						15	
Ala	Gly	Val	Gly	Gly	Gly	Gly	Gly	Tyr	Gly	Xaa	Gly	Gly	Trp	Glu	
			20				25					30			
Thr	Pro	Lys	Arg	Glu	Glu	Xaa	Arg	Ile	Pro	Ala	Thr	Leu	Pro	Cys	Pro
		35					40				45				
Ala	Ala	Pro	Arg	Lys	Ala	Val	Pro	Asp	Phe	Gly	Lys	Arg	Arg	Ser	Xaa
		50				55					60				
Ala	Gln	Glu	Arg	Leu	Leu	Pro	Ala	Ala	Gly	Pro	Gly	Gly	Ala	Leu	Arg
65				70						75				80	
Ala	Arg	Ala	Ala	Pro	Pro	Gly	Leu	Leu	Arg	Val	Thr	Trp	Xaa	Gly	Leu
				85					90					95	
Asp	Phe	Leu	Gly	Arg	Glu	Leu									
					100										

(2) INFORMATION FOR SEQ ID NO:2045:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 542 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..542

- (D) OTHER INFORMATION: / Ceres Seq. ID 1502023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2045:

ggggtagcga	ttacaccttg	acacctaaagg	ccagagattg	gagagagaaa	gaagcagctg	60
agtggagcaa	gaaagaagag	gtcatggcgg	tgtagtctat	cagctgagtg	ggaaagagtg	120
gagcaatggt	ggggggctgt	gccagcggcg	acggcgccgc	cgaagggagc	ctcgcgaggt	180
ggcgaggggc	ggcggccaa	cggatcggcc	tctcatgcgc	ctccttcttc	tcttacgcgc	240
ccctctccctc	cccgctctct	tccaagatca	tctcccactc	cgcaactgaat	gcgcctgatg	300
gagagcagca	aaagatggag	gaaccaccaca	gcaccagagt	ggctgacaag	aattctatgt	360
caatatgttt	ggaactccctc	acacagagca	tcagcagcga	tgtttgacagt	ggtgaggcgg	420
cagcaatctc	cacagcgcag	tgctcccaact	cattcccaact	ycatgcac	gcctccaaca	480
tccggcatgg	caacgtcacg	tgccctatct	gcggtgcaca	atggctgatg	ctaccacgtg	540
ac						

(2) INFORMATION FOR SEQ ID NO:2046:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..139
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502024
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2046:
Met Val Gly Gly Cys Ala Ser Gly Asp Gly Ala Ala Glu Gly Thr Leu
1 5 10 15
Ala Arg Trp Arg Arg Ala Ala Ala Lys Arg Ile Gly Leu Ser Cys Ala
 20 25 30
Ser Phe Phe Ser Tyr Ala Ala Ser Pro Ser Pro Pro Ser Lys Ile
 35 40 45
Ile Ser His Ser Ala Leu Asn Ala Pro Asp Gly Glu Gln Gln Lys Met
 50 55 60
Glu Glu Pro Thr Ser Thr Arg Val Ala Asp Lys Asn Leu Cys Ala Ile
65 70 75 80
Cys Leu Glu Leu Leu Ser Thr Ser Ile Ser Ser Asp Val Asp Ser Gly
 85 90 95
Glu Ala Ala Ala Ile Tyr Thr Ala Gln Cys Ser His Ser Phe His Xaa
 100 105 110
Leu Cys Ile Ala Ser Asn Ile Arg His Gly Asn Val Ser Cys Pro Ile
 115 120 125
Cys Arg Ala Gln Trp Ser Glu Leu Pro Arg Asp
130 135

(2) INFORMATION FOR SEQ ID NO:2047:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..84
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502025
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2047:
Met Arg Leu Met Glu Ser Ser Lys Arg Trp Arg Asn Pro Pro Ala Pro
1 5 10 15
Glu Trp Leu Thr Arg Ile Tyr Val Gln Tyr Val Trp Asn Ser Ser Ala
 20 25 30
Arg Ala Ser Ala Ala Met Leu Thr Val Val Arg Arg Gln Gln Ser Thr
 35 40 45
Gln Arg Ser Ala Pro Thr His Ser Thr Xaa Tyr Ala Ser Pro Pro Thr
 50 55 60
Ser Gly Met Ala Thr Ser Ala Ala Leu Ser Ala Val His Asn Gly Leu
65 70 75 80
Ser Tyr His Val

(2) INFORMATION FOR SEQ ID NO:2048:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 81 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..81
(D) OTHER INFORMATION: / Ceres Seq. ID 1502026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2048:

Met	Glu	Ser	Ser	Lys	Arg	Trp	Arg	Asn	Pro	Pro	Ala	Pro	Glu	Trp	Leu
1				5				10					15		
Thr	Arg	Ile	Trp	Val	Gln	Tyr	Val	Trp	Asn	Ser	Ser	Ala	Arg	Ala	Ser
			20					25					30		
Ala	Ala	Met	Leu	Thr	Val	Val	Arg	Gln	Gln	Ser	Thr	Gln	Arg	Ser	
			35					40					45		
Ala	Pro	Thr	His	Ser	Thr	Xaa	Tyr	Ala	Ser	Pro	Pro	Thr	Ser	Gly	Met
			50				55					60			
Ala	Thr	Ser	Ala	Ala	Leu	Ser	Ala	Val	His	Asn	Gly	Leu	Ser	Tyr	His
					70					75				80	
65															
Val															

(2) INFORMATION FOR SEQ ID NO:2049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..502
(D) OTHER INFORMATION: / Ceres Seq. ID 1502027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049:

acagcacagc	agagaacgca	ggcagaggca	ccataccagt	caaccaccac	cgcttcggtc	60
tcctcccaac	ccgctcgccct	tcgctctcct	ctgggtccca	tctctatca	tccccgagct	120
ccagttctcc	acacctcacg	tctataaata	ataaataagg	cgccccgggt	gccccatcaat	180
tcgtgtccac	gcgtcccgag	agcgcaaatc	attccgcgcg	acgcataaac	cctagcccag	240
ccaccgatcc	ctctcatggc	aaccaccacc	accaggcgga	gcctctctct	ccagaagcag	300
ctaagagatc	tcgcgaagca	cccggtggat	gggttctctg	ctgggctggt	cgacgacagc	360
aatgtcttcg	agtggcagggt	caccatcatc	ggaccgcctg	acactctata	tgatggaggt	420
tacttcaatg	caataatgag	cttcccaaca	aattacccaa	acagcccgcc	atcagtcaga	480
tttacctctg	aaatgkggca	tc				

(2) INFORMATION FOR SEQ ID NO:2050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..49
(D) OTHER INFORMATION: / Ceres Seq. ID 1502028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2050:

Gln	His	Ser	Arg	Glu	Arg	Arg	Gln	Arg	His	His	Thr	Ser	Gln	Pro	Pro
1				5				10					15		
Pro	Leu	Arg	Ser	Pro	Pro	Thr	Pro	Leu	Ala	Phe	Ala	Ser	Phe	Trp	Phe
				20				25					30		
Pro	Ser	Ser	Ile	Ile	Pro	Glu	Leu	Gln	Phe	Ser	Thr	Pro	His	Val	Tyr
			35				40					45			
Lys															

(2) INFORMATION FOR SEQ ID NO:2051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..51
(D) OTHER INFORMATION: / Ceres Seq. ID 1502029
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2051:
Ser Thr Ala Glu Asn Ala Gly Arg Gly Thr Ile Pro Val Asn His His
1 5 10 15
Arg Phe Val Leu Leu Pro His Arg Ser Pro Ser Pro Ser Gly Ser
20 25 30
His Leu Leu Ser Ser Pro Ser Ser Ser Pro His Leu Thr Ser Ile
35 40 45
Asn Asn Lys
50

(2) INFORMATION FOR SEQ ID NO:2052:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..82
(D) OTHER INFORMATION: / Ceres Seq. ID 1502030
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2052:
Met Ala Thr Thr Thr Thr Gln Ala Ser Leu Leu Leu Gln Lys Gln Leu
1 5 10 15
Arg Asp Leu Ala Lys His Pro Val Asp Gly Phe Ser Ala Gly Leu Val
20 25 30
Asp Asp Ser Asn Val Phe Glu Trp Gln Val Thr Ile Ile Gly Pro Pro
35 40 45
Asp Thr Leu Tyr Asp Gly Gly Tyr Phe Asn Ala Ile Met Ser Phe Pro
50 55 60
Gln Asn Tyr Pro Asn Ser Pro Pro Ser Val Arg Phe Thr Ser Glu Met
65 70 75 80
Xaa His

(2) INFORMATION FOR SEQ ID NO:2053:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 526 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..526
(D) OTHER INFORMATION: / Ceres Seq. ID 1502031
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2053:
aattttctta tccccctca tctgtctcac ctccgacctc ggcgcgagacg agcaagccca 60
agtatggcgc gacgcagcgc agccgcctgt gcgtccgggg tctcggcccc gccggccgcg 120
ccgatgaggg cttctgcggg acgcgcgcgt cggctgtcgg tggtaggggc cgcgatatcc 180
ctcgagaagg gcgagaaggc gtacacgggtg cagaagtccg aggaagattt caacgcgcgc 240
aaggagctga tgcctggagg tgtttaactcg ccagtcctgtg ctttcaaatc tgttgggtgg 300
cagccagtag tgttcgaactc tgttaaaagggt tctcgtatgt gggatgttga tgggaatgag 360
tacattgatt acgttgggtc ctgggggtcct gcaatcaatcg gccatcgaga tgataagggtt 420
aatgctgcac tgattgaaac tctgaagaaa ggaactagct ttggtgtctcc atgtttgctg 480
gagaacgtat tggctgagat ggtcatctct gccgtgccaa gtatcg

(2) INFORMATION FOR SEQ ID NO:2054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2054:

Asn Phe Leu Ile Pro Pro His Leu Leu His Leu Arg Pro Arg Ala Arg
1 5 10 15
Arg Ala Ser Pro Ser Met Ala Gly Ala Ala Ala Ala Val Ala Ser
20 25 30
Gly Val Ser Ala Arg Pro Ala Ala Pro Met Arg Ala Ser Ala Gly Arg
35 40 45
Arg Ala Arg Leu Ser Val Val Arg Ala Ala Ile Ser Leu Glu Lys Gly
50 55 60
Glu Lys Ala Tyr Thr Val Gln Lys Ser Glu Glu Ile Phe Asn Ala Ala
65 70 75 80
Lys Glu Leu Met Pro Gly Gly Val Asn Ser Pro Val Arg Ala Phe Lys
85 90 95
Ser Val Gly Gly Gln Pro Val Val Phe Asp Ser Val Lys Gly Ser Arg
100 105 110
Met Trp Asp Val Asp Gly Asn Glu Tyr Ile Asp Tyr Val Gly Ser Trp
115 120 125
Gly Pro Ala Ile Ile Gly His Ala Asp Asp Lys Val Asn Ala Ala Leu
130 135 140
Ile Glu Thr Leu Lys Lys Gly Thr Ser Phe Gly Ala Pro Cys Leu Leu
145 150 155 160
Glu Asn Val Leu Ala Glu Met Val Ile Ser Ala Val Pro Ser Ile
165 170 175

(2) INFORMATION FOR SEQ ID NO:2055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2055:

Met Ala Gly Ala Ala Ala Ala Val Ala Ser Gly Val Ser Ala Arg
1 5 10 15
Pro Ala Ala Pro Met Arg Ala Ser Ala Gly Arg Arg Ala Arg Leu Ser
20 25 30
Val Val Arg Ala Ala Ile Ser Leu Glu Lys Gly Glu Lys Ala Tyr Thr
35 40 45
Val Gln Lys Ser Glu Glu Ile Phe Asn Ala Ala Lys Glu Leu Met Pro
50 55 60
Gly Gly Val Asn Ser Pro Val Arg Ala Phe Lys Ser Val Gly Gly Gln
65 70 75 80
Pro Val Val Phe Asp Ser Val Lys Gly Ser Arg Met Trp Asp Val Asp
85 90 95
Gly Asn Glu Tyr Ile Asp Tyr Val Gly Ser Trp Gly Pro Ala Ile Ile
100 105 110
Gly His Ala Asp Asp Lys Val Asn Ala Ala Leu Ile Glu Thr Leu Lys

115 120 125
Lys Gly Thr Ser Phe Gly Ala Pro Cys Leu Leu Glu Asn Val Leu Ala
130 135 140
Glu Met Val Ile Ser Ala Val Pro Ser Ile
145 150

(2) INFORMATION FOR SEQ ID NO:2056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2056:

Met Arg Ala Ser Ala Gly Arg Arg Ala Arg Leu Ser Val Val Arg Ala
1 5 10 15
Ala Ile Ser Leu Glu Lys Gly Glu Lys Ala Tyr Thr Val Gln Lys Ser
20 25 30
Glu Glu Ile Phe Asn Ala Ala Lys Glu Leu Met Pro Gly Gly Val Asn
35 40 45
Ser Pro Val Arg Ala Phe Lys Ser Val Gly Gly Gln Pro Val Val Phe
50 55 60
Asp Ser Val Lys Gly Ser Arg Met Trp Asp Val Asp Gly Asn Glu Tyr
65 70 75 80
Ile Asp Tyr Val Gly Ser Trp Gly Pro Ala Ile Ile Gly His Ala Asp
85 90 95
Asp Lys Val Asn Ala Ala Leu Ile Glu Thr Leu Lys Lys Gly Thr Ser
100 105 110
Phe Gly Ala Pro Cys Leu Leu Glu Asn Val Leu Ala Glu Met Val Ile
115 120 125
Ser Ala Val Pro Ser Ile
130

(2) INFORMATION FOR SEQ ID NO:2057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..474
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2057:

aaggcaggcg actgcactgc acgcgatgc tgacctgacg acgcgcgcga cagtcaccatc 60
cacactcagg catggcgatg ggcgcgcgtt ccactctact gatgatggtt tcgctggagg 120
ccctgcttct cgcgcgcgcc gccgcgcgcg ggaccatccg tctgcccagc gatgtcggag 180
gcgttgctgc agaccttgct acgcgcgatg cgaggcgag ggcaaggcca aagcatcagc 240
ttcgcgcaga ggagaggcgc tggggggaat gctgcgactt ggccgtatgc gtcaagacgt 300
accgcataac ttctcgtgct ttcgatcggg ttgagcgctg ctccgcagcc tgtaaggagt 360
ccaggtgaaa cgacgaggac gggaggagcg gcggaccgcg tgacgacgac gctg 420

(2) INFORMATION FOR SEQ ID NO:2058:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1502036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2058:

```
Met Ala Met Gly Ala Ala Ser Ile Leu Leu Met Met Val Ser Leu Glu
1      5      10      15
Ala Leu Leu Leu Ala Ala Ala Ala Gly Gly Thr Ile Arg Leu Pro
      20      25      30
Ser Asp Val Gly Gly Val Ala Ala Asp Leu Val Thr Ala Met Ala Arg
      35      40      45
Ala Arg Ala Arg Ala Lys His Gln Leu Arg Asp Glu Glu Arg Pro Trp
      50      55      60
Gly Glu Cys Cys Asp Leu Ala Val Cys Val Lys Thr Tyr Pro Leu Thr
      65      70      75      80
Cys Ser Cys Phe Asp Arg Val Glu Arg Cys Ser Asp Ala Cys Lys Glu
      85      90      95
Cys Val Glu Thr Glu Asp Ser Arg His Val Cys Val Asp Arg Tyr Arg
      100     105     110
Gly Asp Pro Gly Pro Arg Cys His Asp Glu Asp Gly Arg Ser Gly Gly
      115     120     125
Pro Ala Asp Asp Ala
130
```

(2) INFORMATION FOR SEQ ID NO:2059:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1502037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2059:

```
Met Gly Ala Ala Ser Ile Leu Leu Met Met Val Ser Leu Glu Ala Leu
1      5      10      15
Leu Leu Ala Ala Ala Ala Ala Gly Gly Thr Ile Arg Leu Pro Ser Asp
      20      25      30
Val Gly Gly Val Ala Ala Asp Leu Val Thr Ala Met Ala Arg Ala Arg
      35      40      45
Ala Arg Ala Lys His Gln Leu Arg Asp Glu Glu Arg Pro Trp Gly Glu
      50      55      60
Cys Cys Asp Leu Ala Val Cys Val Lys Thr Tyr Pro Leu Thr Cys Ser
      65      70      75      80
Cys Phe Asp Arg Val Glu Arg Cys Ser Asp Ala Cys Lys Glu Cys Val
      85      90      95
Glu Thr Glu Asp Ser Arg His Val Cys Val Asp Arg Tyr Arg Gly Asp
      100     105     110
Pro Gly Pro Arg Cys His Asp Glu Asp Gly Arg Ser Gly Gly Pro Ala
      115     120     125
Asp Asp Asp Ala
130
```

(2) INFORMATION FOR SEQ ID NO:2060:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1502038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2060:

```
Met Met Val Ser Leu Glu Ala Leu Leu Leu Ala Ala Ala Ala Ala Gly
1      5      10      15
Gly Thr Ile Arg Leu Pro Ser Asp Val Gly Gly Val Ala Ala Asp Leu
20      25      30
Val Thr Ala Met Ala Arg Ala Arg Ala Arg Ala Lys His Gln Leu Arg
35      40      45
Asp Glu Glu Arg Pro Trp Gly Glu Cys Cys Asp Leu Ala Val Cys Val
50      55      60
Lys Thr Tyr Pro Leu Thr Cys Ser Cys Phe Asp Arg Val Glu Arg Cys
65      70      75      80
Ser Asp Ala Cys Lys Glu Cys Val Glu Thr Glu Asp Ser Arg His Val
85      90      95
Cys Val Asp Arg Tyr Arg Gly Asp Pro Gly Pro Arg Cys His Asp Glu
100      105      110
Asp Gly Arg Ser Gly Gly Pro Ala Asp Asp Asp Ala
115      120
```

(2) INFORMATION FOR SEQ ID NO:2061:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 895 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..895

(D) OTHER INFORMATION: / Ceres Seq. ID 1502048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2061:

```
atcgaaaaaa aaaaactctc tcgccagatc ctctcctctc cggggatttg aattcgaacc 60
aaaaaatcaa aacaactcag cgattcgatt cgcgcgcgagt caagcgggat gccgccgcgc 120
acggctccgg cgcgacatc aaccocgcgc cggaaggtgc ccctccggaa gctgctgcgt 180
gcgcgctcgg tcgctgcgg ggtgcagttc ggctgggccc tgcagctgtc gttgctgacc 240
ccgtacgtgc aggagctggg catccgcac gcccttgcca gtctcgtctg gctgtgcggt 300
ccgctgtcgc gctcctcgt ccagcccctc gtcggccacc tctccgaccg catcggcccc 360
gccgtctcgc cgctcgggcg ccgcaggccc ttcatcgccg ccggcgccgc gtgcacgcgc 420
gcagccgtgc tcaccgtcgc ctctcctcgt gacctcggcc gactcttcgg cgacagcttc 480
accccgggct caacgcgcct cggcgccatc tgcgtctacc ttgtaggatt ctggtgctc 540
gacgtgggca acaacggcac gcaggggccc tgcaggcgct tctcgcgga cctcacagag 600
aatgacccaa ggagagaggg cgggacacac cgataagtct gctcatttac cattacaggc 660
atcatcaagt ctggaactc ttgtggggtt ggagaagagc acgctgggag ctcttgaatg 720
ctgtgtgctc ttgtgggtgt tgccccgttg agctattttt tgcctgtgtc ccaaatcttt 780
tgtttgtcaa ttcaactcga atgtatgtac gcacgtatgc atgtatgtat ttgtatgtat 840
gtggatcaat tgtagagagc ttaagcaatg aataaaagtt acaggagtta cgttc
```

(2) INFORMATION FOR SEQ ID NO:2062:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1502049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2062:

Arg Lys Lys Lys Leu Ser Pro Ser Pro Leu Leu Ser Gly Val Leu

1	5	10	15
Asn Ser Asn Gln Lys Ile Lys Thr Thr Gln Arg Phe Asp Ser Arg Arg			
	20	25	30
Val Lys Arg Asp Ala Ala Ala His Gly Ser Gly Gly Asp Leu Asn Pro			
	35	40	45
Ala Ala Glu Gly Ala Pro Pro Glu Ala Ala Ala Cys Gly Val Gly Arg			
	50	55	60
Leu Arg Gly Ala Val Arg Leu Gly Ala Ala Ala Val Val Ala Asp Pro			
	65	70	75
Val Arg Ala Gly Ala Gly His Pro Ala Arg Leu Cys Gln Ser Arg Leu			
	85	90	95
Ala Val Arg Ser Ala Val Arg Pro Pro Arg Pro Ala Pro Arg Arg Pro			
	100	105	110
Pro Leu Arg Pro His Arg Pro Arg Arg Phe Ala Ala Arg Ala Pro Gln			
	115	120	125
Ala Leu His Arg Arg Arg Arg Val His Arg Arg Ser Arg Ala His			
	130	135	140
Arg Arg Leu Leu Arg			
145			

(2) INFORMATION FOR SEQ ID NO:2063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2063:

Met Pro Pro Arg Thr Ala Pro Ala Ala Thr Ser Thr Pro Pro Arg Lys	
1	5
Val Pro Leu Arg Lys Leu Leu Arg Ala Ala Ser Val Ala Cys Gly Val	
	10
	15
Gln Phe Gly Trp Ala Leu Gln Leu Ser Leu Leu Thr Pro Tyr Val Gln	
	20
	25
Glu Leu Gly Ile Pro His Ala Phe Ala Ser Leu Val Trp Leu Cys Gly	
	30
	35
Pro Leu Ser Gly Leu Leu Val Gln Pro Leu Val Gly His Leu Ser Asp	
	40
	45
Arg Ile Gly Pro Ala Ala Ser Pro Leu Gly Arg Arg Arg Pro Phe Ile	
	50
	55
Ala Ala Gly Ala Ala Cys Ile Ala Ala Ala Val Leu Thr Val Gly Phe	
	60
	65
Ser Ala Asp Leu Gly Arg Leu Phe Gly Asp Asp Val Thr Pro Gly Ser	
	70
	75
Thr Arg Leu Gly Ala Ile Cys Val Tyr Leu Val Gly Phe Trp Leu Leu	
	80
	85
Asp Val Gly Asn Asn Gly Thr Gln Gly Pro Cys Arg Ala Phe Leu Ala	
	90
	95
Asp Leu Thr Glu Asn Asp Pro Arg Arg Arg Gly Gly Thr His Arg	
	100
	105
	110
	115
	120
	125
	130
	135
	140
	145
	150
	155
	160
	165
	170
	175

(2) INFORMATION FOR SEQ ID NO:2064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..490
(D) OTHER INFORMATION: / Ceres Seq. ID 1502056
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2064:
atcttcgtct ctctccgact ctccctcgcc cgcgcacctt tccgcgccgc ctcttcctct 60
tctctcgctg etctggcgcg cgcaaggatc aaaaggcgcc ggccactaga ggcgagttag 120
tcgcatgtaa acgaccacca gctgctgtga tctcaaaaagg gagcgagaga caaaggagag 180
gcgagcaggt cgtggcgcca gcaatcgttg cgaatcccg cggtattctg tctctgcac 240
cactgcttcc cgctttcccg cccggcgga ggtgtataat tctccaacgc ggttgactgt 300
attgctctc gctctcggtg ggtgggggca tggacgagc agaggagatg caggtggaga 360
ggctgcacga ggaggcgcat gcggggggag ccgacacgga caagctcagc tacgagatat 420
tctccatcct cgagagcaag ttctgttctg gctataccga ccgcgaccag ctctggctgc 480
ccaagccagc

(2) INFORMATION FOR SEQ ID NO:2065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..49
(D) OTHER INFORMATION: / Ceres Seq. ID 1502057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2065:

Ile Phe Val Ser Leu Arg Leu Ser Leu Ala Arg Ala Pro Phe Arg Ala
1 5 10 15
Ala Ser Phe Leu Ser Ser Arg Ala Leu Ala Arg Ala Arg Ile Lys Arg
20 25 30
Arg Arg Pro Leu Glu Ala Ser Glu Ser His Val Asn Asp His Gln Leu
35 40 45
Leu

(2) INFORMATION FOR SEQ ID NO:2066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..53
(D) OTHER INFORMATION: / Ceres Seq. ID 1502058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2066:

Met Asp Glu Ala Glu Glu Met Gln Val Glu Arg Leu His Glu Glu Ala
1 5 10 15
Asp Ala Gly Gly Ala Asp Thr Asp Lys Leu Ser Tyr Glu Ile Phe Ser
20 25 30
Ile Leu Glu Ser Lys Phe Leu Phe Gly Tyr Thr Asp Pro His Gln Leu
35 40 45
Trp Leu Pro Lys Pro
50

(2) INFORMATION FOR SEQ ID NO:2067:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..47
(D) OTHER INFORMATION: / Ceres Seq. ID 1502059
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2067:
Met Gln Val Glu Arg Leu His Glu Ala Asp Ala Gly Gly Ala Asp
1 5 10 15
Thr Asp Lys Leu Ser Tyr Glu Ile Phe Ser Ile Leu Glu Ser Lys Phe
20 25 30
Leu Phe Gly Tyr Thr Asp Pro His Gln Leu Trp Leu Pro Lys Pro
35 40 45

(2) INFORMATION FOR SEQ ID NO:2068:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 566 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..566
(D) OTHER INFORMATION: / Ceres Seq. ID 1502066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2068:

aaaaatcaaa gttagcgctgt gctgccccaa ctcgccaact ccccatcagc tcaccccgat 60
ctagggttttg ggcaccctcc gcttacgcgc ctccccacca agcaaatgtg agggcccgcg 120
gcatctccct tcggggctca tggcggttac agggcaggag ggggatgacg tcgaccacta 180
cgaggtactc tgctccctcg cgggggagga aggcgcggcg ctgaccatcg agcatatoga 240
gaaggccctac cggacgcagt cgcggtcgcg ccaccctgat aagcgccccg acgaccccaa 300
cgccaccgccc gaattccagc tctctctgag ttctacacaa ctctctcgcg acgagtcctc 360
tcgcgcgcag ttcgacgcgc gccttcgcgg ccgcgcgcgc gccgcagccc gcgccgcgcg 420
cacggcgctt aagcgcgcga aggcgcgtct cgacctcgag gagcgcgagc gcgccgyggy 480
cngggccac cccgscgat ccgagcgagt cgccmagcgc gaggcccara gatggccsc 540
gacattgagc gcgagctcgc agcgtt

(2) INFORMATION FOR SEQ ID NO:2069:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..142
(D) OTHER INFORMATION: / Ceres Seq. ID 1502067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2069:

Met Ala Ala Thr Gly Gln Glu Gly Asp Val Asp His Tyr Glu Val
1 5 10 15
Leu Cys Leu Pro Ser Gly Glu Glu Gly Ala Ala Leu Thr Ile Glu His
20 25 30
Ile Glu Lys Ala Tyr Arg Thr Gln Ser Arg Leu Arg His Pro Asp Lys
35 40 45
Arg Pro Asp Asp Pro Asn Ala Thr Ala Asp Phe Gln Leu Leu Ser Ser
50 55 60
Ser Tyr Lys Leu Leu Arg Asp Glu Ser Leu Arg Arg Gln Phe Asp Ala
65 70 75 80
Arg Leu Arg Gly Arg Arg Glu Ala Ala Ala Arg Ala Ala Ala Thr Gly
85 90 95
Val Lys Arg Arg Lys Ala Val Ser Asp Leu Glu Glu Arg Glu Arg Ala
100 105 110
Xaa Xaa Xaa Gly His Pro Xaa Asp Pro Glu Glu Leu Ala Xaa Arg Glu
115 120 125
Ala Xaa Arg Trp Xaa Pro Thr Leu Ser Ala Ser Ser Gln Arg

```
(xi) (A) NAME/KEY: -
      (B) LOCATION: 1..465
      (D) OTHER INFORMATION: / Ceres Seq. ID 1502074
      SEQUENCE DESCRIPTION: SEQ ID NO:2070:
```

(2) INFORMATION FOR SEQ ID NO:2071:

```
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
```

(xi) (A) NAME/KEY: peptide
(B) LOCATION: 1..154
(D) OTHER INFORMATION: / Ceres Seq. ID 1502075
SEQUENCE DESCRIPTION: SEQ ID NO:2071:

(2) INFORMATION FOR SEQ ID NO:2072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
```

(A) NAME/KEY: peptide
(B) LOCATION: 1..128
(D) OTHER INFORMATION: / Ceres Seq. ID 1502076
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2072:
Met Met Gly Gly Ser Gly Arg Ala Ala Leu Leu Ala Leu Val Ala
1 5 10 15
Val Ser Leu Ala Val Glu Ile Gln Ala Asp Ala Gly Tyr Gly Tyr Thr
20 25 30
Pro Thr Pro Thr Pro Ala Thr Pro Thr Pro Lys Pro Glu Lys Pro Pro
35 40 45
Thr Lys Gly Pro Lys Pro Glu Lys Pro Pro Lys Glu His Lys Pro Pro
50 55 60
Lys Glu His Gly Pro Lys Pro Glu Lys Pro Pro Lys Glu His Lys Pro
65 70 75 80
Thr Pro Pro Thr Tyr Thr Pro Ser Pro Lys Pro Thr Pro Pro Thr Tyr
85 90 95
Thr Pro Thr Pro Thr Pro Pro Lys Pro Thr Pro Pro Thr Tyr Thr Pro
100 105 110
Ala Pro Thr Pro His Lys Pro Thr Pro Thr Pro Thr Tyr Thr Pro
115 120 125

(2) INFORMATION FOR SEQ ID NO:2073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2073:

Met Gly Gly Ser Gly Arg Ala Ala Leu Leu Leu Ala Leu Val Ala Val
1 5 10 15
Ser Leu Ala Val Glu Ile Gln Ala Asp Ala Gly Tyr Gly Tyr Thr Pro
20 25 30
Thr Pro Thr Pro Ala Thr Pro Thr Pro Lys Pro Glu Lys Pro Pro Thr
35 40 45
Lys Gly Pro Lys Pro Glu Lys Pro Pro Lys Glu His Lys Pro Pro Lys
50 55 60
Glu His Gly Pro Lys Pro Glu Lys Pro Pro Lys Glu His Lys Pro Thr
65 70 75 80
Pro Pro Thr Tyr Thr Pro Ser Pro Lys Pro Thr Pro Pro Thr Tyr Thr
85 90 95
Pro Thr Pro Thr Pro Pro Lys Pro Thr Pro Pro Thr Tyr Thr Pro Ala
100 105 110
Pro Thr Pro His Lys Pro Thr Pro Thr Pro Thr Tyr Thr Pro
115 120 125

(2) INFORMATION FOR SEQ ID NO:2074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..591
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2074:
atccaggcat ccagcaaatc cagcgggtcc gtactcatct gcttcacctc cgggctccgg 60
ctacggcgccg actcttctct ggcaaccgga ccacagaaac ctctaggcga cgaatcgagc 120
aggttagagga gtaatcaggc atccatggct gagcatcttg cgtccatctt tggcacggag 180
aaggaccgcg tgaactgcgc ctctactctc aagatcgcg catgcscac ggcgaccggt 240
gctcccgccct gcacaacaag ccttccatct ccccgagcgt gctgctctgc aacatgtacc 300
ggtatccagga ggacttcgag gactttctacg aggacatctt cgtggagctg agcaagcagc 360
agcggcgcgga catgatcacc cggggcgctgg acgcgcaggg caaccccacg gaccgggagc 420
ggatccagga ggacttcgag gactttctacg aggacatctt cgtggagctg agcaagcagc 480
gcgagatcga gagcctccac gtctcgagca acctcgcgga ccacatgatc ggggaacgtg 540
acgtggagtt ccgcgaggag gagcaggcgg scgcgcccct gcargcgctg caryggccggc
tactactcgg gccgccccat catcgccgag ttctcgccgg tgactgactt c

(2) INFORMATION FOR SEQ ID NO:2075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2075:

Met Xaa His Gly Asp Arg Cys Ser Arg Leu His Asn Lys Pro Ser Ile
1 5 10 15
Ser Pro Thr Leu Leu Leu Cys Asn Met Tyr Gln Arg Pro Asp Met Ile
20 25 30
Thr Pro Gly Val Asp Ala Gln Gly Asn Pro Ile Asp Pro Glu Arg Ile
35 40 45
Gln Glu Asp Phe Glu Asp Phe Tyr Glu Asp Ile Phe Val Glu Leu Ser
50 55 60
Lys His Gly Glu Ile Glu Ser Leu His Val Cys Asp Asn Leu Ala Asp
65 70 75 80
His Met Ile Gly Asn Val Tyr Val Glu Phe Arg Glu Glu Gln Ala
85 90 95
Xaa Arg Ala Leu Xaa Ala Leu Xaa Gly Arg Leu Leu Leu Gly Pro Pro
100 105 110
His His Arg Arg Val Leu Ala Gly Asp
115 120

(2) INFORMATION FOR SEQ ID NO:2076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2076:

Met Tyr Gln Arg Pro Asp Met Ile Thr Pro Gly Val Asp Ala Gln Gly
1 5 10 15
Asn Pro Ile Asp Pro Glu Arg Ile Gln Glu Asp Phe Glu Asp Phe Tyr
20 25 30
Glu Asp Ile Phe Val Glu Leu Ser Lys His Gly Glu Ile Glu Ser Leu
35 40 45
His Val Cys Asp Asn Leu Ala Asp His Met Ile Gly Asn Val Tyr Val
50 55 60
Glu Phe Arg Glu Glu Glu Gln Ala Xaa Arg Ala Leu Xaa Ala Leu Xaa
65 70 75 80

Gly Arg Leu Leu Leu Gly Pro Pro His His Arg Arg Val Leu Ala Gly
85 90 95
Asp

(2) INFORMATION FOR SEQ ID NO:2077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1502089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2077:

Met	Ile	Thr	Pro	Gly	Val	Asp	Ala	Gln	Gly	Asn	Pro	Ile	Asp	Pro	Glu
1				5					10					15	
Arg	Ile	Gln	Glu	Asp	Phe	Glu	Asp	Phe	Tyr	Glu	Asp	Ile	Phe	Val	Glu
			20				25						30		
Leu	Ser	Lys	His	Gly	Glu	Ile	Glu	Ser	Leu	His	Val	Cys	Asp	Asn	Leu
			35				40					45			
Ala	Asp	His	Met	Ile	Gly	Asn	Val	Tyr	Val	Glu	Phe	Arg	Glu	Glu	Glu
			50			55					60				
Gln	Ala	Xaa	Arg	Ala	Leu	Xaa	Ala	Leu	Xaa	Gly	Arg	Leu	Leu	Leu	Gly
65			70							75					80
Pro	Pro	His	His	Arg	Arg	Val	Leu	Ala	Gly	Asp					
				85					90						

(2) INFORMATION FOR SEQ ID NO:2078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..314

(D) OTHER INFORMATION: / Ceres Seq. ID 1502090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2078:

aaccatttgg	acaccgatcc	atccatccat	ccagccccgt	acgtgtctcg	ctggccgctcc	60
gtatatatag	agagagggcat	cggagatttrg	ccgccacgtt	gccatcgcg	gcrgcgcccg	120
ccggccaag	ccaaccatgc	tggcgagggc	tctcccgccg	cgccgtgtct	ccagcgcgct	180
ttgcctcgcc	cgcgacatc	caagarcmcg	cgccgtcgcg	gccagccgg	nggacgacga	240
ggacgacgac	gacggtcgcg	gcgcgcgcg	cagagggccg	tntctaacgg	gtcargcgcg	300
gcggcgctcg	cagg					

(2) INFORMATION FOR SEQ ID NO:2079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1502091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2079:

Asn	His	Leu	Asp	Thr	Asp	Pro	Ser	Ile	His	Pro	Ala	Pro	Tyr	Val	Ser
1				5					10					15	
Arg	Trp	Pro	Ser	Val	Tyr	Ile	Glu	Arg	Gly	Ile	Gly	Asp	Xaa	Pro	Pro

20 25 30
Arg Cys His Arg Ala Xaa Arg Pro Pro Ala Lys Ala Asn His Ala Gly
35 40 45
Glu Gly Ser Ser Ala Ala Ala Val Leu Gln Arg Arg Leu His Arg Pro
50 55 60
Arg Thr Ser Lys Xaa Xaa Arg Arg Arg Gly Gln Ala Xaa Gly Arg Arg
65 70 75
Gly Arg Arg Arg Arg Ser Arg Arg Arg Arg Gln Arg Pro Xaa Ser Asn
85 90 95
Gly Ser Xaa Ala Ala Val Ala
100

(2) INFORMATION FOR SEQ ID NO:2080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2080:

Pro Phe Gly His Arg Ser Ile His Pro Ser Ser Pro Val Arg Val Ser
1 5 10 15
Leu Ala Val Arg Ile Tyr Arg Glu Arg His Arg Arg Xaa Ala Ala Thr
20 25 30
Leu Pro Ser Arg Xaa Ala Pro Ala Gly Gln Gly Gln Pro Cys Trp Arg
35 40 45
Gly Leu Leu Arg Arg Gly Arg Ala Pro Ala Ala Phe Ala Ser Pro Ala
50 55 60
His Ile Gln Xaa Xaa Pro Pro Ser Arg Pro Gly Arg Xaa Thr Thr Arg
65 70 75 80
Thr Thr Thr Thr Val Ala Ala Ala Ala Glu Ala Ala Xaa
85 90

(2) INFORMATION FOR SEQ ID NO:2081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..59
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2081:

Met Leu Ala Arg Ala Pro Pro Pro Arg Pro Cys Ser Ser Gly Val Cys
1 5 10 15
Ile Ala Arg Ala His Pro Arg Xaa Ala Ala Val Ala Ala Arg Pro Xaa
20 25 30
Asp Asp Glu Asp Asp Asp Gly Arg Gly Gly Gly Arg Gly Arg
35 40 45
Xaa Leu Thr Gly Xaa Arg Arg Arg Pro Ser Gln
50 55

(2) INFORMATION FOR SEQ ID NO:2082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1036

(D) OTHER INFORMATION: / Ceres Seq. ID 1502094

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2082:

accctatgtt	catgccacca	tggaagggct	tcgtattgga	gcaccgatta	tcgaggttta	60
tcattgagaaa	tcttttatct	tacctgatgt	ttcaaggggtg	cttgcttgcc	tttatgagaa	120
ggatgtcaag	tttgagactc	acacagcctc	atacaggagc	ctactcgcat	tcgagggcatc	180
atctcatgct	ccagttccat	tctatgaagg	ccctactttt	ctagaagaat	ccagagaaat	240
ctgcccgttat	atagcagaaa	agtatgaaaa	tcaaggatat	ccgttccctc	ttggaagag	300
tgccccttag	agggtctcaa	ttgaacaatg	gctccacaac	gaggagcatg	ctttcaacc	360
tccgagccgg	gccttgttct	ttcatttgcc	ctttccctcg	ggtagaagg	aagatgatga	420
tattgatgtt	catacaagga	agctagaaga	ggttctggaa	gtttatgagc	aaaggctcag	480
tgacagcgaa	ttccttgttg	gaaacaagtt	cactcttgcc	gacctgtgtc	acctgccaaa	540
ttcccactat	atcaaaagcat	ctaacaagtt	tctttacctt	tatgatctga	ggaaaaatgt	600
aaggaggtgg	tgggatgcta	tttctgaccg	gagttcttgg	aagaaagtgc	tgaggtatat	660
gaagagcgtg	gaggagaaga	acaaacaaga	agaactcaag	aagcagcagc	agcagcagga	720
agaggctctc	agaacctcca	ccgacccaac	tcgggtagac	tcgagaaagc	agagcagaac	780
agagcctcgg	acaatatgtg	ttctctctgc	tgataacgag	tcacatcagct	cgatagtctc	840
tcgaacaaa	aagcctcttc	ctgggtgatca	cttagtgtct	actcaacaaa	ttgatgggtg	900
tggtatgcc	gccacaaatt	gatggtgatg	gtcgtcttag	tggtgtttgt	ctgtctcttt	960
attgtttgg	tctttaacaa	gagttatatt	tttaccttct	gaccaaaag	tggtttaaca	1020
ggatagtc	atgac					

- (2) INFORMATION FOR SEQ ID NO:2083:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..306

(D) OTHER INFORMATION: / Ceres Seq. ID 1502095

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2083:

Pro	Tyr	Val	His	Ala	Thr	Met	Glu	Gly	Leu	Arg	Ile	Gly	Ala	Pro	Ile
1															
Met	Gln	Val	Tyr	His	Glu	Lys	Ser	Phe	Ile	Leu	Pro	Asp	Val	Ser	Arg
Val	Leu	Ala	Cys	Leu	Tyr	Glu	Lys	Asp	Val	Lys	Phe	Glu	Thr	His	Thr
Ala	Ser	Tyr	Arg	Ser	Leu	Leu	Gly	Leu	Gln	Ala	Ser	Ser	His	Ala	Pro
Val	Pro	Phe	Tyr	Glu	Gly	Pro	Thr	Phe	Leu	Glu	Gly	Ser	Arg	Glu	Ile
65															
Cys	Arg	Tyr	Ile	Ala	Glu	Lys	Tyr	Glu	Asn	Gln	Gly	Tyr	Pro	Phe	Leu
Leu	Gly	Lys	Asp	Ala	Leu	Glu	Arg	Ala	Ser	Ile	Glu	Gln	Trp	Leu	His
Asn	Glu	Glu	His	Ala	Phe	Asn	Pro	Pro	Ser	Arg	Ala	Leu	Phe	Phe	His
Leu	Ala	Phe	Pro	Leu	Gly	Glu	Gly	Glu	Asp	Asp	Asp	Ile	Asp	Val	His
Thr	Arg	Lys	Leu	Glu	Glu	Val	Leu	Glu	Val	Tyr	Glu	Gln	Arg	Leu	Ser
145															
Asp	Ser	Glu	Phe	Leu	Val	Gly	Asn	Lys	Phe	Thr	Leu	Ala	Asp	Leu	Val
His	Leu	Pro	Asn	Ser	His	Tyr	Ile	Lys	Ala	Ser	Asn	Lys	Phe	Leu	Tyr
Leu	Tyr	Asp	Ser	Arg	Lys	Asn	Val	Arg	Arg	Trp	Trp	Asp	Ala	Ile	Ser

195	200	205
Asp Arg Ser Ser Trp Lys Lys Val Leu Arg Tyr Met Lys Ser Val Glu		
210	215	220
Glu Lys Asn Lys Gln Glu Glu Leu Lys Lys Gln Gln Gln Gln Glu		
225	230	235
Glu Ala Pro Arg Thr Ser Thr Asp Pro Thr Arg Val Asp Ser Arg Lys		
	245	250
Gln Ser Arg Thr Glu Pro Arg Thr Ile Leu Val Pro Pro Ala Asp Asn		
	260	265
Glu Ser Ser Ala Ser Ile Val Pro Arg Thr Lys Lys Pro Leu Pro Gly		
	275	280
Asp His Leu Val Ser Thr Gln Gln Ile Asp Gly Val Gly Met Pro Ala		
290	295	300
Thr Asn		
305		

(2) INFORMATION FOR SEQ ID NO:2084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..300

(D) OTHER INFORMATION: / Ceres Seq. ID 1502096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2084:

Met Glu Gly Leu Arg Ile Gly Ala Pro Ile Met Gln Val Tyr His Glu	
1	5
Lys Ser Phe Ile Leu Pro Asp Val Ser Arg Val Leu Ala Cys Leu Tyr	10
	20
Glu Lys Asp Val Lys Phe Glu Thr His Thr Ala Ser Tyr Arg Ser Leu	25
	30
Leu Gly Leu Gln Ala Ser Ser His Ala Pro Val Pro Phe Tyr Glu Gly	35
	40
Pro Thr Phe Leu Glu Glu Ser Arg Glu Ile Cys Arg Tyr Ile Ala Glu	45
65	50
Lys Tyr Glu Asn Gln Gly Tyr Pro Phe Leu Leu Gly Lys Asp Ala Leu	55
	60
Glu Arg Ala Ser Ile Glu Gln Trp Leu His Asn Glu Glu His Ala Phe	65
	70
Asn Pro Pro Ser Arg Ala Leu Phe Phe His Leu Ala Phe Pro Leu Gly	75
	80
Glu Gly Glu Asp Asp Asp Ile Asp Val His Thr Arg Lys Leu Glu Glu	85
	90
Val Leu Glu Val Tyr Glu Gln Arg Leu Ser Asp Ser Glu Phe Leu Val	95
145	100
Gly Asn Lys Phe Thr Leu Ala Asp Leu Val His Leu Pro Asn Ser His	105
	110
Tyr Ile Lys Ala Ser Asn Lys Phe Leu Tyr Leu Tyr Asp Ser Arg Lys	115
	120
Asn Val Arg Arg Trp Trp Asp Ala Ile Ser Asp Arg Ser Ser Trp Lys	125
	130
Lys Val Leu Arg Tyr Met Lys Ser Val Glu Glu Lys Asn Lys Gln Glu	135
	140
Glu Leu Lys Lys Gln Gln Gln Gln Glu Glu Ala Pro Arg Thr Ser	145
225	150
Thr Asp Pro Thr Arg Val Asp Ser Arg Lys Gln Ser Arg Thr Glu Pro	155
	160
Arg Thr Ile Leu Val Pro Pro Ala Asp Asn Glu Ser Ser Ala Ser Ile	165
	170
	175
	180
	185
	190
	195
	200
	205
	210
	215
	220
	225
	230
	235
	240
	245
	250
	255
	260
	265
	270

Val Pro Arg Thr Lys Lys Pro Leu Pro Gly Asp His Leu Val Ser Thr
275 280 285
Gln Gln Ile Asp Gly Val Gly Met Pro Ala Thr Asn
290 295 300

(2) INFORMATION FOR SEQ ID NO:2085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2085:

Met Gln Val Tyr His Glu Lys Ser Phe Ile Leu Pro Asp Val Ser Arg
1 5 10 15
Val Leu Ala Cys Leu Tyr Glu Lys Asp Val Lys Phe Glu Thr His Thr
20 25 30
Ala Ser Tyr Arg Ser Leu Leu Gly Leu Gln Ala Ser Ser His Ala Pro
35 40 45
Val Pro Phe Tyr Glu Gly Pro Thr Phe Leu Glu Glu Ser Arg Glu Ile
50 55 60
Cys Arg Tyr Ile Ala Glu Lys Tyr Glu Asn Gln Gly Tyr Pro Phe Leu
65 70 75 80
Leu Gly Lys Asp Ala Leu Glu Arg Ala Ser Ile Glu Gln Trp Leu His
85 90 95
Asn Glu Glu His Ala Phe Asn Pro Pro Ser Arg Ala Leu Phe Phe His
100 105 110
Leu Ala Phe Pro Leu Gly Glu Gly Glu Asp Asp Asp Ile Asp Val His
115 120 125
Thr Arg Lys Leu Glu Glu Val Leu Glu Val Tyr Glu Gln Arg Leu Ser
130 135 140
Asp Ser Glu Phe Leu Val Gly Asn Lys Phe Thr Leu Ala Asp Leu Val
145 150 155 160
His Leu Pro Asn Ser His Tyr Ile Lys Ala Ser Asn Lys Phe Leu Tyr
165 170 175
Leu Tyr Asp Ser Arg Lys Asn Val Arg Arg Trp Trp Asp Ala Ile Ser
180 185 190
Asp Arg Ser Ser Trp Lys Lys Val Leu Arg Tyr Met Lys Ser Val Glu
195 200 205
Glu Lys Asn Lys Gln Glu Glu Leu Lys Lys Gln Gln Gln Glu
210 215 220
Glu Ala Pro Arg Thr Ser Thr Asp Pro Thr Arg Val Asp Ser Arg Lys
225 230 235 240
Gln Ser Arg Thr Glu Pro Arg Thr Ile Leu Val Pro Pro Ala Asp Asn
245 250 255
Glu Ser Ser Ala Ser Ile Val Pro Arg Thr Lys Lys Pro Leu Pro Gly
260 265 270
Asp His Leu Val Ser Thr Gln Gln Ile Asp Gly Val Gly Met Pro Ala
275 280 285
Thr Asn
290

(2) INFORMATION FOR SEQ ID NO:2086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..833

(D) OTHER INFORMATION: / Ceres Seq. ID 1502100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2086:

atcctagaag	gaaacaggaa	caggcagctc	tgaagaagctg	aaactcacgg	ccatggccat	60
cctggggcgc	ctcaggctcg	cgccgtctcc	acccgccctc	gcggcgctg	cgccaccggc	120
tacgtcgccg	tctgcggctg	tacgtctctc	cggtgcactc	cacctcgcca	atgccggcgc	180
cgccgcgctc	ngtcgcgcgc	tcgtctctcg	cgcccgaccc	cgccgtggct	ttcattggag	240
gaggaccgta	cggaagcag	gtgacggcgg	ggcaggacct	caccggcaag	gacttcagcg	300
gccagacact	catcaagcag	gacttcaaga	cgtctatact	gaggcaggcg	aacttcaaa	360
gcgcgaacct	gctcggcgcg	agcttctctg	atgcagacct	cacaagcgct	gatctctctg	420
acgtgatctt	tagaggcgct	gatttgcgc	tggcgaattt	aacgaaggca	aacttatcaa	480
atgcccaact	agaaggggca	cttgccactg	ggaacacttc	tttcaaagg	gcgcacataa	540
ctggggcaga	ttttacogat	gtgccgctgc	gagatgatca	acgggagtac	ctctgcaaaa	600
tcgctgacgg	agtaaatcca	accactggaa	acccaacaaa	ggagactctg	ttctgcagct	660
gatcgacgga	aggacctggg	acttgtgact	tattcaacgt	cttgataaac	ttgcatctgc	720
tgctgtaagc	acgtgaggaa	tgtaaatgta	gttatagagg	gttcctagaa	ataataactg	780
gtaattacgt	gtaaatcaac	caacaataaa	agtgtgtgct	gccctttgaa	tgt	

(2) INFORMATION FOR SEQ ID NO:2087:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1502101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2087:

Met	Ala	Ile	Leu	Gly	Ala	Leu	Arg	Leu	Ala	Pro	Ser	Pro	Pro	Ala	Leu
1			5					10						15	
Ala	Gly	Ala	Ala	Pro	Pro	Ala	Thr	Ser	Ser	Ala	Ala	Val	Arg	Ser	
			20					25				30			
Ser	Val	His	Phe	His	Leu	Ala	Asn	Ala	Gly	Ala	Ala	Leu	Xaa	Arg	
			35				40					45			
Arg	Leu	Ala	Pro	Arg	Arg	Arg	Pro	Arg	Arg	Gly	Phe	His	Trp	Arg	Arg
			50				55				60				
Thr	Val	Arg	Glu	Ala	Gly	Asp	Ala	Gly	Ala	Gly	Pro	His	Arg	Gln	Gly
			65			70			75					80	
Leu	Gln	Arg	Pro	Asp	Thr	His	Gln	Ala	Gly	Leu	Gln	Asp	Val	Tyr	Thr
				85				90				95			
Glu	Ala	Gly	Gly	Leu	Gln	Arg	Arg	Glu	Pro	Ala	Arg	Arg	Glu	Leu	Leu
				100				105					110		
Arg	Cys	Arg	Pro	His	Lys	Arg									

(2) INFORMATION FOR SEQ ID NO:2088:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1502102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2088:

Met	Pro	Ala	Pro	Pro	Arg	Xaa	Val	Ala	Ala	Ser	Leu	Leu	Ala	Ala	Asp
1				5						10				15	

Pro Ala Val Ala Phe Ile Gly Gly Gly Pro Tyr Gly Lys Gln Val Thr
20 25 30
Arg Gly Gln Asp Leu Thr Gly Lys Asp Phe Ser Gly Gln Thr Leu Ile
35 40 45
Lys Gln Asp Phe Lys Thr Ser Ile Leu Arg Gln Ala Asn Phe Lys Gly
50 55 60
Ala Asn Leu Leu Gly Ala Ser Phe Phe Asp Ala Asp Leu Thr Ser Ala
65 70 75 80
Asp Leu Ser Asp Ala Asp Leu Arg Gly Ala Asp Leu Ser Leu Ala Asn
85 90 95
Leu Thr Lys Ala Asn Leu Ser Asn Ala Asn Leu Glu Gly Ala Leu Ala
100 105 110
Thr Gly Asn Thr Ser Phe Lys Gly Ala Asp Ile Thr Gly Ala Asp Phe
115 120 125
Thr Asp Val Pro Leu Arg Asp Asp Gln Arg Glu Tyr Leu Cys Lys Ile
130 135 140
Ala Asp Gly Val Asn Ser Thr Thr Gly Asn Pro Thr Lys Glu Thr Leu
145 150 155 160
Phe Cys Ser

(2) INFORMATION FOR SEQ ID NO:2089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..468
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2089:

atctctatct	catcgtcac	attagaaag	cggaagcctt	ctccgttcct	cctcgacgcg	60
tctcttccac	agccgcaacc	tctatccctc	gtctgggtatc	gtctctccca	cacccctctg	120
ccccaaacca	gaaaaaccct	cgaaaaagcgg	cgggcgccgcg	acatggcgga	ggcgaggct	180
ccagctgctg	cggttgccgc	ggcgaccctc	gaggtggcga	cggtgaccga	ggcgaggacc	240
gtcacggagg	cgaagggtcc	gcataagctg	caccgccagt	ggacctcttg	gtacgacatc	300
cagtcacaag	ccaagcccgg	cgctgcgtgg	ggcacctccc	tcaaaaaagg	gtacaccttc	360
gacacgcteg	aggagttttg	gggcttgtat	gatcatgttt	tccgtccaag	caagttgcct	420
ggaactgctg	attttcacct	attcaagcgt	ggagtagagc	caaaatgg		

(2) INFORMATION FOR SEQ ID NO:2090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2090:

Ile	Ser	Ile	Ser	Ser	Ser	Ser	Leu	Glu	Arg	Pro	Lys	Pro	Ser	Pro	Phe
1															
			5					10					15		
Leu	Leu	Asp	Ala	Ser	Leu	Pro	Gln	Pro	Gln	Pro	Leu	Ser	Leu	Val	Trp
			20					25					30		
Tyr	Arg	Leu	Ser	His	Thr	Pro	Leu	Pro	Gln	Pro	Arg	Lys	Thr	Leu	Glu
			35				40					45			
Lys	Arg	Arg	Arg	Asp	Met	Ala	Glu	Val	Glu	Ala	Pro	Ala	Ala	Ala	
			50		55				60						
Val	Ala	Ala	Ala	Thr	Pro	Glu	Val	Ala	Thr	Val	Thr	Glu	Gly	Gly	Ala

65 70 75 80
Ala Thr Glu Ala Lys Gly Pro His Lys Leu His Arg Gln Trp Thr Phe
85 90 95
Trp Tyr Asp Ile Gln Ser Lys Pro Lys Pro Gly Ala Ala Trp Gly Thr
100 105 110
Ser Leu Lys Lys Ala Tyr Thr Phe Asp Thr Val Glu Glu Phe Trp Gly
115 120 125
Leu Tyr Asp His Val Phe Arg Pro Ser Lys Leu Pro Gly Thr Ala Asp
130 135 140
Phe His Leu Phe Lys Ala Gly Val Glu Pro Lys Trp
145 150 155

(2) INFORMATION FOR SEQ ID NO:2091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1502132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2091:

Met Ala Glu Val Glu Ala Pro Ala Ala Ala Val Ala Ala Thr Pro
1 5 10 15
Glu Val Ala Thr Val Thr Glu Gly Gly Ala Ala Thr Glu Ala Lys Gly
20 25 30
Pro His Lys Leu His Arg Gln Trp Thr Phe Trp Tyr Asp Ile Gln Ser
35 40 45
Lys Pro Lys Pro Gly Ala Ala Trp Gly Thr Ser Leu Lys Lys Ala Tyr
50 55 60
Thr Phe Asp Thr Val Glu Phe Thr Gly Leu Tyr Asp His Val Phe
65 70 75 80
Arg Pro Ser Lys Leu Pro Gly Thr Ala Asp Phe His Leu Phe Lys Ala
85 90 95
Gly Val Glu Pro Lys Trp
100

(2) INFORMATION FOR SEQ ID NO:2092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..513

(D) OTHER INFORMATION: / Ceres Seq. ID 1502133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2092:

aaacaaaaat catttcattcc ccggaaccgg acgccaacg gcagtgctgc aaaagtccgg 60
acaagaactcg cgccgccac cgcaaccgat cgcctcgcc caggcgtgct gccgtccgct 120
cccttctccc gcgcgctcgc ctccgcctac gcccgggccg acccgctgga cccagcgtgc 180
gccgctccac tcggacgcgc cgccgccctc tcgggttgag cgggaggtgc ttggggaccc 240
gcccccatgg cgagcgccgg caacagcggc agcggggacg acgatgcagg agggaaagtc 300
ctggcggtac gctaccagaa gggcgaggtc ctoggcgagg gcacgatagg agtcgtcttc 360
aaggccatcg acaccaagac tggaaataca gtcgcggtaa agccaatccc gataggaaag 420
gacaagaagg aaggtgtcaa ctctactcgc ttgagggaaa ttaactact taaggagctg 480
aaagatccta atattataga gctgattgat tgt

(2) INFORMATION FOR SEQ ID NO:2093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..132
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502134
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2093:
Asn Gln Asn His Phe Ile Pro Gly Thr Gly Arg Arg Thr Ala Val Leu
1 5 10 15
Gln Lys Ser Gly Gln Ser Ser Arg Arg Pro Pro His Pro Ile Arg Leu
 20 25 30
Ala Gln Ala Cys Cys Arg Pro Leu Pro Ser Pro Ala Pro Ser Pro Pro
 35 40 45
Pro Thr Pro Gly Pro Thr Arg Trp Thr Gln Arg Ala Pro Leu His Ser
 50 55 60
Asp Ala Pro Pro Pro Ser Arg Val Glu Ala Glu Val Leu Gly Asp Pro
65 70 75 80
Pro Pro Trp Arg Ala Pro Ala Thr Ala Ala Gly Thr Thr Met Gln
 85 90 95
Glu Gly Ser Ser Trp Arg Ile Ala Thr Arg Arg Ala Arg Ser Ser Ala
 100 105 110
Arg Ala Arg Met Glu Ser Ser Ser Arg Pro Ser Thr Pro Arg Leu Glu
 115 120 125
Ile Gln Ser Arg
130

(2) INFORMATION FOR SEQ ID NO:2094:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..153
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502135
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2094:
Thr Lys Ile Ile Ser Ser Pro Glu Pro Asp Ala Glu Arg Gln Cys Cys
1 5 10 15
Lys Ser Pro Asp Lys Ala Arg Ala Ala His Arg Thr Arg Ser Ala Ser
 20 25 30
Pro Arg Arg Ala Ala Val Arg Ser Leu Leu Pro Arg Arg Arg Leu Arg
 35 40 45
Leu Arg Pro Gly Arg Pro Ala Gly Pro Ser Val Arg Arg Ser Thr Arg
 50 55 60
Thr Arg Arg Arg Pro Leu Gly Leu Arg Arg Arg Cys Leu Gly Thr Arg
65 70 75 80
Pro His Gly Glu Arg Arg Gln Gln Arg Gln Arg Gly Arg Arg Cys Arg
 85 90 95
Arg Glu Ala Pro Gly Gly Ser Leu Pro Glu Gly Arg Gly Pro Arg Arg
 100 105 110
Gly His Val Trp Ser Arg Leu Gln Gly His Arg His Gln Asp Trp Lys
 115 120 125
Tyr Ser Arg Gly Lys Ala Asn Pro Asp Arg Lys Gly Gln Glu Gly Arg
 130 135 140
Cys Gln Leu His Cys Val Glu Gly Asn
145 150

(2) INFORMATION FOR SEQ ID NO:2095:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..89
(D) OTHER INFORMATION: / Ceres Seq. ID 1502136
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2095:
Met Ala Ser Ala Gly Asn Ser Gly Ser Gly Asp Asp Ala Gly Gly
1 5 10 15
Lys Leu Leu Ala Asp Arg Tyr Gln Lys Gly Glu Val Leu Gly Glu Gly
20 25 30
Thr Tyr Gly Val Val Phe Lys Ala Ile Asp Thr Lys Thr Gly Asn Thr
35 40 45
Val Ala Val Lys Arg Ile Arg Ile Gly Lys Asp Lys Lys Glu Gly Val
50 55 60
Asn Phe Thr Ala Leu Arg Glu Ile Lys Leu Leu Lys Glu Leu Lys Asp
65 70 75 80
Pro Asn Ile Ile Glu Leu Ile Asp Cys
85

(2) INFORMATION FOR SEQ ID NO:2096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..522
(D) OTHER INFORMATION: / Ceres Seq. ID 1502153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2096:

aatccctccc gatcagatcc ctgcacaatg gcactccagg cagcctacga gtacctgcag 60
caggccgctcg gccatggcgc gtggctcgctc acgcagacgc tgacgctgct gtcctatgcc 120
gtaccacaccg tactactgct gctagcgctcc ctgcaccaaga gcacgtcgtc gtccggtagg 180
ggcaagccgc cgctccctccc ctgcgcgcgcg ggcaccctcc ccatcgtagg gcacctacac 240
cacatcgggc cccagaccaca catctcgctc caggagctgg tggccaagta cgggcacaa 300
gggttctctgt tctctccgcgc cggcgccgctg cccaccctga tctgtgtcgc gccacagccc 360
gccagagccg tgatgcgcac ccacgaccac atcttcgcgt cccgcccgtg gtccatggcc 420
tcccacatcc tccgtacaa cactgcgcac gtggccttct cgccgctcgg cgaatactgg 480
cagcagacca ggaagctgat gaacacgcac ctgctcagca ac

(2) INFORMATION FOR SEQ ID NO:2097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..174
(D) OTHER INFORMATION: / Ceres Seq. ID 1502154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2097:

Asn Pro Ser Arg Ser Asp Pro Ser Thr Met Ala Leu Gln Ala Ala Tyr
1 5 10 15
Glu Tyr Leu Gln Gln Ala Val Gly His Gly Ala Trp Ser Ser Thr Gln
20 25 30
Thr Leu Thr Leu Leu Leu Ile Ala Val Pro Thr Val Leu Leu Leu Leu
35 40 45

Ala Ser Leu Ala Lys Ser Thr Ser Ser Ser Gly Arg Gly Lys Pro Pro
50 55 60
Leu Pro Pro Ser Pro Gly Thr Leu Pro Ile Val Gly His Leu His
65 70 75 80
His Ile Gly Pro Gln Thr His Ile Ser Leu Gln Glu Leu Val Ala Lys
85 90 95
Tyr Gly His Asn Gly Phe Leu Phe Leu Arg Ala Gly Ala Val Pro Thr
100 105 110
Leu Ile Val Ser Ser Pro Ser Ala Ala Glu Ala Val Met Arg Thr His
115 120 125
Asp His Ile Phe Ala Ser Arg Pro Trp Ser Met Ala Ser His Ile Leu
130 135 140
Arg Tyr Asn Thr Cys Asp Val Ala Phe Ser Pro Leu Gly Glu Tyr Trp
145 150 155 160
Gln Gln Thr Arg Lys Leu Met Asn Thr His Leu Leu Ser Asn
165 170

(2) INFORMATION FOR SEQ ID NO:2098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2098:

Met Ala Leu Gln Ala Ala Tyr Glu Tyr Leu Gln Gln Ala Val Gly His
1 5 10 15
Gly Ala Trp Ser Ser Thr Gln Thr Leu Leu Leu Ile Ala Val
20 25 30
Pro Thr Val Leu Leu Leu Leu Ala Ser Leu Ala Lys Ser Thr Ser Ser
35 40 45
Ser Gly Arg Gly Lys Pro Pro Leu Pro Pro Ser Pro Pro Gly Thr Leu
50 55 60
Pro Ile Val Gly His Leu His His Ile Gly Pro Gln Thr His Ile Ser
65 70 75 80
Leu Gln Glu Leu Val Ala Lys Tyr Gly His Asn Gly Phe Leu Phe Leu
85 90 95
Arg Ala Gly Ala Val Pro Thr Leu Ile Val Ser Ser Pro Ser Ala Ala
100 105 110
Glu Ala Val Met Arg Thr His Asp His Ile Phe Ala Ser Arg Pro Trp
115 120 125
Ser Met Ala Ser His Ile Leu Arg Tyr Asn Thr Cys Asp Val Ala Phe
130 135 140
Ser Pro Leu Gly Glu Tyr Trp Gln Gln Thr Arg Lys Leu Met Asn Thr
145 150 155 160
His Leu Leu Ser Asn
165

(2) INFORMATION FOR SEQ ID NO:2099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..626
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2099:
 aaagccgaaa aggagaaagt accccggttcc gtcggcgcca gtcggcgacc tgcacccacc 60
 gcacgcgcag tcaagccccc cctggaccag ccaacgtgac actccaccgc cgccggcgcc 120
 gggcgagccc gtatgaacgc ccaccgcctg cccatctcct ctctatcccg cgccgcatgg 180
 ccgcgtactt caaccactcc tcgtcttacc cgccgcgcgc tccccgcgcg ggcacttccc 240
 cgtagcgccg gtaccgcac gcctaccgcg cgccgcgcgc acccccgccc gcttacggcg 300
 cctactacga cgcgcgagag caggccctcc cgccgcggga cgaggctccg accctcttca 360
 tcgctggcgt ccccgccgac gccaaagccg gcgaagtcta caacctcttc cgcgatttcc 420
 ccggatacgt ctctctccac ctccgcacgg gcaaatcttc tcaggcgatg gcggtttgctg 480
 tgtttgaga tcaacagtct gcactagctg ccttgagtgc cacaaatgga atggattttg 540
 atcttgagaa aaattgttct cttcatgtag atctcgcaaa atccaattcc agatcaaagc 600
 gcttgagatc agatgatact tcacct

(2) INFORMATION FOR SEQ ID NO:2100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1502166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2100:

Lys	Pro	Lys	Arg	Gly	Lys	Tyr	Pro	Val	Pro	Ser	Ala	Ala	Val	Pro	His
1			5					10					15		
Leu	His	Pro	Pro	His	Ala	Glu	Ser	Arg	Pro	Pro	Trp	Thr	Ser	Gln	Arg
			20					25					30		
Asp	Thr	Pro	Pro	Pro	Pro	Ala	Pro	Arg	Gln	Pro	Val	Ala	Thr	Ala	Thr
			35					40				45			
Ala	Cys	Pro	Ser	Pro	Leu	Tyr	Pro	Ala	Pro	His	Gly	Arg	Val	Leu	Gln
			50				55				60				
Pro	Leu	Leu	Val	Leu	Pro	Ala	Ala	Ala	Ser	Pro	Ala	Gly	His	Phe	Pro
65					70					75				80	
Val	Arg	Arg	Val	Pro	Pro	Arg	Leu	Pro	Ala	Gly	Ala	Gly	Thr	Pro	Gly
					85				90					95	
Arg	Leu	Arg	Arg	Leu	Leu	Arg	Pro	Arg	Arg	Ala	Gly	Pro	Pro	Gly	Ala
					100				105				110		
Gly	Arg	Gly	Pro	His	Pro	Leu	His	Arg	Trp	Pro	Pro	Arg	Arg	Arg	Gln
					115				120				125		
Ala	Ala	Arg	Ser	Leu	Gln	Pro	Leu	Pro	Arg	Phe	Pro	Arg	Ile	Arg	Leu
					130				135			140			
Leu	Pro	Pro	Pro	His	Gly	Gln	Ile	Leu	Ser	Gly	Val	Cys	Val	Cys	Cys
					145					155				160	
Val	Cys	Arg	Ser	Thr	Val	Cys	Thr	Ser	Cys	Leu	Glu	Cys	His	Lys	Trp
					165				170					175	

Asn Gly Ile

(2) INFORMATION FOR SEQ ID NO:2101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2101:

Met Ala Ala Tyr Phe Asn His Ser Ser Ser Tyr Pro Pro Pro Pro

1	5	10	15
Pro	Pro	Gly	Thr
20	25	30	35
Ala	Pro	Ala	Pro
40	45	50	55
Gln	Ala	Leu	Pro
60	65	70	75
Leu	Pro	Ala	Asp
80	85	90	95
Phe	Pro	Gly	Tyr
100	105	110	115
Leu	Ser	Ala	Thr
120	125	130	135
Leu	His	Val	Asp
140	145	150	155
Ser	Asp	Asp	Thr
160	165	170	175

(2) INFORMATION FOR SEQ ID NO:2102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..464
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2102:

acgggaaaagg	agtacggaggt	accggagaca	togtcaacgc	catggccgga	ggagggtgcaa	60
cggtgtgcgt	gaccggagcc	ggcggtgtca	tcgctctgtg	ggtagtgaag	ctcctgtctt	120
cccgcgggta	cacggtgcac	ggcaccgtcc	gccacctcag	tgacgagaag	acaggccacc	180
tgaagcgccct	ggagaatgct	gcccggaaacc	ttaggtatctt	caaggctgac	ctgctggact	240
acgacgcat	ggcagctgcg	gtcgtcgggt	gccaggggggt	tttccatgtg	gccactcctg	300
tgcccttcgga	ggacctgact	gacccagagc	tacaaatgct	gggtcctgct	gttaccggca	360
ccacgaatgt	gctcaaaagt	gctccagcgc	cgaacgtcca	gcgagtggtg	gtgggtgtgt	420
ccatgggttgc	cgctcgagatc	agccccaaag	attggcctga	aggt		

(2) INFORMATION FOR SEQ ID NO:2103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2103:

Gly	Lys	Gly	Val	Arg	Ser	Thr	Gly	Asp	Ile	Val	Asn	Ala	Met	Ala	Gly
1	5	10	15	20	25	30	35	40	45	50	55	60	65	70	75
Gly	Gly	Ala	Thr	Val	Cys	Val	Thr	Gly	Ala	Gly	Gly	Phe	Ile	Ala	Ser
Trp	Val	Val	Lys	Leu	Leu	Ser	Arg	Gly	Tyr	Thr	Val	His	Gly	Thr	
Val	Arg	His	Leu	Ser	Asp	Glu	Lys	Thr	Gly	His	Leu	Lys	Arg	Leu	Glu
Asn	Ala	Ala	Gly	Asn	Leu	Arg	Ile	Phe	Lys	Ala	Asp	Leu	Leu	Asp	Tyr
65	70	75	80	85	90	95	100	105	110	115	120	125	130	135	140

Asp Ala Met Ala Ala Ala Val Val Gly Cys Gln Gly Val Phe His Val
85 90 95
Ala Thr Pro Val Pro Ser Glu Asp Leu Thr Asp Pro Glu Leu Gln Met
100 105 110
Leu Gly Pro Ala Val Thr Gly Thr Asn Val Leu Lys Ala Ala Ser
115 120 125
Ser Ala Asn Val Gln Arg Val Val Val Ser Ser Met Val Ala Val
130 135 140
Glu Ile Ser Pro Lys Asp Trp Pro Glu Gly
145 150

(2) INFORMATION FOR SEQ ID NO:2104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1502170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2104:

Met Ala Gly Gly Ala Thr Val Cys Val Thr Gly Ala Gly Gly Phe
1 5 10 15
Ile Ala Ser Trp Val Val Lys Leu Leu Ser Arg Gly Tyr Thr Val
20 25 30
His Gly Thr Val Arg His Leu Ser Asp Glu Lys Thr Gly His Leu Lys
35 40 45
Arg Leu Glu Asn Ala Ala Gly Asn Leu Arg Ile Phe Lys Ala Asp Leu
50 55 60
Leu Asp Tyr Asp Ala Met Ala Ala Val Val Gly Cys Gln Gly Val
65 70 75 80
Phe His Val Ala Thr Pro Val Pro Ser Glu Asp Leu Thr Asp Pro Glu
85 90 95
Leu Gln Met Leu Gly Pro Ala Val Thr Gly Thr Thr Asn Val Leu Lys
100 105 110
Ala Ala Ser Ser Ala Asn Val Gln Arg Val Val Val Val Ser Ser Met
115 120 125
Val Ala Val Glu Ile Ser Pro Lys Asp Trp Pro Glu Gly
130 135 140

(2) INFORMATION FOR SEQ ID NO:2105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 843 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..843

(D) OTHER INFORMATION: / Ceres Seq. ID 1502189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2105:

tcttcaccca	cattataaag	atcctccact	tcgcactttc	gcgcgcgcct	ctctcctttcc	60
cgagcaggag	gcggacaagg	taagcagcaa	tcgcaggaac	cctagcgccg	cgcgaccocgc	120
aggaatgggt	atcgacctcg	tcgccgggtg	gaggrrkaag	aagaccaacg	gcactgcgcg	180
caagtctgac	gatgtctacc	tcaagctcct	cgtcaagctc	taccgtttcn	ttggtcagga	240
ggaccaaagc	caatttcaac	gcgtgcattc	tcaagaggct	tttcatgagt	aaaaccaaac	300
gaccaccaat	ctccatgcgc	cgctttatgca	agtttatgga	aggaaggagg	aagaacattg	360
ctgtcattgt	tggcacagtc	acagatgaca	aaaggatcca	ggagggtcca	gcaatgaagg	420
ttactgccct	gagggttcacg	gagacagcaa	gggccaggat	tgtcaatgct	ggtggcgagt	480
gcctcacatt	tgaccagctt	gccttcctgt	ctccacttgg	cgagaacacg	gtcctcttga	540

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ggggccccc  gaatgcccg  gaggcagtga  ggcactttgg  caaggctcct  ggagtgccgc  600
acagccacac  caagccggtat  gtgcgctcca  aggggaaggaa  gttcgagaag  gctcgtggca  660
ggaggaacag  ccgtggattc  aaggtttaaa  acaaatgttg  gccctccgtg  ttscatcag  720
catmstgcaa  ccgttgtgtt  tgatcagtcg  acagtaatta  gtcacatc  tgtaccgaga  780
ttmstgacac  aatttgttgt  cctggttga  attytsaga  atatttgatg  tcgtctccyt  840
att

```

(2) INFORMATION FOR SEQ ID NO:2106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2106:

```

Met Ser Thr Ser Ser Ser Ser Ser Ser Thr Val Xaa Leu Val Arg
1      5      10      15
Arg Thr Lys Ser Asn Phe Asn Ala Val Ile Leu Lys Arg Leu Phe Met
      20      25      30
Ser Lys Thr Asn Arg Pro Pro Ile Ser Met Arg Arg Leu Val Lys Phe
      35      40      45
Met Glu Gly Lys Glu Lys Asn Ile Ala Val Ile Val Gly Thr Val Thr
      50      55      60
Asp Asp Lys Arg Ile Gln Glu Val Pro Ala Met Lys Val Thr Ala Leu
      65      70      75      80
Arg Phe Thr Glu Thr Ala Arg Ala Arg Ile Val Asn Ala Gly Gly Glu
      85      90      95
Cys Leu Thr Phe Asp Gln Leu Ala Leu Arg Ala Pro Leu Gly Glu Asn
      100      105      110
Thr Val Leu Leu Arg Gly Pro Lys Asn Ala Arg Glu Ala Val Arg His
      115      120      125
Phe Gly Lys Ala Pro Gly Val Pro His Ser His Thr Lys Pro Tyr Val
      130      135      140
Arg Ser Lys Gly Arg Lys Phe Glu Lys Ala Arg Gly Arg Arg Asn Ser
      145      150      155      160
Arg Gly Phe Lys Val
      165

```

(2) INFORMATION FOR SEQ ID NO:2107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2107:

```

Met Ser Lys Thr Asn Arg Pro Pro Ile Ser Met Arg Arg Leu Val Lys
1      5      10      15
Phe Met Glu Gly Lys Glu Lys Asn Ile Ala Val Ile Val Gly Thr Val
      20      25      30
Thr Asp Asp Lys Arg Ile Gln Glu Val Pro Ala Met Lys Val Thr Ala
      35      40      45
Leu Arg Phe Thr Glu Thr Ala Arg Ala Arg Ile Val Asn Ala Gly Gly
      50      55      60
Glu Cys Leu Thr Phe Asp Gln Leu Ala Leu Arg Ala Pro Leu Gly Glu

```

65				70				75					80		
Asn	Thr	Val	Leu	Leu	Arg	Gly	Pro	Lys	Asn	Ala	Arg	Glu	Ala	Val	Arg
				85				90					95		
His	Phe	Gly	Lys	Ala	Pro	Gly	Val	Pro	His	Ser	His	Thr	Lys	Pro	Tyr
			100					105					110		
Val	Arg	Ser	Lys	Gly	Arg	Lys	Phe	Glu	Lys	Ala	Arg	Gly	Arg	Arg	Asn
			115				120						125		
Ser	Arg	Gly	Phe	Lys	Val										

(2) INFORMATION FOR SEQ ID NO:2108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2108:

Met	Arg	Arg	Leu	Val	Lys	Phe	Met	Glu	Gly	Lys	Glu	Lys	Asn	Ile	Ala
1			5					10					15		
Val	Ile	Val	Gly	Thr	Val	Thr	Asp	Asp	Lys	Arg	Ile	Gln	Glu	Val	Pro
			20					25					30		
Ala	Met	Lys	Val	Thr	Ala	Leu	Arg	Phe	Thr	Glu	Thr	Ala	Arg	Ala	Arg
			35				40					45			
Ile	Val	Asn	Ala	Gly	Gly	Glu	Cys	Leu	Thr	Phe	Asp	Gln	Leu	Ala	Leu
			50			55					60				
Arg	Ala	Pro	Leu	Gly	Glu	Asn	Thr	Val	Leu	Leu	Arg	Gly	Pro	Lys	Asn
			65			70				75				80	
Ala	Arg	Glu	Ala	Val	Arg	His	Phe	Gly	Lys	Ala	Pro	Gly	Val	Pro	His
			85						90				95		
Ser	His	Thr	Lys	Pro	Tyr	Val	Arg	Ser	Lys	Gly	Arg	Lys	Phe	Glu	Lys
			100					105					110		
Ala	Arg	Gly	Arg	Arg	Asn	Ser	Arg	Gly	Phe	Lys	Val				
			115			120									

(2) INFORMATION FOR SEQ ID NO:2109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..819
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2109:

aaatccccac	gaaaacccta	aaccctcgct	accggcgccg	ggctacaagc	tcttcgtcgg	60
ttcagcaccac	tgargccacc	ggctagagga	ggacgttggtg	ggaggggttg	caggttcgat	120
ggcgccggcc	tctgtcgcgg	cgcccgcttg	atcgtccccc	gcctcacccg	tctctccctt	180
ctcgcgctcg	cgccgcttct	cctctggccc	gcggaccggg	acatctccct	ggcccgccctc	240
cacctagcgc	acgtctccgt	cgtggcacgc	cctgcgctcg	cgtctaactat	atccgccacg	300
ctcaaggttc	gcgttcgcac	tcttgacctc	ttcgcgctcg	actacacccc	cctcgacgtc	360
gcctatcgct	accgcggtgc	ggggcttgcc	cggttaacat	ccggcgccgg	acgggtccgg	420
gcgcgcgctg	tctcgtacgt	cgacgccaac	ctgcagctcg	acgggcatac	cgtcgtcgag	480
gacgcgatgt	acctgctgca	ggacctcgcg	caaggatccg	tgcccttcga	caccatcgcc	540
gaggtcgagg	gccaccctcca	ctctcttttc	ctcagcatcc	cggtcaaggg	gagaatatct	600
tgcgtaatgc	atattaatcc	acacaaccaa	accatagtag	atcaggactg	ctatccctgag	660
tgaattgctt	atggcgctga	aatgtggaag	ggtgtgaagt	atgttgcctt	gcgaatggat	720

cggttgattt gtttctaacc ttgtcttcca gtcgtggttg taaaagtaag aaccaactaa 780
gggggtgttg aatgtaatta agctaatagt tagttcgct

(2) INFORMATION FOR SEQ ID NO:2110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1502194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2110:

Met	Xaa	Pro	Pro	Ala	Arg	Gly	Gly	Arg	Gly	Gly	Arg	Gly	Arg	Phe	
1				5				10						15	
Asp	Gly	Gly	Gly	Leu	Cys	Arg	Gly	Gly	Arg	Cys	Ile	Val	Pro	Cys	Leu
				20				25					30		
Thr	Val	Leu	Phe	Leu	Leu	Ala	Leu	Ala	Gly	Phe	Leu	Leu	Trp	Pro	Ala
				35				40					45		
Asp	Pro	Asp	Ile	Ser	Leu	Ala	Arg	Leu	His	Leu	Ala	His	Val	Ser	Val
						55					60				
Val	Ala	Arg	Pro	Ala	Val	Ala	Val	Thr	Ile	Ser	Ala	Thr	Leu	Lys	Val
						70					75			80	
Arg	Val	Arg	Asn	Pro	Asp	Leu	Phe	Ala	Leu	Asp	Tyr	Thr	Arg	Leu	Asp
						85					90			95	
Val	Ala	Ile	Gly	Tyr	Arg	Gly	Ala	Gly	Leu	Gly	Arg	Val	Thr	Ser	Gly
						100							110		
Gly	Gly	Arg	Val	Arg	Ala	Arg	Ala	Val	Ser	Tyr	Val	Asp	Ala	Asn	Leu
						115							125		
Gln	Leu	Asp	Gly	Ile	Arg	Val	Val	Glu	Asp	Ala	Met	Tyr	Leu	Leu	Glu
						130							140		
Asp	Leu	Ala	Gln	Gly	Ser	Val	Pro	Phe	Asp	Thr	Ile	Ala	Glu	Val	Glu
						145							155		160
Gly	His	Leu	His	Phe	Leu	Phe	Leu	Ser	Ile	Pro	Val	Lys	Gly	Arg	Ile
						165								175	
Ser	Cys	Val	Met	His	Ile	Asn	Pro	His	Asn	Gln	Thr	Ile	Val	His	Gln
						180								190	
Asp	Cys	Tyr	Pro	Glu											
															195

(2) INFORMATION FOR SEQ ID NO:2111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 508 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..508

(D) OTHER INFORMATION: / Ceres Seq. ID 1502205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2111:

ataaatcaac	cgccggtgaa	gtctagtgct	ctcgtctgctc	ggtcaccac	ctcagctccg	60
ccgcttgccc	gcttttgctc	tctccctccc	ggctctcgcc	ttcttctaca	cgctaccgct	120
tcacagccgt	aaacgcccct	cccgatcccc	gctagttcgc	caccgcgcgc	cgccgcgcgc	180
cccttcgctc	catcatggcc	gcctgtcgca	cgcaccactc	cgctcacgac	ttcatcgtaa	240
aggatgcgag	cggcacaagac	gttgacctca	gcacctacaa	ggggaaggtt	cttctcattg	300
ttaacgtcgc	atccacagtgt	ggcttaacca	actccaacta	cactgagctgt	gcccagctct	360
atgagaagta	caaggaccaa	ggctttgaaa	tctcggcttt	cccatgcaac	cgatttggtg	420
ggcaggagcc	tggtaaccaat	aaggagattg	tccagtttgc	ctgcacacgc	ttcaaggctg	480
agtaccatc	ttcgacaag	ttgatgtc				

(2) INFORMATION FOR SEQ ID NO:2112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2112:

Met Ala Ala Ser Ser Thr Ala Thr Ser Val His Asp Phe Ile Val Lys
1 5 10 15
Asp Ala Ser Gly Lys Asp Val Asp Leu Ser Thr Tyr Lys Gly Lys Val
20 25 30
Leu Leu Ile Val Asn Val Ala Ser Gln Cys Gly Leu Thr Asn Ser Asn
35 40 45
Tyr Thr Glu Leu Ala Gln Leu Tyr Glu Lys Tyr Lys Asp Gln Gly Phe
50 55 60
Glu Ile Leu Ala Phe Pro Cys Asn Gln Phe Gly Gly Gln Glu Pro Gly
65 70 75 80
Thr Asn Lys Glu Ile Val Gln Phe Ala Cys Thr Arg Phe Lys Ala Glu
85 90 95
Tyr Pro Ser Ser Thr Arg Leu Met
100

(2) INFORMATION FOR SEQ ID NO:2113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..523
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2113:

attggcacgt atgaatgctc agccacatgc gtatgtatac atcacggcca cgttcacggt 60
tcccccttct gcaagcaaac ctaaccaagc ctctgcggct cttcttgcaa tccaactcct 120
ccccgatccc caaaatcgaa cccaagtcca aaccctaacc tcggccttct cgatgtcggc 180
cgccacaacc gccccaaccc ctgcgggtggc caccgccgatg gcgcccgcct cgtcgtaccc 240
ggcctcctcc acgatctccg cctccgtggc cgcgctcggtc gaggaagagg acgacctcta 300
tgccgcgcctc aagtcgctcc agcgcacat ggagttcgtc gagatccagg aggagtacgt 360
taaagacgaa cagaagaacc tcaagcgoga actcctccgt gcgcaggagg aggtcaagcg 420
gtaccagttcc gtaccgntcg tcatcgcca gtttatggag atggtgcgacg gcaacaacgg 480
catcgtgggt tctactacgg gcagcaacta ctatgtcggt atc

(2) INFORMATION FOR SEQ ID NO:2114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2114:

Leu Ala Arg Met Asn Ala Gln Pro His Ala Tyr Val Tyr Ile Thr Ala
1 5 10 15

Thr Phe Thr Leu Pro Pro Ser Ala Ser Lys Pro Asn Gln Ala Ser Ala
20 25 30
Ala Leu Leu Arg Ile Gln Leu Leu Pro Asp Pro Gln Asn Arg Thr Gln
35 40 45
Val Glu Thr Leu Thr Ser Ala Phe Ser Met Ser Ala Ala Thr Thr Ala
50 55 60
Pro Thr Pro Ala Val Ala Thr Pro Met Ala Pro Pro Ser Tyr Pro
65 70 75 80
Ala Ser Ser Thr Ile Ser Ala Ser Val Ala Ala Ser Val Glu Glu Glu
85 90 95
Asp Asp Leu Tyr Gly Arg Leu Lys Ser Leu Gln Arg His Met Glu Phe
100 105 110
Val Glu Ile Gln Glu Glu Tyr Val Lys Asp Glu Gln Lys Asn Leu Lys
115 120 125
Arg Glu Leu Leu Arg Ala Gln Glu Glu Val Lys Arg Ile Gln Ser Val
130 135 140
Pro Xaa Val Ile Gly Gln Phe Met Glu Met Val Asp Gly Asn Asn Gly
145 150 155 160
Ile Val Gly Ser Thr Thr Gly Ser Asn Tyr Tyr Val Arg Ile
165 170

(2) INFORMATION FOR SEQ ID NO:2115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1502222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2115:

Met Asn Ala Gln Pro His Ala Tyr Val Tyr Ile Thr Ala Thr Phe Thr
1 5 10 15
Leu Pro Pro Ser Ala Ser Lys Pro Asn Gln Ala Ser Ala Ala Leu Leu
20 25 30
Arg Ile Gln Leu Leu Pro Asp Pro Gln Asn Arg Thr Gln Val Glu Thr
35 40 45
Leu Thr Ser Ala Phe Ser Met Ser Ala Ala Thr Thr Ala Pro Thr Pro
50 55 60
Ala Val Ala Thr Pro Met Ala Pro Pro Pro Ser Tyr Pro Ala Ser Ser
65 70 75 80
Thr Ile Ser Ala Ser Val Ala Ala Ser Val Glu Glu Asp Asp Leu
85 90 95
Tyr Gly Arg Leu Lys Ser Leu Gln Arg His Met Glu Phe Val Glu Ile
100 105 110
Gln Glu Glu Tyr Val Lys Asp Glu Gln Lys Asn Leu Lys Arg Glu Leu
115 120 125
Leu Arg Ala Gln Glu Glu Val Lys Arg Ile Gln Ser Val Pro Xaa Val
130 135 140
Ile Gly Gln Phe Met Glu Met Val Asp Gly Asn Asn Gly Ile Val Gly
145 150 155 160
Ser Thr Thr Gly Ser Asn Tyr Tyr Val Arg Ile
165 170

(2) INFORMATION FOR SEQ ID NO:2116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2116:

Met	Ser	Ala	Ala	Thr	Thr	Ala	Pro	Thr	Pro	Ala	Val	Ala	Thr	Pro	Met
1				5				10					15		
Ala	Pro	Pro	Pro	Ser	Tyr	Pro	Ala	Ser	Ser	Thr	Ile	Ser	Ala	Ser	Val
			20					25					30		
Ala	Ala	Ser	Val	Glu	Glu	Glu	Asp	Asp	Leu	Tyr	Gly	Arg	Leu	Ser	Ser
		35					40					45			
Leu	Gln	Arg	His	Met	Glu	Phe	Val	Glu	Ile	Gln	Glu	Glu	Tyr	Val	Lys
		50				55					60				
Asp	Glu	Gln	Lys	Asn	Leu	Lys	Arg	Glu	Leu	Leu	Arg	Ala	Gln	Glu	Glu
		65				70				75				80	
Val	Lys	Arg	Ile	Gln	Ser	Val	Pro	Xaa	Val	Ile	Gly	Gln	Phe	Met	Glu
			85						90					95	
Met	Val	Asp	Gly	Asn	Asn	Gly	Ile	Val	Gly	Ser	Thr	Thr	Gly	Ser	Asn
			100					105					110		
Tyr	Tyr	Val	Arg	Ile											
			115												

(2) INFORMATION FOR SEQ ID NO:2117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1058
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2117:

ctcacacgcc	ggccgccgcg	caagagccgt	ggcccccgtc	acgtccgcgc	gcacaggact	60
ctccgagtg	gggattgagc	cgtagttttt	tttttttggt	ggctcggggc	gatatccggt	120
actgtatgag	ggttgccaac	tactagacct	taagatcgct	gattcaatgg	aggcctccga	180
ggcagcacct	gcagcgccgg	ccaccgctcat	ggaagcagag	gatgtgacgc	gcgggaaggg	240
cgaattggtag	gtgcttgggg	agcgggcgct	gatggtgccg	tacacgcggg	agcacgtgcc	300
gcggtaaccac	gactggatgc	aggaccgcgc	gctgctggag	gccaccgcgt	cgagagccct	360
ctccctctcg	caggagttcg	aggtccaccg	ytcatggacc	ctcgaccctc	taagcacac	420
ctccatagtg	ttggataaag	agctcataga	gggagagtgc	gtgccgggca	accgcagat	480
tgaagctatg	gktggkgatg	tgaacatata	tatgaatgac	tctgatgatg	tgcatagcgc	540
ggagatagag	attatgatag	ctgaacataa	gascctgggg	aagggtattg	gtcaagaagc	600
aatcttactg	atgatggcat	ttgcagtaga	gaaatatgga	attcacacgt	tcaggggcaa	660
aattagcgaa	tcaaatatgg	catcgcttaa	gctcttcagg	aagttgggct	tcagggatgc	720
ttcatacagt	gtggtgttca	aggaggtgac	tctggaggca	cccgctgact	cactcccgtt	780
gagatttcc	ctgacattgt	gagactgggt	acgtttgaca	tgccccaa	taattccatg	840
cagacgacac	aagaagctaa	tgctgtttgt	ctgtactatc	tgacccaaat	ttactcgggc	900
tgatatttga	tgaaaaaaat	gaataaaaac	gttgacacgt	tgatgatcaa	ttgcattaga	960
ccagtcgggt	ttttcatgtc	actattttga	agaccgccata	tcttataaac	aaatgtagac	1020
aagttttatc	tcataatttt	tttatagtat	ctcccgtc			

(2) INFORMATION FOR SEQ ID NO:2118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1502225
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2118:
Met Glu Ala Ser Glu Ala Ala Pro Ala Ala Ala Thr Val Met Glu
1 5 10 15
Ala Glu Asp Val Ser Gly Gly Lys Gly Glu Trp Tyr Val Leu Gly Glu
20 25 30
Arg Ala Leu Met Val Pro Tyr Thr Arg Glu His Val Pro Arg Tyr His
35 40 45
Asp Trp Met Gln Asp Pro Ala Leu Leu Glu Ala Thr Ala Ser Glu Pro
50 55 60
Leu Ser Leu Ser Gln Glu Phe Glu Val His Xaa Ser Trp Thr Leu Asp
65 70 75 80
Pro Leu Lys His Thr Phe Ile Val Leu Asp Lys Glu Leu Ile Glu Gly
85 90 95
Glu Phe Val Pro Gly Asn Pro His Ile Glu Ala Met Xaa Xaa Asp Val
100 105 110
Asn Ile Tyr Met Asn Asp Ser Asp Asp Val Gln Ile Ala Glu Ile Glu
115 120 125
Ile Met Ile Ala Glu His Lys Xaa Arg Gly Lys Gly Ile Gly Gln Glu
130 135 140
Ala Ile Leu Leu Met Met Ala Phe Ala Val Glu Lys Tyr Gly Ile His
145 150 155 160
Thr Phe Arg Ala Lys Ile Ser Glu Ser Asn Met Ala Ser Leu Lys Leu
165 170 175
Phe Arg Lys Leu Gly Phe Lys Asp Ala Ser Tyr Ser Val Val Phe Lys
180 185 190
Glu Val Thr Leu Glu Ala Pro Ala Asp Ser Leu Pro Leu Arg Phe Pro
195 200 205
Leu Thr Ile Gly Asp Trp
210

(2) INFORMATION FOR SEQ ID NO:2119:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..200

(D) OTHER INFORMATION: / Ceres Seq. ID 1502226
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2119:
Met Glu Ala Glu Asp Val Ser Gly Gly Lys Gly Glu Trp Tyr Val Leu
1 5 10 15
Gly Glu Arg Ala Leu Met Val Pro Tyr Thr Arg Glu His Val Pro Arg
20 25 30
Tyr His Asp Trp Met Gln Asp Pro Ala Leu Leu Glu Ala Thr Ala Ser
35 40 45
Glu Pro Leu Ser Leu Ser Gln Glu Phe Glu Val His Xaa Ser Trp Thr
50 55 60
Leu Asp Pro Leu Lys His Thr Phe Ile Val Leu Asp Lys Glu Leu Ile
65 70 75 80
Glu Gly Glu Phe Val Pro Gly Asn Pro His Ile Glu Ala Met Xaa Xaa
85 90 95
Asp Val Asn Ile Tyr Met Asn Asp Ser Asp Asp Val Gln Ile Ala Glu
100 105 110
Ile Glu Ile Met Ile Ala Glu His Lys Xaa Arg Gly Lys Gly Ile Gly
115 120 125
Gln Glu Ala Ile Leu Leu Met Met Ala Phe Ala Val Glu Lys Tyr Gly
130 135 140
Ile His Thr Phe Arg Ala Lys Ile Ser Glu Ser Asn Met Ala Ser Leu

145 150 155 160
Lys Leu Phe Arg Lys Leu Gly Phe Lys Asp Ala Ser Tyr Ser Val Val
165 170 175
Phe Lys Glu Val Thr Leu Glu Ala Pro Ala Asp Ser Leu Pro Leu Arg
180 185 190
Phe Pro Leu Thr Ile Gly Asp Trp
195 200

(2) INFORMATION FOR SEQ ID NO:2120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2120:

Met Val Pro Tyr Thr Arg Glu His Val Pro Arg Tyr His Asp Trp Met
1 5 10 15
Gln Asp Pro Ala Leu Leu Glu Ala Thr Ala Ser Glu Pro Leu Ser Leu
20 25 30
Ser Gln Glu Phe Glu Val His Xaa Ser Trp Thr Leu Asp Pro Leu Lys
35 40 45
His Thr Phe Ile Val Leu Asp Lys Glu Leu Ile Glu Gly Glu Phe Val
50 55 60
Pro Gly Asn Pro His Ile Glu Ala Met Xaa Xaa Asp Val Asn Ile Tyr
65 70 75 80
Met Asn Asp Ser Asp Asp Val Gln Ile Ala Glu Ile Glu Ile Met Ile
85 90 95
Ala Glu His Lys Xaa Arg Gly Lys Gly Ile Gly Gln Glu Ala Ile Leu
100 105 110
Leu Met Met Ala Phe Ala Val Glu Lys Tyr Gly Ile His Thr Phe Arg
115 120 125
Ala Lys Ile Ser Glu Ser Asn Met Ala Ser Leu Lys Leu Phe Arg Lys
130 135 140
Leu Gly Phe Lys Asp Ala Ser Tyr Ser Val Val Phe Lys Glu Val Thr
145 150 155 160
Leu Glu Ala Pro Ala Asp Ser Leu Pro Leu Arg Phe Pro Leu Thr Ile
165 170 175
Gly Asp Trp

(2) INFORMATION FOR SEQ ID NO:2121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..640
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2121:

acatccatcc atccatccat ccatccatcc ctataaaatca aggcctacaca ccaacttact 60
ttctagggtct caaattataat ggccctcctcg tctcctcctct tgctgctggc gtcgatggcg 120
gtggcgggcac tctttgtctgt cggctcgtgt ggccggcgcgcc tcaccttcac gatcgccaag 180
gactccagct ccaccaaact atccctcgctc actaacgttg ccatctccga ggtgtcgggtc 240
aaggagaagg gcgcccctgga ctggctggat gatctcaagg agtcgccagc caaaccttc 300
acctctgata gcaaggagcc gattaagggc ccatctcgcg tcgcttcgcg tgtgaaaagg 360

ggtggctacc gcgtcgtcga tgacgtcatc cctgccgact tcaagcctgg ctctgtttac 420
cagacaggcg aacaaatctg agtaatggat tctgctgcgt gcagattata ttgatctcta 480
aaataaaatgt ttgacagaga ctaattaagc acmcaaacaa agcaaggcmc taattcattt 540
cctatgttta ctttgttgga ggcaactgca aaacaatgta ttgtatgcat gttctcctct 600
cacatatggt gbtggtgtgc tgtatatata attaatyycc

(2) INFORMATION FOR SEQ ID NO:2122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1502229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2122:

Ile His Pro Ser Ile His Pro Ser Ile Pro Lys Asn Gln Gly Tyr Thr
1 5 10 15
Pro Thr Tyr Phe Leu Gly Leu Lys Leu Asn Gly Leu Leu Val Leu Leu
20 25 30
Leu Ala Ala Gly Val Asp Gly Gly Gly Gly Thr Leu Cys Arg Arg Leu
35 40 45
Val Trp Arg Arg Ala His Leu His Asp Arg Gln Gly Leu Gln Leu His
50 55 60
Gln Thr Ile Pro Arg His
65 70

(2) INFORMATION FOR SEQ ID NO:2123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1502230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2123:

Met Ala Ser Ser Ser Ser Ser Leu Leu Ala Ser Met Ala Val Ala
1 5 10 15
Ala Leu Phe Val Val Gly Ser Cys Gly Gly Ala Leu Thr Thr Ile
20 25 30
Gly Lys Asp Ser Ser Ser Thr Lys Leu Ser Leu Val Thr Asn Val Ala
35 40 45
Ile Ser Glu Val Ser Val Lys Glu Lys Gly Ala Leu Asp Trp Ser Asp
50 55 60
Asp Leu Lys Glu Ser Pro Ala Lys Thr Phe Thr Leu Asp Ser Lys Glu
65 70 75 80
Pro Ile Lys Gly Pro Ile Ser Val Arg Phe Ala Val Lys Gly Gly Gly
85 90 95
Tyr Arg Val Val Asp Asp Val Ile Pro Ala Asp Phe Lys Pro Gly Ser
100 105 110
Val Tyr Gln Thr Gly Glu Gln Ile
115 120

(2) INFORMATION FOR SEQ ID NO:2124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1502231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2124:

Met Ala Val Ala Ala Leu Phe Val Val Gly Ser Cys Gly Gly Ala Leu
1 5 10 15
Thr Phe Thr Ile Gly Lys Asp Ser Ser Ser Thr Lys Leu Ser Ser Leu Val
20 25 30
Thr Asn Val Ala Ile Ser Glu Val Ser Val Lys Glu Lys Gly Ala Leu
35 40 45
Asp Trp Ser Asp Asp Leu Lys Glu Ser Pro Ala Lys Thr Phe Thr Leu
50 55 60
Asp Ser Lys Glu Pro Ile Lys Gly Pro Ile Ser Val Arg Phe Ala Val
65 70 75 80
Lys Gly Gly Gly Tyr Arg Val Val Asp Asp Val Ile Pro Ala Asp Phe
85 90 95
Lys Pro Gly Ser Val Tyr Gln Thr Gly Glu Gln Ile
100 105

(2) INFORMATION FOR SEQ ID NO:2125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..481

(D) OTHER INFORMATION: / Ceres Seq. ID 1502270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2125:

cggtgctcctc gcttcgcttt gscgcgatt cgatccagge tttggttgga ggcattggcct 60
cgtcgcccg gagcagctac gactgctcct tcaaggctct gcttatcggg gattcggccg 120
tcggcaagag cagcctcctc gtcagcttcg tctcggccg tcacatcgac gacgacatcg 180
cgccaacct aggggtggat tttaaaatca aatttctcag tgtgggtggg aagaaactaa 240
aactgacaat atgggacact gccggtcaag agagggttcag gacaattacc agctcttact 300
acaggggtgc tcatgggatt attttagttt atgacgttac aaagagggag agtttcacaa 360
atttgctga tgtgtggacc aaggaaatag agttacactc aacaaataag gaatgcacaa 420
aaatgcttgt tggaaataaa gtggacaag atgaggacag aatgggtgaca aaagaagaag 480
g

(2) INFORMATION FOR SEQ ID NO:2126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1502271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2126:

Gly Ala Ser Leu Arg Phe Xaa Arg Asp Ser Ile Gln Ala Leu Val Gly
1 5 10 15
Gly Met Ala Ser Ser Pro Ala Ser Ser Tyr Asp Cys Ser Phe Lys Val
20 25 30
Leu Leu Ile Gly Asp Ser Ala Val Gly Lys Ser Ser Leu Leu Val Ser
35 40 45
Phe Val Ser Ala Ala His Ile Asp Asp Asp Ile Ala Pro Thr Ile Gly
50 55 60

Val	Asp	Phe	Lys	Ile	Lys	Phe	Leu	Ser	Val	Gly	Gly	Lys	Lys	Leu	Lys	
65					70					75				80		
Leu	Thr	Ile	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Arg	Phe	Arg	Thr	Ile	Thr	
			85						90					95		
Ser	Ser	Tyr	Tyr	Arg	Gly	Ala	His	Gly	Ile	Ile	Leu	Val	Tyr	Asp	Val	
			100					105					110			
Thr	Lys	Arg	Glu	Ser	Phe	Thr	Asn	Leu	Ala	Asp	Val	Trp	Thr	Lys	Glu	
			115				120						125			
Ile	Glu	Leu	His	Ser	Thr	Asn	Lys	Glu	Cys	Ile	Lys	Met	Leu	Val	Gly	
			130				135					140				
Asn	Lys	Val	Asp	Lys	Asp	Glu	Asp	Arg	Met	Val	Thr	Lys	Glu	Glu		
145					150						155					

(2) INFORMATION FOR SEQ ID NO:2127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142

- (D) OTHER INFORMATION: / Ceres Seq. ID 1502272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2127:

Met	Ala	Ser	Ser	Pro	Ala	Ser	Ser	Tyr	Asp	Cys	Ser	Phe	Lys	Val	Leu	
1				5				10						15		
Leu	Ile	Gly	Asp	Ser	Ala	Val	Gly	Lys	Ser	Ser	Leu	Val	Ser	Phe		
			20					25					30			
Val	Ser	Ala	Ala	His	Ile	Asp	Asp	Ile	Ala	Pro	Thr	Ile	Gly	Val		
			35				40				45					
Asp	Phe	Lys	Ile	Lys	Phe	Leu	Ser	Val	Gly	Gly	Lys	Lys	Leu	Lys	Leu	
			50			55					60					
Thr	Ile	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Arg	Phe	Arg	Thr	Ile	Thr	Ser	
65					70					75				80		
Ser	Tyr	Tyr	Arg	Gly	Ala	His	Gly	Ile	Ile	Leu	Val	Tyr	Asp	Val	Thr	
			85						90					95		
Lys	Arg	Glu	Ser	Phe	Thr	Asn	Leu	Ala	Asp	Val	Trp	Thr	Lys	Glu	Ile	
			100					105					110			
Glu	Leu	His	Ser	Thr	Asn	Lys	Glu	Cys	Ile	Lys	Met	Leu	Val	Gly	Asn	
			115			120						125				
Lys	Val	Asp	Lys	Asp	Glu	Asp	Arg	Met	Val	Thr	Lys	Glu	Glu			
130					135							140				

(2) INFORMATION FOR SEQ ID NO:2128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..344
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2128:

gacgcgcgcg	caggggaagc	ttagcacgga	cgggaccagc	tgacgaccag	gccatgggga	60
agtacatgcg	caagggaacg	atgtccgggg	aggtggccgt	catggaggte	cccggcggcg	120
cgctgctkkg	tgctccgcacc	gtctccgcac	gctcgcgctg	cagagggcgc	agagggcgcg	180
cgacaagggg	gacgcggatg	acgcccggcg	acagtacetc	gagctcagga	gccggangna	240
gaagcctcat	aaggaccatc	agccgctgcc	gctgcgcgcg	cccgcaccgc	cagccaagag	300
gggcgcgcgg	aggaaggccg	cctccgcgcg	cgcgcgcgcg	cacg		

(2) INFORMATION FOR SEQ ID NO:2129:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..114
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502286
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2129:
Pro Arg Gly Arg Gly Ser Leu Ala Arg Thr Gly Pro Ala Asp Asp Gln
1 5 10 15
Ala Met Gly Lys Tyr Met Arg Lys Gly Lys Met Ser Gly Glu Val Ala
 20 25 30
Val Met Glu Val Pro Gly Gly Ala Leu Xaa Xaa Val Arg Thr Ala Pro
 35 40 45
Ala Arg Ser Arg Cys Arg Gly Arg Arg Gly Arg Ser Thr Arg Gly Thr
50 55 60
Arg Met Thr Pro Pro Asp Ser Thr Ser Ser Ser Gly Ala Gly Xaa Arg
65 70 75 80
Ser Leu Ile Arg Thr Ile Ser Arg Cys Arg Cys Arg Arg Pro Pro Pro
 85 90 95
Gln Pro Arg Gly Ala Pro Gly Gly Arg Pro Pro Pro Pro Pro Pro Arg
 100 105 110
Arg Thr

(2) INFORMATION FOR SEQ ID NO:2130:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..97
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502287
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2130:
Met Gly Lys Tyr Met Arg Lys Gly Lys Met Ser Gly Glu Val Ala Val
1 5 10 15
Met Glu Val Pro Gly Gly Ala Leu Xaa Xaa Val Arg Thr Ala Pro Ala
 20 25 30
Arg Ser Arg Cys Arg Gly Arg Arg Gly Arg Ser Thr Arg Gly Thr Arg
35 40 45
Met Thr Pro Pro Asp Ser Thr Ser Ser Ser Gly Ala Gly Xaa Arg Ser
50 55 60
Leu Ile Arg Thr Ile Ser Arg Cys Arg Cys Arg Arg Pro Pro Pro Gln
65 70 75 80
Pro Arg Gly Ala Pro Gly Gly Arg Pro Pro Pro Pro Pro Pro Arg Arg
 85 90 95
Thr

(2) INFORMATION FOR SEQ ID NO:2131:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..93
(D) OTHER INFORMATION: / Ceres Seq. ID 1502288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2131:

Met	Arg	Lys	Gly	Lys	Met	Ser	Gly	Glu	Val	Ala	Val	Met	Glu	Val	Pro
1			5					10					15		
Gly	Gly	Ala	Leu	Xaa	Xaa	Val	Arg	Thr	Ala	Pro	Ala	Arg	Ser	Arg	Cys
			20					25					30		
Arg	Gly	Arg	Arg	Gly	Arg	Ser	Thr	Arg	Gly	Thr	Arg	Met	Thr	Pro	Pro
			35					40					45		
Asp	Ser	Thr	Ser	Ser	Ser	Gly	Ala	Gly	Xaa	Arg	Ser	Leu	Ile	Arg	Thr
			50					55				60			
Ile	Ser	Arg	Cys	Arg	Cys	Arg	Arg	Pro	Pro	Pro	Gln	Pro	Arg	Gly	Ala
			65					70				75		80	
Pro	Gly	Gly	Arg	Pro	Pro	Pro	Pro	Pro	Pro	Arg	Arg	Thr			
								85				90			

(2) INFORMATION FOR SEQ ID NO:2132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..381
(D) OTHER INFORMATION: / Ceres Seq. ID 1502297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2132:

ctcacgcaag	kntntgcttc	cggttaagcc	acaaacacac	agacaccatg	gccttcccag	60
ggactcggc	gaggaagatc	gtaccaggcg	gcttcaccgc	agcacgaacc	gcgtggcca	120
gcgsscgct	cttagcttcg	acctggacgc	cgccggcgac	ttttctggg	gcctgtggca	180
gctcatcaag	cggaaggccg	ccgaggcagc	ggcctacctc	gtgcacctct	tcgcggcgct	240
ggcgagagaag	gcggacgaga	tcttcccgcc	ggagaccgcg	tcggagacgc	tcgcgcagtg	300
gatgcgcgtc	gcgcgcacgc	tggtgattcc	cgccctagt	ggtcgccctc	gtgctttgct	360
gtcgtggtgc	gtcgtgctgc	t				

(2) INFORMATION FOR SEQ ID NO:2133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..126
(D) OTHER INFORMATION: / Ceres Seq. ID 1502298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2133:

Ser	Arg	Lys	Xaa	Xaa	Pro	Pro	Val	Lys	Pro	Gln	Thr	His	Arg	His	His
1			5					10					15		
Gly	Leu	Pro	Arg	Asp	Ser	Gly	Glu	Glu	Asp	Arg	Thr	Arg	Arg	Leu	His
			20					25					30		
Arg	Ser	Thr	Asn	Arg	Arg	Gly	Gln	Xaa	Xaa	Ala	Leu	Ser	Phe	Asp	Leu
			35					40				45			
Asp	Gly	Ala	Gly	Asp	Phe	Phe	Trp	Gly	Leu	Trp	Gln	Leu	Ile	Lys	Ala
			50					55				60			
Lys	Ala	Ala	Glu	Ala	Ala	Ala	Tyr	Leu	Ala	Ala	Leu	Phe	Ala	Ala	Leu
			65					70				75		80	
Ala	Glu	Lys	Ala	Asp	Glu	Ile	Phe	Pro	Pro	Glu	Thr	Arg	Ser	Glu	Thr
			85					90				95			
Leu	Arg	Gln	Trp	Met	Arg	Val	Ala	Val	Thr	Val	Val	Ile	Pro	Gly	Pro
			100					105				110			

Ser Gly Arg Pro Arg Ala Leu Leu Leu Leu Ala Leu Leu Leu
115 120 125

(2) INFORMATION FOR SEQ ID NO:2134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2134:

His	Ala	Xaa	Xaa	Cys	Leu	Arg	Leu	Ser	His	Lys	His	Thr	Asp	Thr	Met
1				5				10						15	
Ala	Phe	Pro	Gly	Thr	Pro	Ala	Arg	Lys	Ile	Val	Pro	Gly	Gly	Phe	Thr
			20					25					30		
Ala	Ala	Arg	Thr	Ala	Val	Ala	Ser	Xaa	Ala	Leu	Leu	Ala	Ser	Thr	Trp
			35					40					45		
Thr	Ala	Pro	Ala	Thr	Phe	Ser	Gly	Ala	Cys	Gly	Ser	Ser	Ser	Arg	Arg
			50					55					60		
Arg	Pro	Pro	Arg	Gln	Arg	Pro	Thr	Ser	Leu	Pro	Ser	Ser	Arg	Arg	Trp
			65					70					75		80
Arg	Arg	Arg	Arg	Thr	Arg	Ser	Ser	Arg	Arg	Arg	Pro	Ala	Arg	Arg	Arg
				85				90					95		
Ser	Gly	Ser	Gly	Cys	Ala	Ser	Pro	Ser	Pro	Trp					
			100					105							

(2) INFORMATION FOR SEQ ID NO:2135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2135:

Met	Ala	Phe	Pro	Gly	Thr	Pro	Ala	Arg	Lys	Ile	Val	Pro	Gly	Gly	Phe
1				5				10						15	
Thr	Ala	Ala	Arg	Thr	Ala	Val	Ala	Ser	Xaa	Ala	Leu	Leu	Ala	Ser	Thr
			20					25					30		
Trp	Thr	Ala	Pro	Ala	Thr	Phe	Ser	Gly	Ala	Cys	Gly	Ser	Ser	Ser	Arg
			35					40					45		
Arg	Arg	Pro	Pro	Arg	Gln	Arg	Pro	Thr	Ser	Leu	Pro	Ser	Ser	Arg	Arg
			50					55					60		
Trp	Arg	Arg	Arg	Arg	Thr	Arg	Ser	Ser	Arg	Arg	Arg	Pro	Ala	Arg	Arg
			65					70					75		80
Arg	Ser	Gly	Ser	Gly	Cys	Ala	Ser	Pro	Ser	Pro	Trp				
			85					90							

(2) INFORMATION FOR SEQ ID NO:2136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

Met	Ala	Thr	Ala	Gln	Val	Leu	Phe	His	Arg	Phe	Tyr	Cys	Lys	Lys	Ser
1				5				10					15		
Phe	Val	Arg	Phe	Ser	Ala	Lys	Arg	Val	Ala	Ala	Ser	Cys	Val	Trp	Leu
			20					25					30		
Ala	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Arg	Lys	Ser	Arg	His	Ile	Ile	Phe
		35					40					45			
Val	Phe	His	Arg	Met	Glu	Cys	Arg	Arg	Glu	Asn	Leu	Pro	Ile	Glu	Phe
	50					55					60				

Leu Asp Val Phe Ser Lys Lys Tyr Ser Glu Leu Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:2139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2139:

gatttggtc	ttgccatgga	ggtgcgcgtc	tccccaccgc	gtgccccacgc	cggcctcctc	60
tgctgcagct	ccaactccgt	cgtctctcggc	ctccgctccc	gctccgccac	cgctccgagc	120
cgccgcgcaa	ggccactcct	tgcccgacaga	accgggacag	ccggagcgac	gaggagaccg	180
cgccggassc	aagatcatca	cggtcggggcg	gccgggggnak	agcggggcggc	ggcgcaacag	240
gaagcagcag	cagcagcagc	agcagacggc	ggcgaaggaa	gaagaagaag	aggagaggga	300
agatgaggac	gacgaggagg	agcgtgacgc	gacgatcccg	gagtggtgac	gaaccgggat	360
atcgcgcggg	gtggcgcgct	cggtggggct	tccgctggcg	ctgggcgtgg	ggtttcttcc	420
cggtgttcta	ctacctgaag	gcgtggcgga	aggtggacgt	gccgacgtgg	atccccctt	

(2) INFORMATION FOR SEQ ID NO:2140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2140:

Asp	Leu	Ala	Leu	Ala	Met	Glu	Val	Pro	Leu	Ser	Pro	Pro	Arg	Ala	His
1					5					10				15	
Ala	Gly	Leu	Leu	Cys	Cys	Ser	Ser	Thr	Pro	Val	Val	Leu	Gly	Leu	Arg
					20					25				30	
Ser	Arg	Ser	Ala	Thr	Ala	Pro	Ser	Arg	Arg	Ala	Arg	Pro	Leu	Leu	Ala
					35					40				45	
Arg	Arg	Thr	Gly	Thr	Ala	Gly	Ala	Thr	Arg	Arg	Pro	Arg	Arg	Xaa	Gln
					50					55				60	
Asp	His	His	Gly	Arg	Ala	Ala	Gly	Xaa	Xaa	Arg	Ala	Ala	Ala	Gln	Gln
					65					70				75	
Glu	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Asp	Gly	Glu	Gly	Arg	Arg	Arg
					85					90				95	
Arg	Gly	Gly	Gly	Arg											
					100										

(2) INFORMATION FOR SEQ ID NO:2141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2141:

Ile Trp Leu Leu Pro Trp Arg Cys Arg Ser Pro His Arg Val Pro Thr

1	5	10	15
Pro Ala Ser Ser Ala Ala Ala Pro Leu Pro Ser Ser Ser Ala Ser Ala	20	25	30
Pro Ala Pro Pro Pro Leu Arg Ala Ala Ala Gln Gly His Ser Leu Pro	35	40	45
Ala Glu Pro Gly Gln Pro Glu Arg Arg Gly Asp Arg Gly Gly Xaa Lys	50	55	60
Ile Ile Thr Val Gly Arg Pro Gly Xaa Ser Gly Arg Arg Arg Asn Arg	65	70	75
Lys Gln Gln Gln Gln Gln Gln Thr Ala Ala Lys Glu Glu Glu Glu	85	90	95
Glu Glu Glu Glu Asp Glu Asp Asp Glu Glu Arg Asp Ala Thr Ile	100	105	110
Pro Glu Trp	115		

(2) INFORMATION FOR SEQ ID NO:2142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1502366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2142:

Phe Gly Ser Cys His Gly Gly Ala Ala Leu Pro Thr Ala Cys Pro Arg	1	5	10	15
Arg Pro Pro Leu Leu Gln Leu His Ser Arg Arg Pro Arg Pro Pro Leu	20	25	30	
Pro Leu Arg His Arg Ser Glu Pro Pro Arg Lys Ala Thr Pro Cys Pro	35	40	45	
Gln Asn Arg Asp Ser Arg Ser Asp Glu Glu Thr Ala Ala Xaa Xaa Arg	50	55	60	
Ser Ser Arg Ser Gly Gly Arg Xaa Xaa Ala Gly Gly Gly Ala Thr Gly	65	70	75	80
Ser Ser Ser Ser Ser Ser Ser Arg Arg Arg Arg Lys Lys Lys Lys	85	90	95	
Arg Arg Arg Lys Met Arg Thr Thr Arg Arg Ser Val Thr Arg Arg Ser	100	105	110	
Arg Ser Gly Asp Glu Pro Asp Asp Ala Ala Gly Trp Ala Arg Arg Trp	115	120	125	
Gly Phe Arg Trp Arg Trp Ala Trp Gly Phe Phe Pro Val Phe Tyr Tyr	130	135	140	
Leu Lys Ala Xaa Ala Lys Val Asp Val Pro Thr Trp Ile Pro	145	150	155	

(2) INFORMATION FOR SEQ ID NO:2143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..477

(D) OTHER INFORMATION: / Ceres Seq. ID 1502367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2143:

ttaacttgat tgatttagct gggagtgcgc gcttgctaa aagtggctcc acaggtgatc	60
gcttgaaaga aactcagtc atcaataaaa gcttgctggc tttgagcgat gtaatcttcg	120

cgatcgcaaa aggagatgac cagcttcggt tcagaaatcc aaaacttaca tacctattgc 180
agccttgccct tggaggtgac tcgaaagctc tcatgtttgt caacatttca ccggagcatc 240
ctccgttggt gagacgatat ghtcgttgag gtttgcttca agggatgaatg cttgtgagat 300
tggaatacca agacgtcaca cataagcccg tcccttcggt ctaggctgaa ttatgggtga 360
aggtagctgt agggatcatg ataattgtat atataatgtg ttggtttgtg ccgcatctgg 420
ccacaaaggt gatgcccac aaaattcttg taactgtgac agtgtaggtg atggtgg

(2) INFORMATION FOR SEQ ID NO:2144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2144:

Asn Leu Ile Asp Leu Ala Gly Ser Glu Arg Leu Ala Lys Ser Gly Ser
1 5 10 15
Thr Gly Asp Arg Leu Lys Glu Thr Gln Ser Ile Asn Lys Ser Leu Ser
20 25 30
Ala Leu Ser Asp Val Ile Phe Ala Lys Gly Asp Asp His Val
35 40 45
Pro Phe Arg Asn Ser Lys Leu Thr Tyr Leu Leu Gln Pro Cys Leu Gly
50 55 60
Gly Asp Ser Lys Ala Leu Met Phe Val Asn Ile Ser Pro Glu His Pro
65 70 75 80
Pro Leu Val Arg Arg Tyr Xaa Arg
85

(2) INFORMATION FOR SEQ ID NO:2145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..388

(D) OTHER INFORMATION: / Ceres Seq. ID 1502373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2145:

attaacagcc aggaagctgg cgtcttgctt gtcttccacc cggctacc 60
cgtcgtcgcc gccgctttcc ccgttggtntc agagctcgag tcggtcagct aggcgcgctg 120
gctaattctcc ctgccttcta taagtacaga gatcaggagg cgggcacact ccattccactg 180
accgctcatg gcgaaggtcc acctctacgt cgccgcggcc tcgcccgtcg tctctcgcgct 240
cgccgcggcc gccctcgccg ggcgaccoga catgctgcag gacgtctgcc cggctgacta 300
cgctctcccg gtgaagctga acgggttcgc gtgcaaggcg aacttttcgg cggacgactt 360
ctttctcgac gggctgagga acnccggc

(2) INFORMATION FOR SEQ ID NO:2146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36

(D) OTHER INFORMATION: / Ceres Seq. ID 1502374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2146:

Leu Thr Ala Arg Lys Leu Ala Ser Cys Leu Ser Leu Phe Phe Ser His
1 5 10 15
Pro Ala Thr Pro Val Val Ala Ala Phe Pro Val Xaa Ser Glu Leu
20 25 30
Glu Ser Ala Ser
35

(2) INFORMATION FOR SEQ ID NO:2147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1502375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2147:

Met Ala Lys Val His Leu Tyr Val Ala Ala Cys Ala Val Val Leu
1 5 10 15
Ala Leu Ala Ala Pro Ala Leu Ala Gly Asp Pro Asp Met Leu Gln Asp
20 25 30
Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu Asn Gly Phe Ala
35 40 45
Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Phe Asp Gly Leu Arg
50 55 60
Asn Xaa Gly
65

(2) INFORMATION FOR SEQ ID NO:2148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..39

(D) OTHER INFORMATION: / Ceres Seq. ID 1502376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2148:

Met Leu Gln Asp Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu
1 5 10 15
Asn Gly Phe Ala Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Phe
20 25 30
Asp Gly Leu Arg Asn Xaa Gly
35

(2) INFORMATION FOR SEQ ID NO:2149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 397 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..397

(D) OTHER INFORMATION: / Ceres Seq. ID 1502381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2149:

ttaaactgttg ctgtcaagac actcaaacat gatgggttgc aggggcataa agagtgggtg 60
gcagaagtgtg attttcttgg aaacottcag catccacatc tagtgaattt ggttggtcac 120
tgcattgaag atgaccagag gttgcttgtg tatgaattta tgcctccgtgg aagtttggag 180

aatcatcttt ttagaaagtc attgcctcta ccatgggcca ttagaatgaa aattgcttt 240
ggtgctgcga aaggcctcgc tttcttcat gaagaagctg aaagaccagt aatctatcgg 300
gacttcaaaa cctccaatat tcttttagat gcggactata acgcaaaact ctctgatttt 360
ggacttgcta aagatggccc tgagggtgat aaaacac

(2) INFORMATION FOR SEQ ID NO:2150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1502382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2150:

Leu	Thr	Val	Ala	Val	Lys	Thr	Leu	Asn	His	Asp	Gly	Leu	Gln	Gly	His
1				5				10					15		
Lys	Glu	Trp	Val	Ala	Glu	Val	Asp	Phe	Leu	Gly	Asn	Leu	Gln	His	Pro
			20				25					30			
His	Leu	Val	Lys	Leu	Val	Gly	Tyr	Cys	Ile	Glu	Asp	Asp	Gln	Arg	Leu
			35				40					45			
Leu	Val	Tyr	Glu	Phe	Met	Pro	Arg	Gly	Ser	Leu	Glu	Asn	His	Leu	Phe
			50				55					60			
Arg	Lys	Ser	Leu	Pro	Leu	Pro	Trp	Ala	Ile	Arg	Met	Lys	Ile	Ala	Leu
			65				70				75				80
Gly	Ala	Ala	Lys	Gly	Leu	Ala	Phe	Leu	His	Glu	Glu	Ala	Glu	Arg	Pro
			85				90							95	
Val	Ile	Tyr	Arg	Asp	Phe	Lys	Thr	Ser	Asn	Ile	Leu	Leu	Asp	Ala	Asp
			100				105						110		
Tyr	Asn	Ala	Lys	Leu	Ser	Asp	Phe	Gly	Leu	Ala	Lys	Asp	Gly	Pro	Glu
			115				120					125			
Gly	Asp	Lys	Thr												
			130												

(2) INFORMATION FOR SEQ ID NO:2151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1502383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2151:

Met	Pro	Arg	Gly	Ser	Leu	Glu	Asn	His	Leu	Phe	Arg	Lys	Ser	Leu	Pro
1				5				10					15		
Leu	Pro	Trp	Ala	Ile	Arg	Met	Lys	Ile	Ala	Leu	Gly	Ala	Ala	Lys	Gly
			20				25					30			
Leu	Ala	Phe	Leu	His	Glu	Glu	Ala	Glu	Arg	Pro	Val	Ile	Tyr	Arg	Asp
			35				40					45			
Phe	Lys	Thr	Ser	Asn	Ile	Leu	Leu	Asp	Ala	Asp	Tyr	Asn	Ala	Lys	Leu
			50				55				60				
Ser	Asp	Phe	Gly	Leu	Ala	Lys	Asp	Gly	Pro	Glu	Gly	Asp	Lys	Thr	
			65				70				75				

(2) INFORMATION FOR SEQ ID NO:2152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..480
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502387
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2152:
aagaactagg gttgtcttct tcttttaac ctgcgcgcgc catccgacgc ccattctctc 60
caccagccgc cngccgcgcgc ctaaggagaa gagggtcgcg cgtctcctt gccccgatgg 120
cgtccgagaa gaagcagtc c aaccgcgatgc gggagatcaa ggtgcagaag ctggtcctca 180
acatatcgtt agggagagcg ggcacgcgct caccgcgcgc gccaaagggtgc tggagcagct 240
cagcggccag acccccgctc tctccaaggc gaggtacacg gtgcgctcgt tcggcatccg 300
gcgtaacgag aagatcgctc gctacgtcac ggtcaggggc gacaaggcca tgcagctgct 360
tgagagcggc ctcaaggta caggagtaaga gctgctcagg aggaacttca gcgacacggc 420
ctgcttcggg ttcggcatcc aagagcacat cgaccttggt atcaagtatg atccatcaac 480

(2) INFORMATION FOR SEQ ID NO:2153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..159
(D) OTHER INFORMATION: / Ceres Seq. ID 1502388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2153:

Arg	Pro	Arg	Val	Ala	Ser	Phe	Leu	Leu	Thr	Ser	Arg	Arg	His	Pro	Thr
1			5						10				15		
Pro	Ile	Ser	Ser	Thr	Gln	Pro	Xaa	Pro	Pro	Pro	Lys	Glu	Lys	Arg	Val
			20					25					30		
Arg	Pro	Ser	Pro	Cys	Pro	Asp	Gly	Val	Arg	Glu	Glu	Ala	Val	Gln	Pro
			35				40					45			
Asp	Ala	Gly	Asp	Gln	Gly	Ala	Glu	Ala	Gly	Pro	Gln	His	Ile	Arg	Arg
			50				55				60				
Glu	Ser	Gly	Asp	Arg	Leu	Thr	Arg	Ala	Ala	Lys	Val	Leu	Glu	Gln	Leu
			65				70			75				80	
Ser	Gly	Gln	Thr	Pro	Val	Phe	Ser	Lys	Ala	Arg	Tyr	Thr	Val	Arg	Ser
					85				90					95	
Phe	Gly	Ile	Arg	Arg	Asn	Glu	Lys	Ile	Ala	Cys	Tyr	Val	Thr	Val	Arg
					100				105					110	
Gly	Asp	Lys	Ala	Met	Gln	Leu	Leu	Glu	Ser	Gly	Leu	Lys	Val	Lys	Glu
					115			120				125			
Tyr	Glu	Leu	Leu	Arg	Arg	Asn	Phe	Ser	Asp	Thr	Gly	Cys	Phe	Gly	Phe
							135				140				
Gly	Ile	Gln	Glu	His	Ile	Asp	Leu	Gly	Ile	Lys	Tyr	Asp	Pro	Ser	
							150				155				

(2) INFORMATION FOR SEQ ID NO:2154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..121
(D) OTHER INFORMATION: / Ceres Seq. ID 1502389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2154:

Met Ala Ser Glu Lys Lys Gln Ser Asn Pro Met Arg Glu Ile Lys Val

1	5	10	15
Gln Lys Leu Val Leu Asn Ile Ser Val Gly Arg Ala Ala Thr Ala Ser			
	20	25	30
Pro Ala Pro Pro Arg Cys Trp Ser Ser Ser Ala Ala Arg Pro Pro Ser			
	35	40	45
Ser Pro Arg Arg Gly Thr Arg Cys Ala Arg Ser Ala Ser Gly Val Thr			
	50	55	60
Arg Arg Ser Pro Ala Thr Ser Arg Ser Gly Ala Thr Arg Pro Cys Ser			
	65	70	75
Cys Leu Arg Ala Ala Ser Arg Ser Arg Ser Thr Ser Cys Ser Gly Gly			
	85	90	95
Thr Ser Ala Thr Pro Ala Ala Ser Gly Ser Ala Ser Lys Ser Thr Ser			
	100	105	110
Thr Leu Val Ser Ser Met Ile His Gln			
	115	120	

(2) INFORMATION FOR SEQ ID NO:2155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1502390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2155:

Met Arg Glu Ile Lys Val Gln Lys Leu Val Leu Asn Ile Ser Val Gly	
	5 10 15
Arg Ala Ala Thr Ala Ser Pro Ala Pro Pro Arg Cys Trp Ser Ser Ser	
	20 25 30
Ala Ala Arg Pro Pro Ser Ser Pro Arg Arg Gly Thr Arg Cys Ala Arg	
	35 40 45
Ser Ala Ser Gly Val Thr Arg Arg Ser Pro Ala Thr Ser Arg Ser Gly	
	50 55 60
Ala Thr Arg Pro Cys Ser Cys Leu Arg Ala Ala Ser Arg Ser Arg Ser	
	65 70 75
Thr Ser Cys Ser Gly Gly Thr Ser Ala Thr Pro Ala Ala Ser Gly Ser	
	85 90 95
Ala Ser Lys Ser Thr Ser Thr Leu Val Ser Ser Met Ile His Gln	
	100 105 110

(2) INFORMATION FOR SEQ ID NO:2156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478

(D) OTHER INFORMATION: / Ceres Seq. ID 1502407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2156:

attcagccca tcgctagctc tcgctgtctc cctgtctctc ctagtagcac aagaccacga	60
gggattaagc gatgacaacc tctaagctcg ctgtctctcac tctgtttgcc ctgctcggtc	120
cctgtgtcatg ccagtcgggt ggctactact tctaccacaac cccgcagcaa ccatctccaa	180
caccacagccc tcctcttagt ccgcaactca tggtcggata ctacaaggac aagtgtgccg	240
cttacgtgga tgttgaagct attgtcaaga agcacgtcaa ggccaccgat gctgcatgc	300
agcccggtct tgctcgcttc ttattccaac actgcttcgt cctgtgatgc gaaggctccg	360
tctctctcga cactgtcagc aacgacacca gctgacccc agagaagttc ggctgcccc	420
acttccccag cctgcggggc ttcgaggtga tcgacgcggc caaggccgag atcgaggg	

(2) INFORMATION FOR SEQ ID NO:2157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2157:

Met	Thr	Thr	Ser	Lys	Leu	Ala	Val	Leu	Thr	Leu	Phe	Ala	Leu	Leu	Gly
1				5					10					15	
Ser	Val	Ser	Cys	Gln	Ser	Gly	Gly	Tyr	Tyr	Phe	Tyr	Pro	Thr	Pro	Gln
			20					25					30		
Gln	Pro	Ser	Pro	Thr	Pro	Ser	Pro	Ser	Ser	Pro	Gln	Leu	Met	Val	
			35				40			45					
Gly	Tyr	Tyr	Lys	Asp	Lys	Cys	Ala	Ala	Tyr	Val	Asp	Val	Glu	Ala	Ile
			50			55				60					
Val	Lys	Lys	His	Val	Lys	Ala	Thr	Asp	Ala	Gly	Met	Gln	Ala	Gly	Leu
65				70					75					80	
Val	Arg	Leu	Leu	Phe	His	Asp	Cys	Phe	Val	Arg	Gly	Cys	Asp	Gly	Ser
			85					90						95	
Val	Leu	Leu	Asp	Thr	Phe	Ser	Asn	Asp	Thr	Ser	Leu	Thr	Pro	Glu	Lys
			100					105					110		
Phe	Gly	Val	Pro	Asn	Phe	Pro	Ser	Leu	Arg	Gly	Phe	Glu	Val	Ile	Asp
			115				120					125			
Ala	Ala	Lys	Ala	Glu	Ile	Glu									
			130			135									

(2) INFORMATION FOR SEQ ID NO:2158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2158:

Met	Val	Gly	Tyr	Tyr	Lys	Asp	Lys	Cys	Ala	Ala	Tyr	Val	Asp	Val	Glu
1					5				10					15	
Ala	Ile	Val	Lys	Lys	His	Val	Lys	Ala	Thr	Asp	Ala	Gly	Met	Gln	Ala
			20					25					30		
Gly	Leu	Val	Arg	Leu	Leu	Phe	His	Asp	Cys	Phe	Val	Arg	Gly	Cys	Asp
			35				40			45					
Gly	Ser	Val	Leu	Leu	Asp	Thr	Phe	Ser	Asn	Asp	Thr	Ser	Leu	Thr	Pro
			50				55			60					
Glu	Lys	Phe	Gly	Val	Pro	Asn	Phe	Pro	Ser	Leu	Arg	Gly	Phe	Glu	Val
65				70					75					80	
Ile	Asp	Ala	Ala	Lys	Ala	Glu	Ile	Glu							
			85												

(2) INFORMATION FOR SEQ ID NO:2159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..437

(D) OTHER INFORMATION: / Ceres Seq. ID 1502420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2159:

aaccotttcg	ctccgcgcgc	cgccctgatg	ctccagcgcc	ctcgccgtcg	gtgcccgcgc	60
tgccgtctct	ccgtctacgag	ctaggcatct	ccttcgccga	tccagcatgg	gtaagacacg	120
tggtatggga	gctggggcgca	asstcaagac	ccacaggag	aaccagaggt	ggtgctgaca	180
aagcctacaa	gaagagccat	cttgccaacg	agtggaaaga	accotttgc	ggaatcatct	240
acgcaaaagg	gatcgtctct	gaaaagatcg	gcacagagcc	caagcagcct	aactctgcta	300
ttcgtaaagt	tgctctgtgt	cagctggtga	agaacggtaa	gaagattgcc	gcctttgtgc	360
cgaacgacgg	ctgcttgaac	tacatcgagg	aaaacgatga	ggtgctgac	gcgggggttcg	420
gtcgtaaggg	ccacgct					

(2) INFORMATION FOR SEQ ID NO:2160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1502421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2160:

Pro	Phe	Arg	Leu	Arg	Arg	Arg	Leu	Ile	Ala	Pro	Ala	Pro	Ser	Pro	Ser	
1			5					10					15			
Ala	Ala	Arg	Leu	Pro	Ser	Ser	Arg	Tyr	Glu	Leu	Gly	Ile	Ser	Phe	Ala	
			20					25					30			
Asp	Pro	Ala	Trp	Val	Arg	His	Val	Val	Trp	Glu	Leu	Gly	Ala	Xaa	Ser	
			35				40						45			
Arg	Pro	Thr	Gly	Gly	Thr	Arg	Gly	Gly	Ala	Asp	Lys	Ala	Tyr	Lys	Lys	
			50			55					60					
Ser	His	Leu	Gly	Asn	Glu	Trp	Lys	Lys	Pro	Phe	Ala	Gly	Ser	Ser	His	
			65			70				75					80	
Ala	Lys	Gly	Ile	Val	Leu	Glu	Lys	Ile	Gly	Ile	Glu	Ala	Lys	Gln	Pro	
			85					90						95		
Asn	Ser	Ala	Ile	Arg	Lys	Cys	Ala	Arg	Val	Gln	Leu	Val	Lys	Asn	Gly	
			100				105							110		
Lys	Lys	Ile	Ala	Ala	Phe	Val	Pro	Asn	Asp	Gly	Cys	Leu	Asn	Tyr	Ile	
			115				120							125		
Glu	Glu	Asn	Asp	Glu	Val	Leu	Ile	Ala	Gly	Phe	Gly	Arg	Lys	Gly	His	
			130			135						140				
Ala																
145																

(2) INFORMATION FOR SEQ ID NO:2161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..501

(D) OTHER INFORMATION: / Ceres Seq. ID 1502422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2161:

aaagtgaata	cagaaaacct	cagccccagg	ccaattctc	gaccgcatcg	ccaccacacc	60
catctctcatg	gtacacctcg	cgacctcacc	gcggggaaga	aggtggtgct	cttcgcgcgtg	120
ccggsscgct	tcacgcccac	gcacaccag	aagcacctcc	cggggttcgt	gcgcaaggcc	180
ggggagctcc	gcgccaaggg	ctcgacacgg	tggctgctgt	ctccgtcaac	gacgccttcg	240

tgtatgcgcgc	gtggaaggag	agtcctgggga	tcggggacga	ggtgctgctc	ctgtcggagc	300
gcaacggcga	gctggcgcg	gcattggctc	gagctcgacc	tctccgacaa	gcccgtaggg	360
tcggcgctcc	gtcccgccgc	tacgsgctgc	tcgcggagga	cggcgtggtc	aaggtgatca	420
acctcgagga	ggcgggcgcg	ttcaccaaca	gcagcgccga	ggacatgctc	aacgcgctct	480
gaactcgcga	cgccatgggt	g				

(2) INFORMATION FOR SEQ ID NO:2162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2162:

Lys	Val	Asn	Thr	Glu	Thr	Ser	Ser	Pro	Arg	Pro	Ile	Pro	Arg	Pro	His
1				5				10					15		
Arg	His	Pro	Pro	His	Leu	His	Gly	Tyr	Leu	Arg	Asp	Leu	Thr	Ala	Gly
				20				25					30		
Lys	Lys	Val	Val	Leu	Phe	Ala	Val	Pro	Xaa	Xaa	Phe	Thr	Pro	Thr	Cys
				35				40					45		
Thr	Gln	Lys	His	Leu	Pro	Gly	Phe	Val	Ala	Lys	Ala	Gly	Glu	Leu	Arg
				50				55					60		
Ala	Lys	Gly	Ser	Thr	Pro	Trp	Pro	Ala	Ser	Pro	Ser	Thr	Thr	Pro	Ser
65					70					75				80	

(2) INFORMATION FOR SEQ ID NO:2163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2163:

Ser	Glu	Tyr	Arg	Asn	Leu	Gln	Pro	Gln	Ala	Asn	Ser	Ser	Thr	Ala	Ser
1				5				10					15		
Pro	Pro	Thr	Pro	Ser	Pro	Trp	Leu	Pro	Pro	Arg	Pro	His	Arg	Gly	Glu
				20				25					30		
Glu	Gly	Gly	Ala	Leu	Arg	Arg	Ala	Arg	Xaa	Val	His	Ala	His	Leu	His
				35				40					45		
Pro	Glu	Ala	Pro	Pro	Gly	Val	Arg	Gly	Gln	Gly	Arg	Gly	Ala	Pro	Arg
				50				55					60		
Gln	Gly	Leu	Asp	Thr	Val	Ala	Cys	Val	Ser	Val	Asn	Asp	Ala	Phe	Val
65					70					75				80	
Met	Arg	Ala	Trp	Lys	Glu	Ser	Leu	Gly	Ile	Gly	Asp	Glu	Val	Leu	Leu
				85				90					95		
Leu	Ser	Asp	Gly	Asn	Gly	Glu	Leu	Ala	Arg	Ala	Trp	Ala	Arg	Ala	Arg
				100				105					110		
Pro	Leu	Arg	Gln	Ala	Arg	Gly	Val	Gly	Val	Arg	Ser	Arg	Arg	Tyr	Xaa
				115				120					125		
Leu	Leu	Ala	Glu	Asp	Gly	Val	Val	Lys	Val	Ile	Asn	Leu	Glu	Glu	Gly
				130				135					140		
Gly	Ala	Phe	Thr	Asn	Ser	Ser	Ala	Glu	Asp	Met	Leu	Asn	Ala	Leu	
145					150					155					

(2) INFORMATION FOR SEQ ID NO:2164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2164:

Met	Ala	Thr	Ser	Ala	Thr	Ser	Pro	Arg	Gly	Arg	Arg	Trp	Cys	Ser	Ser	
1				5					10					15		
Pro	Cys	Pro	Xaa	Arg	Ser	Arg	Pro	Pro	Ala	Pro	Arg	Ser	Thr	Ser	Arg	
			20						25				30			
Gly	Ser	Trp	Pro	Arg	Pro	Gly	Ser	Ser	Ala	Pro	Arg	Ala	Arg	His	Arg	
			35				40					45				
Gly	Leu	Arg	Leu	Arg	Gln	Arg	Arg	Leu	Arg	Asp	Ala	Arg	Val	Glu	Gly	
			50			55					60					
Glu	Ser	Gly	Asp	Arg	Gly	Arg	Gly	Ala	Ala	Pro	Val	Gly	Arg	Gln	Arg	
65				70						75				80		
Arg	Ala	Gly	Ala	Arg	Met	Gly	Ser	Ser	Ser	Thr	Ser	Pro	Thr	Ser	Pro	
				85					90					95		
Trp	Gly	Arg	Arg	Pro	Val	Pro	Pro	Leu	Xaa	Ala	Ala	Arg	Gly	Gly	Arg	
			100					105					110			
Arg	Gly	Gln	Gly	Asp	Gln	Pro	Arg	Gly	Gly	Arg	Arg	Val	His	Gln	Gln	
			115				120					125				
Gln	Arg	Arg	Gly	His	Ala	Gln	Arg	Ala	Leu	Asn	Ser	Arg	Arg	His	Gly	
			130			135					140					

(2) INFORMATION FOR SEQ ID NO:2165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..398
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2165:

acgatacacac	accactccac	agcagtagca	agagggatag	agcaaggcca	cacacacaca	60
caccactagg	ctaggttagc	cttttagtcg	tcgtcgagga	gcaagaaggg	cgcgacgcga	120
agcaggcaag	caagaagaga	gccgatcgac	cgagagctag	cacgcgatgg	cgaggtcttc	180
caagatgatg	gttcggcgas	stctgtctggc	cttgccctcg	gccgtgtcga	ccgccgaggg	240
gaggaacatc	aagacgcgca	cgacggagaa	gaaggacgac	gcggtgtgtc	agccgcagac	300
attccccgcc	ttcgaccgcc	tcggcgggcg	gcgtccccgg	cgttcggcgg	cttccccggg	360
ggcagcattc	ctggcgcagc	cattccccgg	ttcagcat			

(2) INFORMATION FOR SEQ ID NO:2166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1502430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2166:

Met Ala Arg Ser Lys Met Met Val Ala Ala Xaa Leu Leu Ala Leu
1 5 10 15
Ala Leu Ala Val Ser Thr Ala Glu Ala Arg Asn Ile Lys Thr Thr Thr
20 25 30
Thr Glu Lys Lys Asp Asp Ala Val Val Gln Pro Gln Thr Phe Pro Pro
35 40 45
Phe Asp Arg Leu Gly Gly Ala Arg Pro Arg Arg Ser Ala Ala Ser Pro
50 55 60
Ala Ala Ala Phe Leu Ala Ala Ala Phe Pro Gly Ser Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:2167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1502431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2167:

Met Met Val Ala Ala Xaa Leu Leu Ala Leu Ala Val Ser Thr
1 5 10 15
Ala Glu Ala Arg Asn Ile Lys Thr Thr Thr Thr Glu Lys Lys Asp
20 25 30
Ala Val Val Gln Pro Gln Thr Phe Pro Pro Phe Asp Arg Leu Gly Gly
35 40 45
Ala Arg Pro Arg Arg Ser Ala Ala Ser Pro Ala Ala Ala Phe Leu Ala
50 55 60
Ala Ala Phe Pro Gly Ser Ala
65 70

(2) INFORMATION FOR SEQ ID NO:2168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1502432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2168:

Met Val Ala Ala Xaa Leu Leu Ala Leu Ala Val Ser Thr Ala
1 5 10 15
Glu Ala Arg Asn Ile Lys Thr Thr Thr Thr Glu Lys Lys Asp Asp Ala
20 25 30
Val Val Gln Pro Gln Thr Phe Pro Pro Phe Asp Arg Leu Gly Gly Ala
35 40 45
Arg Pro Arg Arg Ser Ala Ala Ser Pro Ala Ala Ala Phe Leu Ala Ala
50 55 60
Ala Phe Pro Gly Ser Ala
65 70

(2) INFORMATION FOR SEQ ID NO:2169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..362
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502441
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2169:
aggttcacgg gaggcgagga ccttgccccc ctgcattcct cgggtcgctg gacctccggc 60
acaaccagct gacgggcccc atccggcgcg gctggtgcag gggcagttcc ggtcgctggt 120
cctgtcctac aaccagctca cgggccccat ccgcgcgcac gacgcgnanc gagatcaaca 180
ccgtgcacct ctccacaac aggtccaccg gcgaccocctc ccactcgttt cgccgccggc 240
cgccccattc ggcaagggtg acctgtcgtg gaactaccto aacttcgacc tcagcaggct 300
ggtgttcccg ggcgagctca cgtacctgga cctgtcccaac aacctcatcc gcggcaccgt 360
gc

(2) INFORMATION FOR SEQ ID NO:2170:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..120
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502442
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2170:
Gly Ser Arg Glu Ala Arg Thr Leu Pro Pro Cys Ile Pro Pro Val Ala
1 5 10 15
Gly Pro Pro Ala Gln Pro Ala Asp Gly Pro His Pro Gly Gly Leu Val
20 25 30
Gln Gly Gln Phe Arg Ser Leu Val Leu Ser Tyr Asn Gln Leu Thr Gly
35 40 45
Pro Ile Pro Arg Asp Asp Ala Xaa Arg Asp Gln His Arg Arg Pro Leu
50 55 60
Pro Gln Gln Ala His Arg Arg Pro Leu Pro Pro Val Ser Pro Pro Ala
65 70 75 80
Gly Pro Phe Gly Lys Val Asp Leu Ser Trp Asn Tyr Leu Asn Phe Asp
85 90 95
Leu Ser Arg Leu Val Phe Pro Pro Glu Leu Thr Tyr Leu Asp Leu Ser
100 105 110
His Asn Leu Ile Arg Gly Thr Val
115 120

(2) INFORMATION FOR SEQ ID NO:2171:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..120
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502443
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2171:
Val His Gly Arg Arg Gly Pro Cys Pro Pro Ala Phe Leu Arg Ser Leu
1 5 10 15
Asp Leu Arg His Asn Gln Leu Thr Gly Pro Ile Pro Ala Gly Trp Cys
20 25 30
Arg Gly Ser Ser Gly Arg Trp Ser Cys Pro Thr Thr Ser Ser Arg Ala
35 40 45
Pro Ser Arg Ala Thr Thr Xaa Xaa Glu Ile Asn Thr Val Asp Leu Ser

50 55 60
His Asn Arg Leu Thr Gly Asp Pro Ser His Leu Phe Arg Arg Arg Pro
65 70 75 80
Ala His Ser Ala Arg Trp Thr Cys Arg Gly Thr Thr Ser Thr Ser Thr
85 90 95
Ser Ala Gly Trp Cys Ser Arg Arg Ser Ser Arg Thr Trp Thr Cys Pro
100 105 110
Thr Thr Ser Ser Ala Ala Pro Cys
115 120

(2) INFORMATION FOR SEQ ID NO:2172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..396
(D) OTHER INFORMATION: / Ceres Seq. ID 1502461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2172:

aaaacctag ccaacctag tcgcgcgans stntcgcgcg cgcacactcc tcccgcgtgcc 60
ccctccctcg cgccggccat ccacgcgggc cgtctccgcg cgcaaccacg gggggcgcac 120
ggcntgagct ctccggcccg accccgcgcg tgggggncgt caactccggc aaggkcgcg 180
tcggaaagaa saccaccacc gccaacctcg ccgcctctct cgcgcgcctc ggcctccagc 240
ccgtcgccgt cgacgcgat gctggcctcc gcaacctcga cctcctgctc ggcctcgaga 300
accgcgtcca cctcaccgcc gccgcactcc tcgcgggaga ctgcgcgact gaccaggcgc 360
tcgtccgcca ccgcgcgtt ccacgacctc cactcc

(2) INFORMATION FOR SEQ ID NO:2173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..132
(D) OTHER INFORMATION: / Ceres Seq. ID 1502462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2173:

Lys Thr Leu Ala Asn Pro Ser Pro Pro Xaa Xaa Ser Arg Ala Ala Pro
1 5 10 15
Pro Pro Ala Ala Pro Ser Ser Gly Gly Gly Ile His Ala Gly Arg Leu
20 25 30
Arg Ala Gln Pro Arg Gly Ala His Gly Xaa Ser Ser Arg Ala Arg Pro
35 40 45
Arg Ala Trp Trp Xaa Ser Pro Pro Ala Arg Xaa Ser Glu Arg Xaa
50 55 60
Pro Pro Pro Pro Thr Ser Pro Pro Leu Ser Arg Ala Ser Ala Ser Gln
65 70 75 80
Pro Ser Pro Ser Thr Pro Met Leu Ala Ser Ala Thr Ser Thr Ser Cys
85 90 95
Ser Ala Ser Arg Thr Ala Ser Thr Ser Pro Pro Pro Xaa Ser Ser Arg
100 105 110
Glu Thr Ala Asp Ser Thr Arg Arg Ser Ser Ala Thr Ala Phe His
115 120 125
Asp Leu His Leu
130

(2) INFORMATION FOR SEQ ID NO:2174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..497
(D) OTHER INFORMATION: / Ceres Seq. ID 1502479
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2174:
caaaggatgt caagaaggag gctccaaagg aggcccccaa gccaaagggtg gttgaggcac 60
cagcagaaga ggaagcacca aagccaaagc caaagaatcc tcttgacttg ctgccaccaa 120
gcaagatggt ccttgatgac tgaagaggcg tatactcaaa cacaaagact aacttcggg 180
agggttgcct caaagggttc tgggacatgt acgaccocaga ggctactctt tgtgtgtctg 240
tgactacaag tacaatgatg agaacaccgt ctccctttgtg acctgaaca aggttggtgg 300
attcctgcag cggatggacc tgtgccgcaa gtacgccttt gggaagatgc tcgtgatagg 360
ctctgagcca cccttcaagc tgaaggggct ttggctcttc cgtggccagg atgttcccaa 420
gtttgtaatg gacgaggtct atgacatgga gctctacgag tgggaccaag gtggacatct 480
ctgatgaggc cagaagg
(2) INFORMATION FOR SEQ ID NO:2175:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..80
(D) OTHER INFORMATION: / Ceres Seq. ID 1502480
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2175:
Gln Arg Met Ser Arg Arg Arg Leu Gln Arg Arg Pro Pro Ser Gln Arg
1 5 10 15
Trp Leu Arg His Gln Gln Lys Arg Lys His Gln Ser Gln Ser Gln Arg
20 25 30
Ile Leu Leu Thr Cys Cys His Gln Ala Arg Trp Ser Leu Met Thr Gly
35 40 45
Arg Gly Tyr Thr Gln Thr Gln Arg Leu Thr Ser Gly Arg Leu Pro Ser
50 55 60
Lys Val Ser Gly Thr Cys Thr Thr Gln Arg Leu Leu Phe Val Val Leu
65 70 75 80
(2) INFORMATION FOR SEQ ID NO:2176:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..92
(D) OTHER INFORMATION: / Ceres Seq. ID 1502481
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2176:
Lys Asp Val Lys Lys Glu Ala Pro Lys Glu Ala Pro Lys Pro Lys Val
1 5 10 15
Val Glu Ala Pro Ala Glu Glu Glu Ala Pro Lys Pro Lys Pro Lys Asn
20 25 30
Pro Leu Asp Leu Leu Pro Pro Ser Lys Met Val Leu Asp Asp Trp Lys
35 40 45
Arg Leu Tyr Ser Asn Thr Lys Thr Asn Phe Arg Glu Val Ala Ile Lys

50 55 60
Gly Phe Trp Asp Met Tyr Asp Pro Glu Ala Thr Leu Cys Gly Ser Val
65 70 75 80
Thr Thr Ser Thr Met Met Arg Thr Pro Ser Pro Leu
85 90

(2) INFORMATION FOR SEQ ID NO:2177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2177:

Met Ser Arg Arg Arg Leu Gln Arg Arg Pro Pro Ser Gln Arg Trp Leu
1 5 10 15
Arg His Gln Gln Lys Arg Lys His Gln Ser Gln Ser Gln Arg Ile Leu
20 25 30
Leu Thr Cys Cys His Gln Ala Arg Trp Ser Leu Met Thr Gly Arg Gly
35 40 45
Tyr Thr Gln Thr Gln Arg Leu Thr Ser Gly Arg Leu Pro Ser Lys Val
50 55 60
Ser Gly Thr Cys Thr Thr Gln Arg Leu Leu Phe Val Val Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO:2178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..455
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2178:

tttgatgttt tctattaat tttagacttga tccaaaaggt cggatacatc ttttatcaga 60
tttggtgaat cccctctccc tctcacgctc caccactgat catgggggcta ctcagcatta 120
tccgcaagat caagcgcaag gagaaggaga tgcgcactcct catggttggtg cttgacaaact 180
caggggaagac aaccatcggt ctcaagatca atggggaggga caccagcgctc attagcccaa 240
cccttggtatt caacatcaag accatcaagt accacaaata ctctttgaac atattgggatg 300
ttggaggaca gaagacaatc aggtcttact ggagaaacta ctttgagcag actgatggat 360
tagtttggtt tgttgatagt tcagacataa ggaggcgtta tgattgccgt gctgaactcc 420
acaatctctt gaaagaagag agactagttg gagct

(2) INFORMATION FOR SEQ ID NO:2179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2179:

Met Gly Leu Leu Ser Ile Ile Arg Lys Ile Lys Arg Lys Glu Lys Glu
1 5 10 15

Met Arg Ile Leu Met Val Gly Leu Asp Asn Ser Gly Lys Thr Thr Ile
20 25 30
Val Leu Lys Ile Asn Gly Glu Asp Thr Ser Val Ile Ser Pro Thr Leu
35 40 45
Gly Phe Asn Ile Lys Thr Ile Lys Tyr His Lys Tyr Ser Leu Asn Ile
50 55 60
Trp Asp Val Gly Gly Gln Lys Thr Ile Arg Ser Tyr Trp Arg Asn Tyr
65 70 75 80
Phe Glu Gln Thr Asp Gly Leu Val Trp Val Val Asp Ser Ser Asp Ile
85 90 95
Arg Arg Leu Asp Asp Cys Arg Ala Glu Leu His Asn Leu Leu Lys Glu
100 105 110
Glu Arg Leu Val Gly Ala
115

(2) INFORMATION FOR SEQ ID NO:2180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2180:

Met Arg Ile Leu Met Val Gly Leu Asp Asn Ser Gly Lys Thr Thr Ile
1 5 10 15
Val Leu Lys Ile Asn Gly Glu Asp Thr Ser Val Ile Ser Pro Thr Leu
20 25 30
Gly Phe Asn Ile Lys Thr Ile Lys Tyr His Lys Tyr Ser Leu Asn Ile
35 40 45
Trp Asp Val Gly Gly Gln Lys Thr Ile Arg Ser Tyr Trp Arg Asn Tyr
50 55 60
Phe Glu Gln Thr Asp Gly Leu Val Trp Val Val Asp Ser Ser Asp Ile
65 70 75 80
Arg Arg Leu Asp Asp Cys Arg Ala Glu Leu His Asn Leu Leu Lys Glu
85 90 95
Glu Arg Leu Val Gly Ala
100

(2) INFORMATION FOR SEQ ID NO:2181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2181:

Met Val Gly Leu Asp Asn Ser Gly Lys Thr Thr Ile Val Leu Lys Ile
1 5 10 15
Asn Gly Glu Asp Thr Ser Val Ile Ser Pro Thr Leu Gly Phe Asn Ile
20 25 30
Lys Thr Ile Lys Tyr His Lys Tyr Ser Leu Asn Ile Trp Asp Val Gly
35 40 45
Gly Gln Lys Thr Ile Arg Ser Tyr Trp Arg Asn Tyr Phe Glu Gln Thr
50 55 60
Asp Gly Leu Val Trp Val Val Asp Ser Ser Asp Ile Arg Arg Leu Asp

65 70 75 80
Asp Cys Arg Ala Glu Leu His Asn Leu Leu Lys Glu Glu Arg Leu Val
85 90 95
Gly Ala

(2) INFORMATION FOR SEQ ID NO:2182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..462
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2182:

```
aacatcctaa tcgaaaaaaa gctctctgct tccctctcca ttttttcac tcattcggcg      60
ccggcggaacc cctgctcgt cactcgcgat ggcccggatc aagtgacag agctgcgcgg      120
aaagagcaag acggatctgc aagcgcmast caaggagctt aaatcggagc tctccctcct      180
acgcgtcgcc awggtcacgc gcgggggtcc caacaagctc tccaaaatca agattgtgcg      240
cacctccatc gctcgcgtgc tcacgcgttat ctgcgagaag cagaagtcgg cgctgcgtga      300
ggcgtacaag aagaagaagc ttctcccgct cgatctccgc cccaagaaga cccgcgcgat      360
tcgcaggcgc ctacccaagc accagctctc ctgtaagacc gagagggaaa agaagcgtga      420
gaagtatttt cccatgcgga agtaacgttat caaggcctag at
```

(2) INFORMATION FOR SEQ ID NO:2183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2183:

```
His Pro Asn Arg Lys Lys Ala Leu Cys Phe Pro Leu His Phe Phe Ile
1 5 10 15
Ser Phe Gly Ala Ala Pro Pro Ala Arg His Ser Arg Trp Pro Gly
20 25 30
Ser Arg Cys Thr Ser Cys Ala Glu Arg Ala Arg Arg Ile Cys Lys Arg
35 40 45
Xaa Ser Arg Ser Leu Asn Arg Ser Ser Pro Ser Tyr Ala Ser Pro Xaa
50 55 60
Ser Pro Ala Gly Leu Pro Thr Ser Ser Pro Lys Ser Arg Leu Cys Ala
65 70 75 80
Pro Pro Ser Leu Ala Cys Ser Pro Leu Ser Arg Arg Ser Arg Ser Arg
85 90 95
Arg Cys Val Arg Arg Thr Arg Arg Arg Ser Phe Ser Arg Ser Ile Ser
100 105 110
Ala Pro Arg Arg Pro Ala Pro Phe Ala Gly Ala Ser Pro Ser Thr Ser
115 120 125
Ser Pro
130
```

(2) INFORMATION FOR SEQ ID NO:2184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1502516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2184:

Met	Ala	Arg	Ile	Lys	Val	His	Glu	Leu	Arg	Gly	Lys	Ser	Lys	Thr	Asp	
1				5				10					15			
Leu	Gln	Ala	Xaa	Xaa	Lys	Glu	Leu	Lys	Ser	Glu	Leu	Ser	Leu	Leu	Arg	
				20				25					30			
Val	Ala	Xaa	Val	Thr	Gly	Gly	Ala	Pro	Asn	Lys	Leu	Ser	Lys	Ile	Lys	
				35				40					45			
Ile	Val	Arg	Thr	Ser	Ile	Ala	Arg	Val	Leu	Thr	Val	Ile	Ser	Gln	Lys	
				50				55				60				
Gln	Lys	Ser	Ala	Leu	Arg	Glu	Ala	Tyr	Lys	Lys	Lys	Lys	Leu	Leu	Pro	
65				70				75							80	
Leu	Asp	Leu	Arg	Pro	Lys	Lys	Thr	Arg	Ala	Ile	Arg	Arg	Arg	Leu	Thr	
				85				90						95		
Lys	His	Gln	Leu	Ser	Leu	Lys	Thr	Glu	Arg	Glu	Lys	Lys	Arg	Glu	Lys	
				100				105						110		
Tyr	Phe	Pro	Met	Arg	Lys	Tyr	Ala	Ile	Lys	Ala						
				115				120								

(2) INFORMATION FOR SEQ ID NO:2185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..437

(D) OTHER INFORMATION: / Ceres Seq. ID 1502517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2185:

tccattgacg	tcgaggaatc	ggaaggactg	gtactttacat	cacaatccat	actacaattg	60
agcgaattct	tcttggagat	aaaagctctt	acgatcttgc	caaaactgta	aagaatttta	120
gatcccaacg	acctgggatg	gtccaaacag	aggaacaata	caagtcttgc	tacagggcaa	180
ttgctgtacg	agctgaaaga	cctgctaaat	tcagatcatt	gaggtgggtc	acatgagacg	240
gacagcaacg	ckkctagcat	tattacgttt	tttttagaca	tttctatgtg	aaggaacact	300
taccctttag	aggagtgaat	tagtcaatct	cagttctctt	taaacatagt	tgtgtctagt	360
caaaatctat	gtaataaaaa	atctatcata	tgtagaagta	tgctatgttt	tigactaatc	420
gttgctatta	ctaccgt					

(2) INFORMATION FOR SEQ ID NO:2186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1502518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2186:

His	Cys	Ser	Ala	Gly	Ile	Gly	Arg	Thr	Gly	Thr	Tyr	Ile	Thr	Ile	His	
1				5				10					15			
Thr	Thr	Ile	Glu	Arg	Ile	Leu	Leu	Gly	Asp	Lys	Ser	Ser	Tyr	Asp	Leu	
				20				25					30			
Ala	Lys	Thr	Val	Lys	Asn	Phe	Arg	Ser	Gln	Arg	Pro	Gly	Met	Val	Gln	
				35				40					45			
Thr	Glu	Glu	Gln	Tyr	Lys	Phe	Cys	Tyr	Arg	Ala	Ile	Ala	Val	Arg	Ala	

50 55 60
Glu Arg Pro Ala Lys Phe Arg Ser Leu Arg Trp Val Thr
65 70 75

(2) INFORMATION FOR SEQ ID NO:2187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..469
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2187:

attctccag	ccacaaatcg	atcggaacg	cacgcccctt	tctcttcgcc	ttttcgcgtc	60
gtccagatct	cagtcgttct	tcgctccatg	agctaggaat	ccgaggtgtc	ctctagggcta	120
agcgaagtgtg	gccggcggcg	gctaggatgg	gggtgatatc	cgggatgatg	atgggggtca	180
ttgttggcgt	cgcatcatgg	ccggctggag	ccgcgtcatg	cgccgacgca	gcacgaagcg	240
catcgccaag	gctgcggata	tcaaggtgct	tgggtctctc	agcagggacg	acctcaggaa	300
gctgtgcgnt	gataacttcc	cggagtgatg	atccttcccg	cagtttgagc	aggttaaatg	360
gttgaacaag	catctgagca	aactttggcc	ttttgttgta	gaagctgcaa	cagttagtgg	420
taagggaatc	cgttgaacca	ctgctagatg	attaccggcc	tccaggaat		

(2) INFORMATION FOR SEQ ID NO:2188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2188:

Met	Gly	Leu	Ile	Ser	Gly	Met	Met	Met	Gly	Val	Ile	Val	Gly	Val	Ala
1		5						10					15		
Ser	Trp	Pro	Ala	Gly	Ala	Ala	Ser	Arg	Cys	Ala	Asp	Ala	Ala	Arg	Ser
		20						25					30		
Ser	Pro	Arg	Leu	Arg	Ile	Ser	Arg	Cys	Leu	Gly	Leu	Ser	Ala	Gly	Thr
		35						40					45		
Thr	Ser	Gly	Ser	Cys	Ala	Xaa	Ile	Thr	Ser	Arg	Ser	Gly	Tyr	Pro	Ser
		50						55					60		
Arg	Ser	Leu	Ser	Arg	Leu	Asn	Gly								
65								70							

(2) INFORMATION FOR SEQ ID NO:2189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2189:

Met	Ala	Gly	Trp	Ser	Arg	Val	Met	Arg	Arg	Arg	Ser	Thr	Lys	Arg	Ile
1			5							10				15	
Ala	Lys	Ala	Ala	Asp	Ile	Lys	Val	Leu	Gly	Ser	Leu	Ser	Arg	Asp	Asp
			20							25				30	

Leu Arg Lys Leu Cys Xaa Asp Asn Phe Pro Glu Trp Ile Ser Phe Pro
35 40 45
Gln Phe Glu Gln Val Lys Trp Leu Asn Lys His Leu Ser Lys Leu Trp
50 55 60
Pro Phe Val Val Glu Ala Ala Thr Val Val Val Lys Gly Ile Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:2190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..72

- (D) OTHER INFORMATION: / Ceres Seq. ID 1502522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2190:

Met Arg Arg Arg Ser Thr Lys Arg Ile Ala Lys Ala Ala Asp Ile Lys
1 5 10 15
Val Leu Gly Ser Leu Ser Arg Asp Asp Leu Arg Lys Leu Cys Xaa Asp
20 25 30
Asn Phe Pro Glu Trp Ile Ser Phe Pro Gln Phe Glu Gln Val Lys Trp
35 40 45
Leu Asn Lys His Leu Ser Lys Leu Trp Pro Phe Val Val Glu Ala Ala
50 55 60
Thr Val Val Val Lys Gly Ile Arg
65 70

(2) INFORMATION FOR SEQ ID NO:2191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..419

- (D) OTHER INFORMATION: / Ceres Seq. ID 1502527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2191:

atagacagga agattgaatt tccaaatcct aacgaggatt cacgtttcga tatcttgaag 60
atccattcaa gaaaaatgaa cttagtcggt gccattgatc tgaaaaagat cgcggaaaaa 120
atgaatgggg cctcaggagc tgagctcaag gccgtctgca cagaggctgg aatgtttgct 180
cttcgtgaga gaaggggtgca cgttaccacag gaggactctcg agatggcagt ggccaaggtg 240
atgaagaaga acacggagaa gaacatgtcc ctgcgcaass tctggaagtg aggcctcgtgc 300
ccaccttcaa cggcctcccc gaagctagtgt gcagtcgctt catatccata tcttttacca 360
aagcagtgga atggtgtaac ggcagtctct ggacaatggt atctcaagtt gcgcgcgcgc

(2) INFORMATION FOR SEQ ID NO:2192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..96

- (D) OTHER INFORMATION: / Ceres Seq. ID 1502528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2192:

Ile Asp Arg Lys Ile Glu Phe Pro Asn Pro Asn Glu Asp Ser Arg Phe
1 5 10 15

Asp	Ile	Leu	Lys	Ile	His	Ser	Arg	Lys	Met	Asn	Leu	Met	Arg	Gly	Ile	
	20							25					30			
Asp	Leu	Lys	Lys	Ile	Ala	Glu	Lys	Met	Asn	Gly	Ala	Ser	Gly	Ala	Glu	
	35						40					45				
Leu	Lys	Ala	Val	Cys	Thr	Glu	Ala	Gly	Met	Phe	Ala	Leu	Arg	Glu	Arg	
	50					55				60						
Arg	Val	His	Val	Thr	Gln	Glu	Asp	Phe	Glu	Met	Ala	Val	Ala	Lys	Val	
	65				70				75					80		
Met	Lys	Lys	Asp	Thr	Glu	Lys	Asn	Met	Ser	Leu	Arg	Xaa	Xaa	Trp	Lys	
			85					90						95		

(2) INFORMATION FOR SEQ ID NO:2193:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..71
(D) OTHER INFORMATION: / Ceres Seq. ID 1502529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2193:

Met	Asn	Leu	Met	Arg	Gly	Ile	Asp	Leu	Lys	Lys	Ile	Ala	Glu	Lys	Met	
1				5				10					15			
Asn	Gly	Ala	Ser	Gly	Ala	Glu	Leu	Lys	Ala	Val	Cys	Thr	Glu	Ala	Gly	
			20				25					30				
Met	Phe	Ala	Leu	Arg	Glu	Arg	Arg	Val	His	Val	Thr	Gln	Glu	Asp	Phe	
		35				40					45					
Glu	Met	Ala	Val	Ala	Lys	Val	Met	Lys	Lys	Asp	Thr	Glu	Lys	Asn	Met	
		50				55					60					
Ser	Leu	Arg	Xaa	Xaa	Trp	Lys										
					70											

(2) INFORMATION FOR SEQ ID NO:2194:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..68
(D) OTHER INFORMATION: / Ceres Seq. ID 1502530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2194:

Met	Arg	Gly	Ile	Asp	Leu	Lys	Lys	Ile	Ala	Glu	Lys	Met	Asn	Gly	Ala	
1				5				10					15			
Ser	Gly	Ala	Glu	Leu	Lys	Ala	Val	Cys	Thr	Glu	Ala	Gly	Met	Phe	Ala	
			20				25					30				
Leu	Arg	Glu	Arg	Arg	Val	His	Val	Thr	Gln	Glu	Asp	Phe	Glu	Met	Ala	
		35				40					45					
Val	Ala	Lys	Val	Met	Lys	Lys	Asp	Thr	Glu	Lys	Asn	Met	Ser	Leu	Arg	
		50				55					60					
Xaa	Xaa	Trp	Lys													

(2) INFORMATION FOR SEQ ID NO:2195:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 511 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..511
(D) OTHER INFORMATION: / Ceres Seq. ID 1502542

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2195:

gcaccgaggc	cacagcctcg	cgtcgctgcc	ccacagccac	gcgagccsnc	gccgatccgc	60
gagcgagat	cgcgaagcca	ggcggcgag	agggagctcg	agggcgccga	ggaagcggtt	120
cgacacgtcg	ctgatttccc	tggggaagag	atggggctct	cctttggtta	gctgttcacg	180
cgctcttccg	ccaagaagga	gatgaggatt	ctcatgtctg	ggctcgatgc	cgccggttaag	240
accacatcc	tctacaagct	caagctcgcc	gagatcgctca	ccaccatccc	cactatcgga	300
ttcaatgtg	aaactgttga	gtataagaac	attagcttca	ctgtttggga	tggtgtgtgc	360
caggacaaga	tcaggccctc	gtggaggcac	tactttcaga	acacacaggg	acttattttt	420
gtgttagaca	gcaacgacag	ggaacgtgtt	gttgaggcta	gagatgagct	ccacaggatg	480
ctgaatgagg	atgagctcgc	tgacgctgtg	c			

- (2) INFORMATION FOR SEQ ID NO:2196:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..170
(D) OTHER INFORMATION: / Ceres Seq. ID 1502543

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2196:

Ala	Pro	Arg	Pro	Gln	Pro	Arg	Val	Val	Ala	Pro	Gln	Pro	Arg	Glu	Xaa
1			5					10						15	
Xaa	Pro	Ile	Arg	Glu	Arg	Arg	Ser	Arg	Ser	Gln	Ala	Ala	Xaa	Arg	Glu
			20					25				30			
Leu	Glu	Ala	Ala	Glu	Glu	Gly	Val	Arg	Thr	Val	Ala	Asp	Phe	Pro	Gly
			35					40				45			
Glu	Glu	Met	Gly	Leu	Ser	Phe	Gly	Lys	Leu	Phe	Ser	Arg	Leu	Phe	Ala
			50					55				60			
Lys	Lys	Glu	Met	Arg	Ile	Leu	Met	Val	Gly	Leu	Asp	Ala	Ala	Gly	Lys
			65					70				75			80
Thr	Thr	Ile	Leu	Tyr	Lys	Leu	Lys	Leu	Gly	Glu	Ile	Val	Thr	Thr	Ile
			85					90						95	
Pro	Thr	Ile	Gly	Phe	Asn	Val	Glu	Thr	Val	Glu	Tyr	Lys	Asn	Ile	Ser
			100					105					110		
Phe	Thr	Val	Trp	Asp	Val	Gly	Gly	Gln	Asp	Lys	Ile	Arg	Pro	Leu	Trp
			115					120				125			
Arg	His	Tyr	Phe	Gln	Asn	Thr	Gln	Gly	Leu	Ile	Phe	Val	Val	Asp	Ser
			130					135				140			
Asn	Asp	Arg	Glu	Arg	Val	Val	Glu	Ala	Arg	Asp	Glu	Leu	His	Arg	Met
			145					150			155				160
Leu	Asn	Glu	Asp	Glu	Leu	Arg	Asp	Ala	Val						
			165					170							

- (2) INFORMATION FOR SEQ ID NO:2197:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..120
(D) OTHER INFORMATION: / Ceres Seq. ID 1502544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2197:

Met	Gly	Leu	Ser	Phe	Gly	Lys	Leu	Phe	Ser	Arg	Leu	Phe	Ala	Lys	Lys
1			5					10						15	
Glu	Met	Arg	Ile	Leu	Met	Val	Gly	Leu	Asp	Ala	Ala	Gly	Lys	Thr	Thr
			20					25					30		
Ile	Leu	Tyr	Lys	Leu	Lys	Leu	Gly	Glu	Ile	Val	Thr	Thr	Ile	Pro	Thr
			35					40					45		
Ile	Gly	Phe	Asn	Val	Glu	Thr	Val	Glu	Tyr	Lys	Asn	Ile	Ser	Phe	Thr
			50					55				60			
Val	Trp	Asp	Val	Gly	Gly	Gln	Asp	Lys	Ile	Arg	Pro	Leu	Trp	Arg	His
								70				75			80
Tyr	Phe	Gln	Asn	Thr	Gln	Gly	Leu	Ile	Phe	Val	Val	Asp	Ser	Asn	Asp
															95
Arg	Glu	Arg	Val	Val	Glu	Ala	Arg	Asp	Glu	Leu	His	Arg	Met	Leu	Asn
															110
Glu	Asp	Glu	Leu	Arg	Asp	Ala	Val								
															120

(2) INFORMATION FOR SEQ ID NO:2198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2198:

Met	Arg	Ile	Leu	Met	Val	Gly	Leu	Asp	Ala	Ala	Gly	Lys	Thr	Thr	Ile
1			5					10						15	
Leu	Tyr	Lys	Leu	Lys	Leu	Gly	Glu	Ile	Val	Thr	Thr	Ile	Pro	Thr	Ile
			20					25					30		
Gly	Phe	Asn	Val	Glu	Thr	Val	Glu	Tyr	Lys	Asn	Ile	Ser	Phe	Thr	Val
			35					40					45		
Trp	Asp	Val	Gly	Gly	Gln	Asp	Lys	Ile	Arg	Pro	Leu	Trp	Arg	His	Tyr
			50					55				60			
Phe	Gln	Asn	Thr	Gln	Gly	Leu	Ile	Phe	Val	Val	Asp	Ser	Asn	Asp	Arg
								70				75			80
Glu	Arg	Val	Val	Glu	Ala	Arg	Asp	Glu	Leu	His	Arg	Met	Leu	Asp	Glu
															95
Asp	Glu	Leu	Arg	Asp	Ala	Val									
															100

(2) INFORMATION FOR SEQ ID NO:2199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..488
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2199:

aggaggaggcg	cgccatggag	cggggggcac	ctgcgcgtgc	tcgcgcgcgc	cacgctgggtg	60
cagacgttcg	gccagcgcaa	ccacgtgtgc	ctgcaggagc	gtcccatcac	cgtcccgccc	120
tacgccgacc	cgggcaagat	gcaggcgcac	ctcatcagcc	ccggcacgcc	gcgctccatc	180
ttcgtctact	tcaggggcct	cttctacgac	atgggcaacg	accccgaggg	cggtactact	240
gccagggggc	tcgcgcgtcg	gtgtgggaga	acttcaagga	caaccgcgtg	ttcgacatct	300
cgacggagca	cccgtcgacg	tactacgagg	acatgcagcg	cgccatcttc	tgccgtgtgc	360

cgctgggggtg ggcgcctctg agcccccggc tgggtggaggc ggtgggtgttc ggggtcatcc 420
ccgtcatcat cgcgcagac atcgtgctgc cgttcgcgga cgccatcccc tggggaggaca 480
tcagcgtg

(2) INFORMATION FOR SEQ ID NO:2200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1502574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2200:

Arg	Arg	Ser	Ala	Pro	Trp	Ser	Gly	Gly	Ile	Leu	Pro	Leu	Leu	Arg	Arg
1				5					10					15	
Ala	Thr	Leu	Val	Gln	Thr	Phe	Gly	Gln	Arg	Asn	His	Val	Cys	Leu	Gln
			20					25					30		
Asp	Gly	Ser	Ile	Thr	Val	Pro	Pro	Tyr	Ala	Asp	Pro	Gly	Lys	Met	Gln
			35				40					45			
Ala	His	Leu	Ile	Ser	Pro	Gly	Thr	Pro	Arg	Ser	Ile	Phe	Val	Tyr	Phe
			50				55				60				
Arg	Gly	Leu	Phe	Tyr	Asp	Met	Gly	Asn	Asp	Pro	Glu	Gly	Gly	Tyr	Tyr
			65			70			75					80	
Ala	Arg	Gly	Leu	Ala	Arg	Arg	Cys	Gly	Arg	Thr	Ser	Arg	Thr	Thr	Arg
			85						90					95	
Cys	Ser	Thr	Ser	Arg	Arg	Ser	Thr	Arg	Arg	Arg	Thr	Thr	Arg	Thr	Cys
			100					105					110		
Ser	Ala	Pro	Ser	Ser	Ala	Cys	Ala	Arg	Trp	Gly	Gly	Arg	Pro	Gly	Ala
			115				120					125			
Pro	Gly	Trp	Trp	Arg	Arg	Trp	Cys	Ser	Gly	Ala	Ser	Pro	Ser	Ser	Ser
			130				135					140			
Pro	Thr	Thr	Ser	Cys	Cys	Arg	Ser	Arg	Thr	Pro	Ser	Pro	Gly	Arg	Thr
				150						155				160	
Ser	Ala														

(2) INFORMATION FOR SEQ ID NO:2201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1502575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2201:

Gly	Gly	Ala	Arg	His	Gly	Ala	Gly	Ala	Ser	Cys	Arg	Cys	Ser	Ala	Ala
1				5				10						15	
Pro	Arg	Trp	Cys	Arg	Arg	Ser	Ala	Ser	Ala	Thr	Thr	Cys	Ala	Cys	Arg
			20					25					30		
Thr	Ala	Pro	Ser	Pro	Ser	Arg	Pro	Thr	Pro	Thr	Arg	Ala	Arg	Cys	Arg
			35				40					45			
Arg	Thr	Ser	Ser	Ala	Pro	Ala	Arg	Arg	Ala	Pro	Ser	Ser	Ser	Thr	Ser
			50				55					60			
Gly	Ala	Ser	Ser	Thr	Thr	Trp	Ala	Thr	Thr	Pro	Arg	Ala	Ala	Thr	Thr
			65			70			75					80	
Pro	Gly	Ala	Ser	Arg	Val	Gly	Val	Gly	Glu	Leu	Gln	Gly	Gln	Pro	Ala
				85					90					95	

Val Arg His Leu Asp Gly Ala Pro Val Asp Val Leu Arg Gly His Ala
100 105 110
Ala Arg His Leu Leu Pro Val Pro Ala Gly Val Gly Ala Leu Glu Pro
115 120 125
Pro Ala Gly Gly Gly Gly Val Arg Val His Pro Arg His His Arg
130 135 140
Arg Arg His Arg Ala Ala Val Arg Gly Arg His Pro Leu Gly Gly His
145 150 155 160
Gln Arg

(2) INFORMATION FOR SEQ ID NO:2202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1502576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2202:

Glu Glu Arg Ala Met Glu Arg Gly His Pro Ala Ala Pro Pro Arg
1 5 10 15
His Ala Gly Ala Asp Val Arg Pro Ala Gln Pro Arg Val Pro Ala Gly
20 25 30
Arg Leu His His Arg Pro Ala Leu Arg Arg Pro Gly Gln Asp Ala Gly
35 40 45
Ala Pro His Gln Pro Arg His Ala Ala Leu His Leu Arg Leu Leu Gln
50 55 60
Gly Pro Leu Leu Arg His Gly Gln Arg Pro Arg Gly Arg Leu Leu Arg
65 70 75 80
Gln Gly Pro Arg Ala Ser Val Trp Glu Asn Phe Lys Asp Asn Pro Leu
85 90 95
Phe Asp Ile Ser Thr Glu His Pro Ser Thr Tyr Tyr Glu Asp Met Gln
100 105 110
Arg Ala Ile Phe Cys Leu Cys Pro Leu Gly Trp Ala Pro Trp Ser Pro
115 120 125
Arg Leu Val Glu Ala Val Val Phe Gly Cys Ile Pro Val Ile Ile Ala
130 135 140
Asp Asp Ile Val Leu Pro Phe Ala Asp Ala Ile Pro Trp Glu Asp Ile
145 150 155 160
Ser Val

(2) INFORMATION FOR SEQ ID NO:2203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..493

(D) OTHER INFORMATION: / Ceres Seq. ID 1502613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2203:

ctctccgtct ccggtctcca gtctcgctgc ttccacaagt ccacaaccgt accagcacca 60
ccgcgcctat gcgtctctcg ccgatccmga tgccgccacg ccaccatccg cncgcgacgc 120
ggagcccaga cggaaggcag tccgcgtggt ggtgaagggg ccgctcacgg gggtgggggtt 180
ccgcgactgg actgcgtcac gccgcgagtc ctcggctcgc cggctggggtc cgcaaccgcc 240
gtgacggcag tgtggaggcc ctctctctcg gagaccgcc gaagatcgaa gacatgataa 300

cccgccgcct ccccgctggc cccccagccg ccaccgtcac cgccgtcgtc ccgtccackg 360
ccgagcccggt ggtatccgtc caccggcttc ggagatcaag ttcaccgtct gacccccccg 420
tcccgcgaca ggttcgctgc tcgcccgcgc ggtcttgaac ggtctattgc tgcactacta 480
ctgcgaatct gcg

(2) INFORMATION FOR SEQ ID NO:2204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2204:

Leu	Ser	Val	Ser	Gly	Leu	Gln	Ser	Arg	Cys	Phe	His	Lys	Ser	Thr	Thr	
				5						10					15	
Val	Pro	Ala	Pro	Pro	Arg	His	Gly	Val	Leu	Arg	Arg	Ser	Xaa	Cys	Arg	
				20				25					30			
His	Ala	Thr	Ile	Arg	Xaa	Ala	Ala	Gly	Ala	Arg	Thr	Glu	Gly	Ser	Pro	
				35			40						45			
Arg	Gly	Gly	Glu	Gly	Ala	Arg	His	Gly	Gly	Gly	Val	Pro	Arg	Leu	Asp	
				50			55				60					
Cys	Val	Thr	Ala	Glu	Ser	Leu	Gly	Ser	Pro	Ala	Gly	Ser	Ala	Thr	Ala	
				65		70			75					80		
Val	Thr	Ala	Val	Trp	Arg	Pro	Ser	Ser	Pro	Glu	Thr	Pro	Arg	Arg	Ser	
				85					90					95		
Lys	Thr															

(2) INFORMATION FOR SEQ ID NO:2205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2205:

Ser	Pro	Ser	Pro	Val	Ser	Ser	Leu	Ala	Ala	Ser	Thr	Ser	Pro	Gln	Pro	
				5						10				15		
Tyr	Gln	His	His	Arg	Ala	Met	Ala	Ser	Ser	Ala	Asp	Xaa	Asp	Ala	Ala	
				20				25					30			
Thr	Pro	Pro	Ser	Xaa	Pro	Gln	Pro	Glu	Pro	Ala	Arg	Lys	Ala	Val	Arg	
				35			40					45				
Val	Val	Val	Lys	Gly	Arg	Val	Thr	Gly	Val	Gly	Phe	Arg	Asp	Trp	Thr	
				50			55				60					
Ala	Ser	Arg	Pro	Ser	Arg	Ser	Ala	Arg	Arg	Leu	Gly	Pro	Gln	Pro	Pro	
				65		70				75				80		

(2) INFORMATION FOR SEQ ID NO:2206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1502616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2206:

Met Ala Ser Ser Ala Asp Xaa Asp Ala Ala Thr Pro Pro Ser Xaa Pro
1 5 10 15
Gln Pro Glu Pro Ala Arg Lys Ala Val Arg Val Val Val Lys Gly Arg
20 25 30
Val Thr Gly Val Gly Phe Arg Asp Trp Thr Ala Ser Arg Pro Ser Arg
35 40 45
Ser Ala Arg Arg Leu Gly Pro Gln Pro Pro
50 55

(2) INFORMATION FOR SEQ ID NO:2207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1502621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2207:

aagatcaagc caccaccacc gccagcaaga gcagagaggc gagaccgcga gagtgtacgt 60
gccaccagca gcagcagcaa tggccgcgcg cggcaccacc tctctatcct cccaccgtct 120
ctctctctcc cgccagcagg sscctcccta cgatgccgcc tctcttctct cggccagccc 180
agaaggcccg gc

(2) INFORMATION FOR SEQ ID NO:2208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1502622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2208:

Lys Ile Lys Pro Pro Pro Pro Ala Arg Ala Glu Arg Arg Asp Arg
1 5 10 15
Glu Ser Val Arg Ala Thr Ser Ser Ser Ser Asn Gly Arg Arg Arg His
20 25 30
His Leu Leu Ile Leu Pro Pro Ala Pro Pro Leu Pro Pro Ala Xaa Xaa
35 40 45
Ser Leu Arg Cys Arg Leu Ser Phe Leu Gly Gln Pro Arg Arg Pro Gly
50 55 60

(2) INFORMATION FOR SEQ ID NO:2209:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1502623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2209:

Arg Ser Ser His His Arg Gln Gln Glu Gln Arg Gly Glu Thr Ala
1 5 10 15
Arg Val Tyr Val Pro Pro Ala Ala Ala Met Ala Ala Ala Thr
20 25 30
Thr Ser Ser Ser Ser His Leu Leu Leu Ser Arg Gln Xaa Pro
35 40 45
Pro Tyr Asp Ala Ala Ser Pro Ser Ser Ala Ser Pro Glu Gly Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:2210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1502624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2210:

Asp Gln Ala Thr Thr Thr Ala Ser Lys Ser Arg Glu Ala Arg Pro Arg
1 5 10 15
Glu Cys Thr Cys His Gln Gln Gln Gln Trp Pro Pro Pro Pro
20 25 30
Pro Pro His Pro Pro Thr Cys Ser Ser Ser Pro Ala Ser Arg Xaa Leu
35 40 45
Pro Thr Met Pro Pro Leu Leu Pro Arg Pro Ala Gln Lys Ala Arg
50 55 60

(2) INFORMATION FOR SEQ ID NO:2211:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..327

(D) OTHER INFORMATION: / Ceres Seq. ID 1502635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2211:

agtgtgtgtg cctagcgccg ccgccgcccc aactgcctt gcgtgactga aagctcgctg 60
gcttcgctcc acgcgagaag cgagagcatg gacacccagg tgaagcttgc tgtgtggtg 120
aaggtgatgg gcaggaccgg ctccaggggg caggbgacc aggtcagagt taagttcttg 180
gatgaccaga accggctcat catgaggaat gtcaaggggg ccgtccgcga ggggtgacatc 240
ctcaccctgc tcgagtcga gatggatgcc akgagggtgc gctgaagccc tagcgttctt 300
gggtcatccaa gaacttaact ctgacct

(2) INFORMATION FOR SEQ ID NO:2212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1502636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2212:

Met Asp Thr Gln Val Lys Leu Ala Val Val Val Lys Val Met Gly Arg

1 5 10 15
Thr Gly Ser Arg Gly Gln Xaa Thr Gln Val Arg Val Lys Phe Leu Asp
20 25 30
Asp Gln Asn Arg Leu Ile Met Arg Asn Val Lys Gly Pro Val Arg Glu
35 40 45
Gly Asp Ile Leu Thr Leu Leu Glu Ser Glu Met Asp Ala Xaa Arg Leu
50 55 60

Arg
65

(2) INFORMATION FOR SEQ ID NO:2213:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..52
(D) OTHER INFORMATION: / Ceres Seq. ID 1502637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2213:

Met Gly Arg Thr Gly Ser Arg Gly Gln Xaa Thr Gln Val Arg Val Lys
1 5 10 15
Phe Leu Asp Asp Gln Asn Arg Leu Ile Met Arg Asn Val Lys Gly Pro
20 25 30
Val Arg Glu Gly Asp Ile Leu Thr Leu Leu Glu Ser Glu Met Asp Ala
35 40 45
Xaa Arg Leu Arg
50

(2) INFORMATION FOR SEQ ID NO:2214:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..39
(D) OTHER INFORMATION: / Ceres Seq. ID 1502638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2214:

Met Ser Arg Gly Pro Ser Ala Arg Val Thr Ser Ser Pro Cys Ser Ser
1 5 10 15
Pro Arg Trp Met Pro Xaa Gly Cys Ala Glu Ala Leu Ala Phe Leu Val
20 25 30
Ile Gln Glu Leu Asn Ser Asp
35

(2) INFORMATION FOR SEQ ID NO:2215:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 454 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..454
(D) OTHER INFORMATION: / Ceres Seq. ID 1502643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2215:

gcgtgtgcaa attacgttcc ctctagtctc tactctagcc ccctctctct ctcacacaca
cacacacccc tatcacttgg actgtgctag tataggtagc cgccgtgtaa tggagcagga

60
120

gctcagcctt gagtcacccc tcttcacccc ctggtctctg ccggaaccgc cgggctattt 180
cgctcgcacg tactgcgacc gcaagttctt cacctcgcag gctctcggtg gccaccagaa 240
cgcgacacaag tacgagcgcm sactggccaa gcgccggcgg agatcgccac cgccctgcgc 300
gcgcacgggg cgcccgccac cgccacgggc gtccaggacg cgccgctatg ggctctcgcg 360
atgtccccgc cagccccaag gcacgggtag cgggtccgcac aagagcgcaa caagatgga 420
taagcacaag ggcgctgctg atgatgccc tccc

(2) INFORMATION FOR SEQ ID NO:2216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1502644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2216:

Leu Leu Gln Ile Thr Phe Pro Leu Val Ser Thr Leu Ala Pro Ser Leu
1 5 10 15
Ser His Thr His Thr His Pro Tyr His Leu Asp Cys Ala Ser Ile Gly
20 25 30
Ser Arg Arg Val Met Glu Gln Glu Leu Ser Leu Glu Leu Thr Leu Phe
35 40 45
His Pro Ser Val Ser Pro Glu Pro Pro Gly Tyr Phe Val Cys Thr Tyr
50 55 60
Cys Asp Arg Lys Phe Phe Thr Ser Gln Ala Leu Gly Gly His Gln Asn
65 70 75 80
Ala His Lys Tyr Glu Arg Xaa Leu Ala Lys Arg Arg Arg Ser Pro
85 90 95
Pro Pro Cys Ala Arg Thr Gly Arg Pro Pro Pro Arg Ala Ser Arg
100 105 110
Thr Arg Arg Tyr Gly Leu Ser Arg Cys Pro Arg Gln Pro Gln Gly Thr
115 120 125
Gly Ser Gly Ala Asp Lys Ser Ala Thr Arg Met Asp Lys His Lys Ala
130 135 140
Pro Ala Asp Asp Ala Ala Pro
145 150

(2) INFORMATION FOR SEQ ID NO:2217:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1502645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2217:

Met Glu Gln Glu Leu Ser Leu Glu Leu Thr Leu Phe His Pro Ser Val
1 5 10 15
Ser Pro Glu Pro Pro Gly Tyr Phe Val Cys Thr Tyr Cys Asp Arg Lys
20 25 30
Phe Phe Thr Ser Gln Ala Leu Gly Gly His Gln Asn Ala His Lys Tyr
35 40 45
Glu Arg Xaa Leu Ala Lys Arg Arg Arg Ser Pro Pro Pro Cys Ala
50 55 60
Arg Thr Gly Arg Pro Pro Pro Pro Arg Ala Ser Arg Thr Arg Arg Tyr
65 70 75 80
Gly Leu Ser Arg Cys Pro Arg Gln Pro Gln Gly Thr Gly Ser Gly Ala

85 90 95
Asp Lys Ser Ala Thr Arg Met Asp Lys His Lys Ala Pro Ala Asp Asp
100 105 110
Ala Ala Pro
115

(2) INFORMATION FOR SEQ ID NO:2218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..451
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2218:

atcagcagac	caccacccaa	tcacaccagc	tctctctaga	gctagccctc	tcttctccca	60
acaacttggtg	atccctctcc	atctctctca	gccttcttca	ctgaatttct	ggccgggtcga	120
tcgtcatgca	cagctacaga	gccatgcacc	cgtacactca	tcactcgtac	cagcaccaca	180
cgcgggccgn	ggcccacca	agcacggcca	cggccacgga	catggacatg	gccatggcga	240
cgaggaggac	gaccagtcac	gctgctctcc	tcctctggc	ctctggcac	caccacggca	300
acgcgctgct	tcattgcgct	gctcgtctcc	cccgatctgc	gccassgcca	ccaccacctc	360
tatggcagcc	gctgcctcct	cccccgcttc	ttacccttgg	gctcaccacc	caaagccttt	420
acaataatgc	cggctggggc	ggtaggggag	c			

(2) INFORMATION FOR SEQ ID NO:2219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2219:

Ser	Ala	Asp	His	His	Pro	Ile	Thr	Pro	Ala	Leu	Ser	Arg	Ala	Ser	Pro	
1			5					10					15			
Leu	Phe	Leu	Gln	His	Leu	Leu	Ile	Pro	Ser	His	Leu	Leu	Lys	Pro	Ser	
			20					25					30			
Ser	Leu	Asn	Phe	Trp	Pro	Val	Asp	Arg	His	Ala	Gln	Leu	Gln	Ser	His	
			35				40					45				
Ala	Pro	Val	His	Ser	Ser	Leu	Val	Pro	Ala	Pro	His	Arg	Gly	Xaa	Ala	
			50				55					60				
Pro	Thr	Lys	His	Gly	His	Gly	His	Gly	His	Gly	His	Gly	His	Gly	Asp	
			65				70					75			80	
Glu	Glu	Asp	Asp	Gln	Ser	Cys	Cys	Ser	Ser	Pro	Ser	Gly	Leu	Leu	Ala	
				85				90					95			
Pro	Pro	Arg	Gln	Arg	Ala	Ala	Ser	Ser	Ala	Cys	Ser	Ser	Pro	Pro	Ile	
			100				105						110			
Cys	Ala	Xaa	Ala	Thr	Thr	Thr	Ser	Met	Ala	Ala	Ala	Ala	Ser	Ser	Pro	
			115				120					125				
Ala	Ser	Tyr	Pro	Trp	Ala	His	Pro	Pro	Lys	Pro	Leu	Gln				
			130				135					140				

(2) INFORMATION FOR SEQ ID NO:2220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1502651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2220:

Met	His	Ser	Tyr	Arg	Ala	Met	His	Pro	Tyr	Thr	His	His	Ser	Tyr	Gln	
1			5						10					15		
His	His	Thr	Ala	Ala	Xaa	Arg	Pro	Pro	Ser	Thr	Ala	Thr	Ala	Thr	Asp	
			20					25					30			
Met	Asp	Met	Ala	Met	Ala	Thr	Arg	Arg	Thr	Thr	Ser	His	Ala	Ala	Pro	
			35					40				45				
Leu	Pro	Leu	Ala	Ser	Trp	His	His	His	Gly	Asn	Ala	Leu	Leu	His	Arg	
			50				55				60					
Arg	Ala	Arg	Leu	Pro	Arg	Ser	Ala	Pro	Xaa	Pro	Pro	Pro	Pro	Leu	Trp	
			65				70			75				80		
Gln	Pro	Leu	Pro	Pro	Pro	Pro	Leu	Leu	Thr	Leu	Gly	Leu	Thr	His	Gln	
						85			90					95		
Ser	Leu	Tyr	Asn	Asn	Ala	Gly	Cys	Gly	Gly	Arg	Gly					
			100					105								

(2) INFORMATION FOR SEQ ID NO:2221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1502652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2221:

Met	His	Pro	Tyr	Thr	His	His	Ser	Tyr	Gln	His	His	Thr	Ala	Ala	Xaa	
1			5						10						15	
Arg	Pro	Pro	Ser	Thr	Ala	Thr	Ala	Thr	Asp	Met	Asp	Met	Ala	Met	Ala	
			20					25					30			
Thr	Arg	Arg	Thr	Thr	Ser	His	Ala	Ala	Pro	Leu	Pro	Leu	Ala	Ser	Trp	
			35				40					45				
His	His	His	Gly	Asn	Ala	Leu	Leu	His	Arg	Arg	Ala	Arg	Leu	Pro	Arg	
			50				55				60					
Ser	Ala	Pro	Xaa	Pro	Pro	Pro	Pro	Leu	Trp	Gln	Pro	Leu	Pro	Pro	Pro	
			65				70			75				80		
Pro	Leu	Leu	Thr	Leu	Gly	Leu	Thr	His	Gln	Ser	Leu	Tyr	Asn	Asn	Ala	
				85					90					95		
Gly	Cys	Gly	Gly	Arg	Gly											
			100													

(2) INFORMATION FOR SEQ ID NO:2222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 443 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..443

(D) OTHER INFORMATION: / Ceres Seq. ID 1502653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2222:

ggggaggtag	tgatatcaaa	gggtgataat	ccagatgctg	ttgttctcgg	tctaatggct	60
gctgggtgaag	casstgtgca	tctgttcatg	gtgcgaatag	gctaggcgca	aattcgcttc	120
ttgacatag	tgtttttggc	agagcttctg	caaacagggt	agcagatatt	tctaaaccag	180

gtgagaagca gaaacctctg gaaaaagatg ctggagaaaa gaccatagcc tgggtggaca 240
agctgaggaa tgcgaatggg tcattgccaa cttccaagat ccgtctcaac atgcagcgtg 300
ttatgcaaaa taatgctgct gtattccgta cacaagaata cacttgaaga aggttggtag 360
ctgattagca aaacatggga aagttttcca tgatgtgaag ctcagttgac cggagtctca 420
tttggaaact tgacctgata gag

(2) INFORMATION FOR SEQ ID NO:2223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..34

(D) OTHER INFORMATION: / Ceres Seq. ID 1502654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2223:

Gly Glu Val Val Asp Ile Lys Gly Asp Asn Pro Asp Ala Val Val Pro
1 5 10 15
Gly Leu Met Ala Ala Gly Glu Ala Xaa Val His Leu Phe Met Val Arg
20 25 30
Ile Gly

(2) INFORMATION FOR SEQ ID NO:2224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1502655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2224:

Met Arg Met Gly His Cys Gln Leu Pro Arg Ser Val Ser Thr Cys Ser
1 5 10 15
Val Leu Cys Lys Ile Met Leu Leu Tyr Ser Val His Lys Asn Thr Leu
20 25 30
Glu Glu Gly Cys Glu Leu Ile Ser Lys Thr Trp Glu Ser Phe Pro
35 40 45

(2) INFORMATION FOR SEQ ID NO:2225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45

(D) OTHER INFORMATION: / Ceres Seq. ID 1502656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2225:

Met Gly His Cys Gln Leu Pro Arg Ser Val Ser Thr Cys Ser Val Leu
1 5 10 15
Cys Lys Ile Met Leu Leu Tyr Ser Val His Lys Asn Thr Leu Glu Glu
20 25 30
Gly Cys Glu Leu Ile Ser Lys Thr Trp Glu Ser Phe Pro
35 40 45

(2) INFORMATION FOR SEQ ID NO:2226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..386
(D) OTHER INFORMATION: / Ceres Seq. ID 1502682
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2226:
ttccccctcc ctctgccaat ctggccagct agccagccca gtccccacgc ccattcccatc 60
ccattctaaa actgcatcga atctctgcgc cgcacccgct agactcagcc gacgssatgc 120
cgccgcccac ctccgctccc cgctctgcgc ttcccgcaat ggcccgatcc cagaccacga 180
cccagtcaca gggagaccct gacttccgct cctcatctc cgacctcacc tccctgctcc 240
tccactcccc cgccagcgcc ggccgcggtg gctccggacc cgtcttctcc tctctctccc 300
tttccatccc cactcccaaa cccaagccga accccagtcc cacatcagca ggcgcgcgca 360
ccccgctggc gcgcgcggcc atcggg
(2) INFORMATION FOR SEQ ID NO:2227:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..128
(D) OTHER INFORMATION: / Ceres Seq. ID 1502683
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2227:
Ser Pro Ser Leu Cys Gln Ser Gly Gln Leu Ala Ser Pro Val Pro Thr
1 5 10 15
Pro Ile Pro Ser His Leu Lys Thr Ala Ser Asn Pro Arg Arg Arg Thr
20 25 30
Ala Arg Leu Ser Arg Xaa Xaa Ala Ala Gln Leu Arg Ser Pro Pro
35 40 45
Arg Ala Ser Arg Asn Gly Pro Ile Pro Asp Pro Asp Pro Val Pro Gly
50 55 60
Arg Pro Arg Leu Pro Val Pro His Leu Arg Pro His Leu Pro Ala Pro
65 70 75 80
Pro Leu Pro Arg Gln Arg Arg Arg Arg Trp Leu Arg Thr Arg Leu Leu
85 90 95
Leu Leu Leu Pro Phe His Pro His Ser Gln Thr Gln Ala Glu Pro Gln
100 105 110
Ser His Ile Ser Ser Ala Ala Asp Pro Ala Gly Ala Arg Gly His Arg
115 120 125
(2) INFORMATION FOR SEQ ID NO:2228:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..90
(D) OTHER INFORMATION: / Ceres Seq. ID 1502684
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2228:
Met Pro Pro Pro Asn Ser Ala Pro Arg Leu Ala Leu Pro Ala Met Ala
1 5 10 15

Arg Ser Gln Thr Gln Thr Gln Ser Gln Gly Asp Leu Asp Phe Pro Ser
20 25 30
Leu Ile Ser Asp Leu Thr Ser Leu Leu Leu His Ser Pro Ala Ser Ala
35 40 45
Gly Ala Gly Gly Ser Gly Pro Val Phe Ser Ser Ser Leu Ser Ile
50 55 60
Pro Thr Pro Lys Pro Lys Pro Asn Pro Ser Pro Thr Ser Ala Ala Pro
65 70 75 80
Pro Thr Pro Leu Ala Arg Ala Ala Ile Gly
85 90

(2) INFORMATION FOR SEQ ID NO:2229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1502685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2229:

Met Ala Arg Ser Gln Thr Gln Thr Gln Ser Gln Gly Asp Leu Asp Phe
1 5 10 15
Pro Ser Leu Ile Ser Asp Leu Thr Ser Leu Leu Leu His Ser Pro Ala
20 25 30
Ser Ala Gly Ala Gly Gly Ser Gly Pro Val Phe Ser Ser Ser Leu
35 40 45
Ser Ile Pro Thr Pro Lys Pro Lys Pro Asn Pro Ser Pro Thr Ser Ala
50 55 60
Ala Pro Pro Thr Pro Leu Ala Arg Ala Ala Ile Gly
65 70 75

(2) INFORMATION FOR SEQ ID NO:2230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..491

(D) OTHER INFORMATION: / Ceres Seq. ID 1502713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2230:

ttgatgatga ggagaggccc tatttaccta agcacattct ctacaggcaa aaggaaacagt 60
tcagtgatgg tgttgggtat agttggatcg atggattgaa ggaccatgcc agccaacatg 120
tctccgattc catgatgatg aatgctggct ttgtttaccg agagaacaca cccacaacaa 180
aagaagggtg ctactacaga atgatattcg agaaattctt tcccaagcct gcagcaagggt 240
caactgttcc tggagggtcct agtgtggcct gcagcactgc caaagctggt gaatgggatg 300
catcctggtc caagaacctt gatccttctg ggcgtgctgc ttgggtgttt cacgatgctg 360
cgtatgaaga cactgcaggg gaaactcctg cctctgctga tctgtctca gacaagggcc 420
ctgctccagc tattggcgaa asstaggac acccgttgct tcagccacag ctgtctaacc 480
ttatgtttat c

(2) INFORMATION FOR SEQ ID NO:2231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..147
(D) OTHER INFORMATION: / Ceres Seq. ID 1502714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2231:

Asp Asp Glu Glu Arg Pro Tyr Leu Pro Lys His Ile Leu Tyr Arg Gln
1 5 10 15
Lys Glu Gln Phe Ser Asp Gly Val Gly Tyr Ser Trp Ile Asp Gly Leu
20 25 30
Lys Asp His Ala Ser Gln His Val Ser Asp Ser Met Met Met Asn Ala
35 40 45
Gly Phe Val Tyr Pro Glu Asn Thr Pro Thr Thr Lys Glu Gly Tyr Tyr
50 55 60
Tyr Arg Met Ile Phe Glu Lys Phe Phe Pro Lys Pro Ala Ala Arg Ser
65 70 75 80
Thr Val Pro Gly Gly Pro Ser Val Ala Cys Ser Thr Ala Lys Ala Val
85 90 95
Glu Trp Asp Ala Ser Trp Ser Lys Asn Leu Asp Pro Ser Gly Arg Ala
100 105 110
Ala Leu Gly Val His Asp Ala Ala Tyr Glu Asp Thr Ala Gly Glu Thr
115 120 125
Pro Ala Ser Ala Asp Pro Val Ser Asp Lys Gly Leu Arg Pro Ala Ile
130 135 140
Gly Glu Xaa
145

(2) INFORMATION FOR SEQ ID NO:2232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..104
(D) OTHER INFORMATION: / Ceres Seq. ID 1502715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2232:

Met Met Met Asn Ala Gly Phe Val Tyr Pro Glu Asn Thr Pro Thr Thr
1 5 10 15
Lys Glu Gly Tyr Tyr Tyr Arg Met Ile Phe Glu Lys Phe Phe Pro Lys
20 25 30
Pro Ala Ala Arg Ser Thr Val Pro Gly Gly Pro Ser Val Ala Cys Ser
35 40 45
Thr Ala Lys Ala Val Glu Trp Asp Ala Ser Trp Ser Lys Asn Leu Asp
50 55 60
Pro Ser Gly Arg Ala Ala Leu Gly Val His Asp Ala Ala Tyr Glu Asp
65 70 75 80
Thr Ala Gly Glu Thr Pro Ala Ser Ala Asp Pro Val Ser Asp Lys Gly
85 90 95
Leu Arg Pro Ala Ile Gly Glu Xaa
100

(2) INFORMATION FOR SEQ ID NO:2233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..103
(D) OTHER INFORMATION: / Ceres Seq. ID 1502716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2233:
Met Met Asn Ala Gly Phe Val Tyr Pro Glu Asn Thr Pro Thr Thr Lys
1 5 10 15
Glu Gly Tyr Tyr Tyr Arg Met Ile Phe Glu Lys Phe Phe Pro Lys Pro
20 25 30
Ala Ala Arg Ser Thr Val Pro Gly Gly Pro Ser Val Ala Cys Ser Thr
35 40 45
Ala Lys Ala Val Glu Trp Asp Ala Ser Trp Ser Lys Asn Leu Asp Pro
50 55 60
Ser Gly Arg Ala Ala Leu Gly Val His Asp Ala Ala Tyr Glu Asp Thr
65 70 75 80
Ala Gly Glu Thr Pro Ala Ser Ala Asp Pro Val Ser Asp Lys Gly Leu
85 90 95
Arg Pro Ala Ile Gly Glu Xaa
100

(2) INFORMATION FOR SEQ ID NO:2234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..384
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2234:

atcatctaca cgcgcgaggc gccgacaacc acttgccgac catgagcacg ggcacggacg 60
ccgtccggct gccgtgsssc cgcgcaassc ccgcccatca acaagtacgc cttcgctcgc 120
gccctgctcg cctccatgaa ctccgtcctc ctccgctatg acatctcggt gatgagcggc 180
gcgcassgtg ttcatgaagg aggacctcaa gatacggagc acgctagatc gagatccctgc 240
ccggcgctcat caacatctac tcgctcttcg gmtccctcgc cgcgggcytc acctccgamt 300
ggytcggccg ccgctacacc atggtgctgg cggccgcatc cttcttcacg ggcgcgctcc 360
tcattggcct cgcccgggac tacg

(2) INFORMATION FOR SEQ ID NO:2235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2235:

Met Asn Ser Val Leu Leu Gly Tyr Asp Ile Ser Val Met Ser Gly Ala
1 5 10 15
Xaa Xaa Phe His Glu Gly Gly Pro Gln Asp His Gly His Ala Arg Ser
20 25 30
Arg Ser Ser Pro Ala Ser Ser Thr Ser Thr Arg Ser Ser Xaa Pro Ser
35 40 45
Pro Arg Xaa Ser Pro Pro Xaa Xaa Ser Ala Ala Ala Thr Pro Trp Cys
50 55 60
Trp Arg Pro Pro Ser Ser Ser Arg Ala Arg Ser Ser Trp Ala Ser Pro
65 70 75 80
Gly Thr Thr

(2) INFORMATION FOR SEQ ID NO:2236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..71
(D) OTHER INFORMATION: / Ceres Seq. ID 1502719
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2236:
Met Ser Gly Ala Xaa Xaa Phe His Glu Gly Gly Pro Gln Asp His Gly
1 5 10 15
His Ala Arg Ser Arg Ser Ser Pro Ala Ser Ser Thr Ser Thr Arg Ser
20 25 30
Ser Xaa Pro Ser Pro Arg Xaa Ser Pro Pro Xaa Xaa Ser Ala Ala Ala
35 40 45
Thr Pro Trp Cys Trp Arg Pro Pro Ser Ser Ser Arg Ala Arg Ser Ser
50 55 60
Trp Ala Ser Pro Gly Thr Thr
65 70

(2) INFORMATION FOR SEQ ID NO:2237:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..63
(D) OTHER INFORMATION: / Ceres Seq. ID 1502720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2237:
Met Lys Glu Asp Leu Lys Ile Thr Asp Thr Leu Asp Arg Asp Pro Arg
1 5 10 15
Arg Arg His Gln His Leu Leu Ala Leu Arg Xaa Pro Arg Arg Gly Xaa
20 25 30
His Leu Arg Xaa Xaa Arg Pro Pro Leu His His Gly Ala Gly Gly Arg
35 40 45
His Leu Leu His Gly Arg Ala Pro His Gly Pro Arg Pro Gly Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:2238:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 484 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..484
(D) OTHER INFORMATION: / Ceres Seq. ID 1502721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2238:
tatgcaatca gagagaacat tgagaaggat attgagagg aaaggcggag aaaggacaaac 60
cctgaggcga tggagggaaga tgaagtggat gagatcgccg agatcagggc cctcacttc 120
gaggagtcca tgaagtatgc tcggcgtagt gtcagtgatg ctgatatccg caagtaccag 180
gcgtttgcc agactttgca gcagtcgccg gggtttgcca gtgagttccg ctctctggat 240
cagccggcga casstggtgc tgctgtgtgca sscgatccgt ttgcttctgc ggtgtgtgcg 300
gctgatgacg acgatctata cagctagtgt ggtgtgtcaa tatcagtcgc gtcactcatc 360
tgtttaaaaa tgatcatact aaacacgcgt gtcatgcaat gatatttatt tgcgtacatc 420
ttggacgtcg ctgagatgc gactctcgc ccttcggtta ccttttcagt ccatattctc 480
catg

(2) INFORMATION FOR SEQ ID NO:2239:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..108
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502722
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2239:
Tyr Ala Ile Arg Glu Asn Ile Glu Lys Asp Ile Glu Arg Glu Arg Arg
1 5 10 15
Arg Lys Asp Asn Pro Glu Ala Met Glu Glu Asp Glu Val Asp Glu Ile
 20 25 30
Ala Glu Ile Arg Ala Pro His Phe Glu Glu Ser Met Lys Tyr Ala Arg
 35 40 45
Arg Ser Val Ser Asp Ala Asp Ile Arg Lys Tyr Gln Ala Phe Ala Gln
 50 55 60
Thr Leu Gln Gln Ser Arg Gly Phe Gly Ser Glu Phe Arg Phe Ser Asp
65 70 75 80
Gln Pro Ala Thr Xaa Gly Ala Ala Ala Xaa Asp Pro Phe Ala Ser
 85 90 95
Ala Gly Ala Ala Ala Asp Asp Asp Asp Leu Tyr Ser
 100 105
(2) INFORMATION FOR SEQ ID NO:2240:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..85
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502723
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2240:
Met Glu Glu Asp Glu Val Asp Glu Ile Ala Glu Ile Arg Ala Pro His
1 5 10 15
Phe Glu Glu Ser Met Lys Tyr Ala Arg Arg Ser Val Ser Asp Ala Asp
 20 25 30
Ile Arg Lys Tyr Gln Ala Phe Ala Gln Thr Leu Gln Gln Ser Arg Gly
 35 40 45
Phe Gly Ser Glu Phe Arg Phe Ser Asp Gln Pro Ala Thr Xaa Gly Ala
 50 55 60
Ala Ala Ala Xaa Asp Pro Phe Ala Ser Ala Gly Ala Ala Ala Asp Asp
65 70 75 80
Asp Asp Leu Tyr Ser
 85
(2) INFORMATION FOR SEQ ID NO:2241:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..76
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502724
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2241:

Met Leu Gly Val Val Ser Val Met Leu Ile Ser Ala Ser Thr Arg Arg
1 5 10 15
Leu Pro Arg Leu Cys Ser Ser Pro Gly Gly Leu Ala Val Ser Ser Ala
20 25 30
Ser Arg Ile Ser Arg Arg Xaa Xaa Val Leu Leu Leu Xaa Xaa Ile Arg
35 40 45
Leu Leu Leu Arg Val Leu Arg Leu Met Thr Thr Ile Tyr Thr Ala Ser
50 55 60
Trp Val Ala Gln Tyr Gln Ser Arg His Ser Ser Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:2242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..309
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2242:

gaagcgagcc aaccagagcca tggagaagcg gatgatcg gacgggggtcc tctgtggcgca	60
cctcctcccc tccccctccg ccgctctctc gcagcctcag ctgtcggtcg cggtgtgcgc	120
ggcggtggag agcgccgcct accagaggtc ctctctctc ggggacgatg tctgtctgct	180
cgctgcctac aggcagcgca tatgcaagcg caagcgagga ggttcaagg acacctacc	240
agaggacctc ctctactgtt ttctcaagcg tgttctggac aacactagaa tcaatccagc	300
tgacatcgg	

(2) INFORMATION FOR SEQ ID NO:2243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2243:

Lys Arg Ala Asn Pro Ala Met Glu Lys Ala Ile Asp Arg Gln Arg Val
1 5 10 15
Leu Leu Ala His Leu Leu Pro Ser Pro Ser Ala Ala Ser Ser Gln Pro
20 25 30
Gln Leu Ala Ala Ser Ala Cys Ala Ala Gly Asp Ser Ala Ala Tyr Gln
35 40 45
Arg Ser Ser Ser Phe Gly Asp Asp Val Val Val Ala Ala Tyr Arg
50 55 60
Thr Pro Ile Cys Lys Ala Lys Arg Gly Gly Phe Lys Asp Thr Tyr Pro
65 70 75 80
Glu Asp Leu Leu Thr Val Val Leu Lys Ala Val Leu Asp Asn Thr Arg
85 90 95
Ile Asn Pro Ala Asp Ile
100

(2) INFORMATION FOR SEQ ID NO:2244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1502728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2244:

```
Ser Glu Pro Thr Gln Pro Trp Arg Arg Arg Ser Ile Gly Ser Gly Ser
1      5      10      15
Ser Trp Arg Thr Ser Ser Pro Pro Pro Pro Pro Pro Pro Arg Ser Leu
      20      25      30
Ser Leu Arg Arg Arg Ala Arg Pro Gly Thr Ala Pro Pro Thr Arg
      35      40      45
Gly Pro Pro Pro Ser Gly Thr Met Ser Ser Ser Ser Leu Pro Thr Gly
50      55      60
Arg Arg Tyr Ala Arg Pro Ser Glu Glu Ala Ser Arg Thr Pro Thr Gln
65      70      75      80
Arg Thr Ser Ser Leu Leu Phe Ser Arg Leu Phe Trp Thr Thr Leu Glu
      85      90      95
Ser Ile Gln Leu Thr Ser
      100
```

(2) INFORMATION FOR SEQ ID NO:2245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1502729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2245:

```
Met Glu Lys Ala Ile Asp Arg Gln Arg Val Leu Leu Ala His Leu Leu
1      5      10      15
Pro Ser Pro Ser Ala Ala Ser Ser Gln Pro Gln Leu Ala Ala Ser Ala
      20      25      30
Cys Ala Ala Gly Asp Ser Ala Ala Tyr Gln Arg Ser Ser Ser Phe Gly
      35      40      45
Asp Asp Val Val Val Val Ala Ala Tyr Arg Thr Pro Ile Cys Lys Ala
50      55      60
Lys Arg Gly Gly Phe Lys Asp Thr Tyr Pro Glu Asp Leu Leu Thr Val
65      70      75      80
Val Leu Lys Ala Val Leu Asp Asn Thr Arg Ile Asn Pro Ala Asp Ile
      85      90      95
```

(2) INFORMATION FOR SEQ ID NO:2246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 496 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..496

(D) OTHER INFORMATION: / Ceres Seq. ID 1502730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2246:

```
gagaatcgag cagagccacc gatcgctcct gagcactttc cacattccag ttccactccg      60
cttcgcgtgc cggctgcgcgt ctccgagact ccgacagtcc gaccgcaaga aggatgagtg      120
aagaggataa gactgctgct tctgctgagc agccgaagag ggcccctaag ctcaatgaaa      180
ggatcctctc ttctctgtcc aggagggtcc tagctgtcca tccatggcat gatcttgaga      240
```

tcggtctctga	tgctctctgct	gttttcaatg	ttgtaagtac	cagcattacc	ttagaacggt	300
ttgatgtgtt	atatgttcgg	tgctgtgggg	acttaggttg	tctggaacca	tctacgggaa	360
ggttgttgag	atcacaagg	gaagcaaagt	taaatatgag	cttgacaaga	aaactggact	420
gattaaggtt	gatcgagtc	tgttactcat	cagttgtata	cctcacaat	tatggtttcg	480
ttccaaagga	ctcttt					

(2) INFORMATION FOR SEQ ID NO:2247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2247:

Met	Ser	Glu	Glu	Asp	Lys	Thr	Ala	Ala	Ser	Ala	Glu	Gln	Pro	Lys	Arg	
1				5						10				15		
Ala	Pro	Lys	Leu	Asn	Glu	Arg	Ile	Leu	Ser	Ser	Leu	Ser	Arg	Arg	Ser	
			20					25					30			
Val	Ala	Ala	His	Pro	Trp	His	Asp	Leu	Glu	Ile	Gly	Pro	Asp	Ala	Pro	
			35				40					45				
Ala	Val	Phe	Asn	Val	Val	Ser	Thr	Ser	Ile	Thr	Leu	Glu	Pro	Phe	Asp	
			50				55				60					
Val	Leu	Tyr	Val	Arg	Cys	Cys	Gly	Asp	Leu	Gly	Cys	Leu	Glu	Pro	Ser	
			65			70		75					80			
Thr	Gly	Arg	Leu	Leu	Arg	Ser	Gln	Arg	Glu	Ala	Lys	Leu	Asn	Met	Ser	
			85					90					95			
Leu	Thr	Arg	Lys	Leu	Asp											
																100

(2) INFORMATION FOR SEQ ID NO:2248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2248:

acatcaatcc	attccctttc	ctctcccgct	ccacttccat	gggcaaggtt	cggtcctttc	60
tctcgcgctc	cgcgcagcgc	aagcgcgcgc	gscgcgagag	caggctcgtc	ctgcgcgcac	120
tctcgcgcgc	ccagcgcgc	gcgcgcgcgc	tccccactcc	cgaggaggtc	achgtcgtcg	180
tcgtcaacca	caaccagggg	acgagacgga	gcgcgtgttc	cgcgaagttc	acgcgaacgc	240
cgacgggcag	atctcgcggt	ccgagc				

(2) INFORMATION FOR SEQ ID NO:2249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2249:

Thr Ser Ile His Ser Leu Ser Ser Pro Ala Pro Leu Pro Trp Ala Arg

1 5 10 15
Phe Gly Pro Ser Ser Arg Ala Pro Ala Ala Ser Ala Ala Xaa Arg
20 25 30
Arg Ala Gly Ser Ser Ser Pro His Ser Ser Ala Ala Ser Ala Pro Pro
35 40 45
Ser Pro Ser Pro Leu Pro Arg Arg Ser Xaa Ser Ser Ser Thr Thr
50 55 60
Thr Arg Gly Arg Asp Gly Ala Arg Val Pro Gln Val Arg Arg Glu Arg
65 70 75 80
Arg Arg Ala Asp Leu Ala Val Arg
85

(2) INFORMATION FOR SEQ ID NO:2250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1502757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2250:

His Gln Ser Ile Pro Phe Pro Leu Pro Leu His Phe His Gly Gln Gly
1 5 10 15
Ser Val Leu Leu Leu Ala Leu Pro Gln Arg Gln Ala Arg Gln Xaa Gly
20 25 30
Glu Gln Ala Arg Pro Arg Arg Thr Pro Pro Arg Pro Ala Arg Arg Arg
35 40 45
Pro Arg Pro His Ser Arg Gly Gly His Xaa Arg Arg Arg Gln Pro Gln
50 55 60
Pro Gly Asp Glu Thr Glu Arg Val Phe Arg Lys Phe Asp Ala Asn Gly
65 70 75 80
Asp Gly Gln Ile Ser Arg Ser Glu
85

(2) INFORMATION FOR SEQ ID NO:2251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1502758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2251:

Ile Asn Pro Phe Pro Phe Leu Ser Arg Ser Thr Ser Met Gly Lys Val
1 5 10 15
Arg Ser Phe Phe Ser Arg Ser Arg Ser Gly Lys Arg Gly Xaa Pro Glu
20 25 30
Ser Arg Leu Val Leu Ala Ala Leu Leu Arg Gly Gln Arg Ala Ala Val
35 40 45
Pro Val Pro Thr Pro Glu Glu Val Xaa Val Val Val Asn His Asn
50 55 60
Gln Gly Thr Arg Arg Ser Ala Cys Ser Ala Ser Thr Arg Thr Ala
65 70 75 80
Thr Gly Arg Ser Arg Gly Pro Ser
85

(2) INFORMATION FOR SEQ ID NO:2252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..479
(D) OTHER INFORMATION: / Ceres Seq. ID 1502759
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2252:
ttggagatgc ggttttcata cctgctgggt gtctctcatca agtacggaat ctaaagtctt 60
gcaccaagat agctctggat ttgtatcac cagagaacat tcagcaatgt ctcagcttaa 120
ccgaggattt ccgagactt ccagtgggcc acaggggaaa agaagataaa cttagaggtga 180
agaagatgat cgtctatgcc gttgagcatg cttggcgat tctgaaagag ccttgacac 240
cccgcgagtc cgctgaaca agctggcatc atatctgggt ttctgctagt caacgagggg 300
aactagagaa catgatgcga tggtgtgcga cagtagacgt ggggtagcgc tagttgcttt 360
gcttgctggc acaaataata atcttggaat tattactaat aagggcctcg ttagggaagg 420
atttgaggag attaatTTTT ttttatttta actgaataga aagagatttg atgagatcc
(2) INFORMATION FOR SEQ ID NO:2253:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..55
(D) OTHER INFORMATION: / Ceres Seq. ID 1502760
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2253:
Trp Arg Cys Gly Phe His Thr Cys Trp Val Ser Ser Ser Ser Thr Glu
1 5 10 15
Ser Lys Val Leu His Gln Asp Ser Ser Gly Phe Cys Ile Thr Arg Glu
20 25 30
His Ser Ala Met Ser Gln Leu Asn Arg Gly Phe Pro Glu Thr Ser Ser
35 40 45
Gly Pro Gln Gly Lys Arg Arg
50 55
(2) INFORMATION FOR SEQ ID NO:2254:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..84
(D) OTHER INFORMATION: / Ceres Seq. ID 1502761
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2254:
Gly Asp Ala Val Phe Ile Pro Ala Gly Cys Pro His Gln Val Arg Asn
1 5 10 15
Leu Lys Ser Cys Thr Lys Ile Ala Leu Asp Phe Val Ser Pro Glu Asn
20 25 30
Ile Gln Gln Cys Leu Ser Leu Thr Glu Asp Phe Arg Arg Leu Pro Val
35 40 45
Gly His Arg Ala Lys Glu Asp Lys Leu Glu Val Lys Lys Met Ile Val
50 55 60
Tyr Ala Val Glu His Ala Leu Ala Ile Leu Lys Glu Pro Cys Thr Pro
65 70 75 80
Arg Glu Ser Ala

(2) INFORMATION FOR SEQ ID NO:2255:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..43
(D) OTHER INFORMATION: / Ceres Seq. ID 1502762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2255:

Met Leu Cys Asp Ser Arg Arg Gly Val Ala Leu Val Ala Leu Val
1 5 10 15
Gly Thr Asn Asn Asn Leu Gly Asn Ile Thr Asn Lys Gly Ser Val Arg
20 25 30
Lys Gly Phe Glu Glu Ile Asn Phe Phe Leu Phe
35 40

(2) INFORMATION FOR SEQ ID NO:2256:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 478 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..478
(D) OTHER INFORMATION: / Ceres Seq. ID 1502763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2256:

agatcagatg cgagacaaaa taaggatcac ggakttgcag agatatccaa tccaagcaca 60
tcggagggtgc tcattgaaga gagaagatcc ttgggtcccg aaaaggagac gagatccctgt 120
cctggggcagc gcaggagggg aggagttaat acctgcgtcc cctggcacgt gtgggtcgcc 180
ctgccccgcc ccgaagaag cgcgcccccc gcsstggtat ataagcgcgc mssacgggcc 240
caaggctggg caagacggcg ggtcgtcgga gtcgacaggg ggtccaaagc ttcagatggc 300
cagcgtcgtg ggagcagtg ccggggggcgt gggggcgccg acgcgcacgt cctcgcggtg 360
gacgacagct cgtcgacccg cgccatcatc gccgccatac tccggagctc ccggtttcgt 420
gtgactcgcg tggaaagtgg gaagagggcc ctggaactgt taggcacgga gccgaacg

(2) INFORMATION FOR SEQ ID NO:2257:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..159
(D) OTHER INFORMATION: / Ceres Seq. ID 1502764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2257:

Arg Ser Asp Gly Arg Gln Asn Lys Asp His Gly Xaa Ala Glu Ile Ser
1 5 10 15
Asn Pro Ser Thr Ser Glu Val Leu Ile Glu Arg Arg Ser Leu Gly
20 25 30
Pro Glu Lys Glu Thr Arg Ser Cys Pro Gly Gln Arg Arg Gly Gly
35 40 45
Val Asn Thr Cys Val Pro Trp His Val Trp Val Ala Leu Pro Arg Pro
50 55 60
Ala Arg Ser Ala Pro Pro Xaa Xaa Val Tyr Lys Arg Xaa Xaa Pro Ala
65 70 75 80

Gln Gly Trp Ala Arg Arg Arg Val Val Gly Val Asp Arg Gly Val Gln
85 90 95
Ala Ser Asp Gly Gln Arg Arg Trp Ser Ser Gly Arg Gly Arg Gly Gly
100 105 110
Ala Asp Ala His Val Leu Ala Val Asp Asp Ser Ser Val Asp Arg Ala
115 120 125
Ile Ile Ala Ala Ile Leu Arg Ser Ser Arg Phe Arg Val Thr Ala Val
130 135 140
Glu Ser Gly Lys Arg Ala Leu Glu Leu Gly Thr Glu Pro Asn
145 150 155

(2) INFORMATION FOR SEQ ID NO:2258:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..140
(D) OTHER INFORMATION: / Ceres Seq. ID 1502765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2258:

Asp Gln Met Ala Asp Lys Ile Arg Ile Thr Xaa Leu Gln Arg Tyr Pro
1 5 10 15
Ile Gln Ala His Arg Arg Cys Ser Leu Lys Arg Glu Asp Pro Trp Val
20 25 30
Arg Lys Arg Arg Arg Asp Pro Val Leu Gly Ser Ala Gly Gly Glu Glu
35 40 45
Leu Ile Pro Ala Ser Pro Gly Thr Cys Gly Ser Pro Cys Pro Ala Pro
50 55 60
Gln Glu Ala Arg Pro Pro Xaa Trp Tyr Ile Ser Ala Xaa Xaa Arg Pro
65 70 75 80
Lys Ala Gly Gln Asp Gly Gly Ser Ser Glu Ser Thr Gly Glu Ser Lys
85 90 95
Leu Gln Met Ala Ser Val Gly Gly Ala Val Ala Gly Gly Val Gly Ala
100 105 110
Pro Thr Arg Thr Ser Ser Arg Trp Thr Thr Ala Pro Ser Thr Ala Pro
115 120 125
Ser Ser Pro Pro Tyr Ser Gly Ala Pro Gly Phe Val
130 135 140

(2) INFORMATION FOR SEQ ID NO:2259:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..138
(D) OTHER INFORMATION: / Ceres Seq. ID 1502766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2259:

Met Ala Asp Lys Ile Arg Ile Thr Xaa Leu Gln Arg Tyr Pro Ile Gln
1 5 10 15
Ala His Arg Arg Cys Ser Leu Lys Arg Glu Asp Pro Trp Val Arg Lys
20 25 30
Arg Arg Arg Asp Pro Val Leu Gly Ser Ala Gly Gly Glu Glu Leu Ile
35 40 45
Pro Ala Ser Pro Gly Thr Cys Gly Ser Pro Cys Pro Ala Pro Gln Glu
50 55 60
Ala Arg Pro Pro Xaa Trp Tyr Ile Ser Ala Xaa Xaa Arg Pro Lys Ala

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..95
(D) OTHER INFORMATION: / Ceres Seq. ID 1502769
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2262:
Met Asp Leu Lys Asp Ser Leu Ser Lys Phe Lys Gln Gln Gln Glu Arg
1 5 10 15
Cys Gln Ser Ser Leu Ala Ser Ile Ala Ala Ser Thr Ser Lys Pro Lys
20 25 30
His Arg Ala Gln Pro Ala His Ala Pro Asn Val Pro Ala Arg Pro Ser
35 40 45
Gln Pro Ile Lys Phe Ser Asn Asp Thr Glu Arg Leu Gln His Ile Asn
50 55 60
Ser Ile Arg Lys Ser Pro Val Gly Ala Gln Ile Lys Leu Val Ile Glu
65 70 75 80
Leu Leu Tyr Lys Thr Arg Gln Ala Phe Thr Ala Glu Gln Xaa Lys
85 90 95

(2) INFORMATION FOR SEQ ID NO:2263:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..70
(D) OTHER INFORMATION: / Ceres Seq. ID 1502770
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2263:
Met Leu Pro Thr Ser Gln Gln Asp His His Asn Leu Leu Ser Phe Gln
1 5 10 15
Met Ile Gln Lys Gly Cys Ser Thr Ser Ile Arg Leu Gly Asn Leu Leu
20 25 30
Leu Glu His Arg Ser Ser Leu Ser Ser Asn Phe Phe Thr Arg Gln Asp
35 40 45
Lys Leu Leu Leu Gln Ser Arg Xaa Asn Glu Ala Thr Tyr Val Asp Ile
50 55 60
His Gly Asn Lys Ala Val
65 70

(2) INFORMATION FOR SEQ ID NO:2264:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..486
(D) OTHER INFORMATION: / Ceres Seq. ID 1502771
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2264:
gtgggacgag aacaagttca cagctgatga gctgcagact ctgacaacaa acctatgcta 60
cacgtacgct aggtgcaccc gctccgtgtc aattgtgccc ccggcataact atgctcatct 120
ggcagccttc cgagctcgct tctacatgga gccagatacc tctgacagtg gctcaatggc 180
cagtggtgccc cgtggccctc caccaggtgc ggcacssagc atgagaggag cggggagtgt 240
tcgggtcagg cccctacctg ctctcaagga aaacgtgaag cgtgtcatgt tttactgctg 300

agatgctgag ctaccttcac caagaaaata tctgacttg ttccatgtac ccgcactggt 360
tcggtgatac tatctgacac cgaatttatg cattaagtct tccagtggtc tggagatttt 420
aagtaacgcc tgtttttatt cgtgagtgt aacgctgcag ttcgaggagc ttcagtgtctg 480
tatgat

(2) INFORMATION FOR SEQ ID NO:2265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2265:

Trp Asp Glu Asn Lys Phe Thr Ala Asp Glu Leu Gln Thr Leu Thr Asn
1 5 10 15
Asn Leu Cys Tyr Thr Tyr Ala Arg Cys Thr Arg Ser Val Ser Ile Val
20 25 30
Pro Pro Ala Tyr Tyr Ala His Leu Ala Ala Phe Arg Ala Arg Phe Tyr
35 40 45
Met Glu Pro Asp Thr Ser Asp Ser Gly Ser Met Ala Ser Gly Ala Arg
50 55 60
Gly Pro Pro Pro Gly Ala Ala Xaa Ser Met Arg Gly Ala Gly Ser Val
65 70 75 80
Ala Val Arg Pro Leu Pro Ala Leu Lys Glu Asn Val Lys Arg Val Met
85 90 95
Phe Tyr Cys

(2) INFORMATION FOR SEQ ID NO:2266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2266:

Met Glu Pro Asp Thr Ser Asp Ser Gly Ser Met Ala Ser Gly Ala Arg
1 5 10 15
Gly Pro Pro Pro Gly Ala Ala Xaa Ser Met Arg Gly Ala Gly Ser Val
20 25 30
Ala Val Arg Pro Leu Pro Ala Leu Lys Glu Asn Val Lys Arg Val Met
35 40 45
Phe Tyr Cys
50

(2) INFORMATION FOR SEQ ID NO:2267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2267:
atcagyaaya acttcaggct tggagaaaga agaaaggcat agcagcgggc agcggcatgg 60
gcaccakccc cgtcatccct gcgacgatgc tcttcgtcgc tcttctgtgn nctgtctgct 120
tc

(2) INFORMATION FOR SEQ ID NO:2268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2268:

Ser	Xaa	Xaa	Thr	Ser	Gly	Leu	Glu	Lys	Glu	Glu	Arg	His	Ser	Ser	Gly
1			5						10					15	
Gln	Arg	His	Gly	His	Xaa	Pro	Arg	His	Pro	Cys	Asp	Asp	Ala	Leu	Arg
			20					25					30		
Arg	Ser	Ser	Ser	Cys	Xaa	Cys	Leu	Leu							
			35				40								

(2) INFORMATION FOR SEQ ID NO:2269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2269:

Gln	Xaa	Xaa	Leu	Gln	Ala	Trp	Arg	Lys	Lys	Gly	Ile	Ala	Ala	Gly
1			5						10					15
Ser	Gly	Met	Gly	Thr	Xaa	Pro	Val	Ile	Pro	Ala	Thr	Met	Leu	Phe
			20				25						30	
Ala	Leu	Leu	Xaa	Xaa	Val	Cys	Phe							
			35				40							

(2) INFORMATION FOR SEQ ID NO:2270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2270:

accttactas sagcagacgg tatcggtcaa ggtccccata ctgctacaga agacgcaggt 60
ssaccttctg ttctgcatac ctaccgccgg cacaggtaca gatctgtctc caagtcattcc 120
agtcatctc c

(2) INFORMATION FOR SEQ ID NO:2271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..43
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502785
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2271:
Thr Leu Leu Xaa Ala Asp Gly Ile Val Gln Gly Pro His Thr Ala Thr
1 5 10 15
Glu Asp Ala Gly Xaa Pro Ser Val Ser Pro Tyr Tyr Arg Arg His Arg
 20 25 30
Tyr Arg Ser Val Ser Lys Ser Ser Ser Ser
 35 40
(2) INFORMATION FOR SEQ ID NO:2272:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..43
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502786
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2272:
Pro Tyr Xaa Xaa Gln Thr Val Ser Phe Lys Val Pro Ile Leu Leu Gln
1 5 10 15
Lys Thr Gln Xaa Xaa Leu Leu Phe Arg His Thr Thr Ala Gly Thr Gly
 20 25 30
Thr Asp Leu Ser Pro Ser His Pro Val His Leu
 35 40
(2) INFORMATION FOR SEQ ID NO:2273:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..43
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502787
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2273:
Leu Thr Xaa Ser Arg Arg Tyr Arg Ser Arg Ser Pro Tyr Cys Tyr Arg
1 5 10 15
Arg Arg Arg Xaa Thr Phe Cys Phe Ala Ile Leu Pro Pro Ala Gln Val
 20 25 30
Gln Ile Cys Leu Gln Val Ile Gln Phe Ile Ser
 35 40
(2) INFORMATION FOR SEQ ID NO:2274:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 473 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..473
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502805
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2274:
agattccctt ccctttccgt tagcaggata gagagggaga ggagcagaag atagcagagg

gccagaggcg cagaaggcag tcgcgagacg gaggaagagg aagaagaagc ggcavsgcga 120
ggatgcgctg cctgaacgtg tcgaccaacg tgaacctgga ggggggtggac acctccgcga 180
tctctgcgca agcctccaag tccgtcgcca acatcatcgg caagcccgag gcctacgtga 240
tggtgtttct caagggttcg gtgcctatgg cattttgagg taccaggag ccagcagctt 300
acggtagact ggtttccatc ggaggcctga accctgatgt gaacaagaag cttagtgctg 360
gcacgcgttc tatcctggag tcaaatgctg ctgttcccaa gtcacgcttc tacctcaagt 420
tctatgactc gaaggctcat cctgcacaag aaatgctca atgtttgcat gct

(2) INFORMATION FOR SEQ ID NO:2275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2275:

Met Pro Cys Leu Asn Val Ser Thr Asn Val Asn Leu Glu Gly Val Asp
1 5 10 15
Thr Ser Ala Ile Leu Ala Glu Ala Ser Lys Ser Val Ala Asn Ile Ile
20 25 30
Gly Lys Pro Glu Ala Tyr Val Met Val Val Leu Lys Gly Ser Val Pro
35 40 45
Met Ala Phe Gly Gly Thr Gln Glu Pro Ala Ala Tyr Gly Glu Leu Val
50 55 60
Ser Ile Gly Gly Leu Asn Pro Asp Val Asn Lys Lys Leu Ser Ala Gly
65 70 75 80
Ile Ala Ser Ile Leu Glu Ser Lys Leu Ser Val Pro Lys Ser Arg Phe
85 90 95
Tyr Leu Lys Phe Tyr Asp Ser Lys Ala His Pro Ala Gln Glu Asn Ala
100 105 110
Gln Cys Leu His Ala
115

(2) INFORMATION FOR SEQ ID NO:2276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2276:

Met Val Val Leu Lys Gly Ser Val Pro Met Ala Phe Gly Gly Thr Gln
1 5 10 15
Glu Pro Ala Ala Tyr Gly Glu Leu Val Ser Ile Gly Gly Leu Asn Pro
20 25 30
Asp Val Asn Lys Lys Leu Ser Ala Gly Ile Ala Ser Ile Leu Glu Ser
35 40 45
Lys Leu Ser Val Pro Lys Ser Arg Phe Tyr Leu Lys Phe Tyr Asp Ser
50 55 60
Lys Ala His Pro Ala Gln Glu Asn Ala Gln Cys Leu His Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:2277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..69
(D) OTHER INFORMATION: / Ceres Seq. ID 1502808
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2277:
Met Ala Phe Gly Gly Thr Gln Glu Pro Ala Ala Tyr Gly Glu Leu Val
1 5 10 15
Ser Ile Gly Gly Leu Asn Pro Asp Val Asn Lys Lys Leu Ser Ala Gly
20 25 30
Ile Ala Ser Ile Leu Glu Ser Lys Leu Ser Val Pro Lys Ser Arg Phe
35 40 45
Tyr Leu Lys Phe Tyr Asp Ser Lys Ala His Pro Ala Gln Glu Asn Ala
50 55 60
Gln Cys Leu His Ala
65

(2) INFORMATION FOR SEQ ID NO:2278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..410
(D) OTHER INFORMATION: / Ceres Seq. ID 1502809
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2278:

agactgtctg ccagtgagc cgagggagcg cctccgcctc agatccaacc cccaccgatg 60
cgagctccgg cgatgctccg ctgggccgcg gcggssctcg cggggctcct cgccgctcac 120
cgccgcgcgc gttttacctt cccggcgctg cgcccaacga cttccataag aaagatccac 180
ttttggtgaa ggtgaataag ctgacatcca cgaagacgca acttccctac tcatattact 240
ctcttccttt ctgtaaacca aacacgatag ttgacagtcg agagaatctt ggagaagtgc 300
tgcggtgtga tgcattgag aactctcctt atgtggctcg tactagatta ctgcttgata 360
catattcagc attgtaattt gtaatgtacc aaatcactta gtcgtcatgc

(2) INFORMATION FOR SEQ ID NO:2279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..62
(D) OTHER INFORMATION: / Ceres Seq. ID 1502810
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2279:

Arg Leu Ser Ala Ser Gly Arg Glu Gly Ala Pro Pro Gln Ile Gln
1 5 10 15
Pro Pro Pro Met Arg Ala Pro Ala Met Leu Arg Trp Ala Ala Ala Xaa
20 25 30
Leu Ala Gly Leu Leu Ala Ala His Arg Pro Pro Arg Phe Thr Tyr Pro
35 40 45
Ala Trp Arg Pro Thr Thr Ser Ile Arg Lys Ile His Phe Trp
50 55 60

(2) INFORMATION FOR SEQ ID NO:2280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..124
(D) OTHER INFORMATION: / Ceres Seq. ID 1502811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2280:

Thr	Val	Cys	Gln	Trp	Thr	Arg	Gly	Ser	Ala	Ser	Ala	Ser	Asp	Pro	Thr	
1			5				10						15			
Pro	Thr	Asp	Ala	Ser	Ser	Gly	Asp	Ala	Pro	Leu	Gly	Arg	Gly	Xaa	Xaa	
			20				25						30			
Arg	Gly	Ala	Pro	Arg	Arg	Ser	Pro	Ala	Ala	Ala	Phe	Tyr	Leu	Pro	Gly	
			35				40					45				
Val	Ala	Pro	Asn	Asp	Phe	His	Lys	Lys	Asp	Pro	Leu	Leu	Val	Lys	Val	
			50				55				60					
Asn	Lys	Leu	Thr	Ser	Thr	Lys	Thr	Gln	Leu	Pro	Tyr	Ser	Tyr	Tyr	Ser	
			70						75						80	
Leu	Pro	Phe	Cys	Lys	Pro	Asn	Thr	Ile	Val	Asp	Ser	Ala	Glu	Asn	Leu	
			85						90					95		
Gly	Glu	Val	Leu	Arg	Gly	Asp	Arg	Ile	Glu	Asn	Ser	Pro	Tyr	Val	Val	
			100				105						110			
Ser	Thr	Arg	Leu	Leu	Leu	Val	Thr	Tyr	Ser	Ala	Leu					
			115				120									

(2) INFORMATION FOR SEQ ID NO:2281:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 443 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..443
(D) OTHER INFORMATION: / Ceres Seq. ID 1502820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2281:

aacatccttaa	tcgaaaaacg	gaagtttcgg	cgggssggcg	tgtctgtgat	ctcaacccaa	60
ggcgtgcctc	cgctccggtc	accctgcgt	ccacgcaacc	atgtcgagga	ggaagaccag	120
ggagcccaag	gaggagaacg	tacaccttgc	accaactgtc	cgtgaaggag	agatgtctct	180
ttgtgttcgt	cacactcttg	catccttcga	tgacaccttc	attcatatac	ctgatttgct	240
tgggagggaat	actctggttc	ggatcacccg	tggcatgaag	gtgaaggctg	accgtgacga	300
gtcgtccact	tacgtctcta	tgtctgtctc	tcaagacgtc	gcacagcgct	gcaagagcgt	360
tggcattact	gcactgcaca	ttaagctctg	cgccaccgga	gcaacaagac	caagaccctt	420
ggacctgggt	ccagctctgc	cct				

(2) INFORMATION FOR SEQ ID NO:2282:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..91
(D) OTHER INFORMATION: / Ceres Seq. ID 1502821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2282:

His	Pro	Asn	Arg	Lys	Thr	Glu	Val	Ser	Ala	Ala	Xaa	Arg	Ala	Arg	Asp	
1			5				10					15				
Leu	Asn	Pro	Arg	Arg	Ala	Ser	Ala	Pro	Val	Thr	Arg	Arg	Ser	Thr	Gln	
			20				25					30				
Pro	Cys	Arg	Gly	Gly	Arg	Pro	Gly	Ser	Pro	Arg	Arg	Arg	Thr	Ser	Pro	

(2) INFORMATION FOR SEQ ID NO:2283:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1502822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2283:

(2) INFORMATION FOR SEQ ID NO:2284:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 442 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..442

(D) OTHER INFORMATION: / Ceres Seq. ID 1502834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2284:

ttaactcgag	agaggagttaa	gaatcccgga	attgagatacc	tgtatgcttt	gcaacaaatga	60
acgaactcga	agaagctctt	gcgcgcaaaa	awaagcaaaa	gcgaatcgctt	gaatttgtgtg	120
caagctctg	taggagagacc	aacagagagt	gcgctctaaa	tctattatat	tcgaagacccc	180
gagagctctg	aaagtcaagat	attatgatat	cgctcttatgt	atttaaagaa	gggtgaaccac	240
tgtatgaacc	actgttatgtt	catcgcgatg	ctctgctaact	tttttggaa	gaaagagaag	300
ttgcagatgt	ccccacagat	catcctctc	gcagcaagca	acatcgagtt	cttcaataca	360
tgtattctga	gaaggagcaa	ctgatggcca	tactgacgaa	gagaataaag	ccttawtwtga	420
taqatcttga	taqgcaaaat	gg				

(2) INFORMATION FOR SEQ ID NO:2285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..146
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502835
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2285:
Asn Ser Arg Gly Glu Ala Ser Arg Asn Gly Asp Pro Asp Ala Leu
1 5 10 15
Ala Thr Met Asn Ala Thr Ala Glu Ala Leu Glu Ala Lys Xaa Lys Gln
 20 25 30
Lys Pro Ser Phe Glu Leu Ser Gly Lys Leu Ala Glu Glu Thr Asn Arg
 35 40 45
Val Ala Gly Val Asn Leu Leu Tyr Ser Glu Pro Pro Glu Ala Arg Lys
50 55 60
Ser Glu Ile Arg Trp Arg Leu Tyr Val Phe Lys Asp Gly Glu Pro Leu
65 70 75
Asn Glu Pro Leu Tyr Val His Arg Met Thr Cys Tyr Leu Phe Gly Arg
 85 90 95
Glu Xaa Lys Val Ala Asp Val Pro Thr Asp His Pro Ser Cys Ser Lys
 100 105 110
Gln His Ala Val Leu Gln Tyr Arg Leu Val Glu Lys Glu Gln Leu Asp
 115 120 125
Gly Ile Leu Thr Lys Arg Ile Arg Pro Xaa Leu Met Asp Leu Asp Ser
130 135 140
Thr Asn
145

(2) INFORMATION FOR SEQ ID NO:2286:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..128
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2286:

Met Asn Ala Thr Ala Glu Ala Leu Glu Ala Lys Xaa Lys Gln Lys Pro
1 5 10 15
Ser Phe Glu Leu Ser Gly Lys Leu Ala Glu Glu Thr Asn Arg Val Ala
 20 25 30
Gly Val Asn Leu Leu Tyr Ser Glu Pro Pro Glu Ala Arg Lys Ser Glu
 35 40 45
Ile Arg Trp Arg Leu Tyr Val Phe Lys Asp Gly Glu Pro Leu Asn Glu
50 55 60
Pro Leu Tyr Val His Arg Met Thr Cys Tyr Leu Phe Gly Arg Glu Xaa
65 70 75 80
Lys Val Ala Asp Val Pro Thr Asp His Pro Ser Cys Ser Lys Gln His
 85 90 95
Ala Val Leu Gln Tyr Arg Leu Val Glu Lys Glu Gln Leu Asp Gly Ile
 100 105 110
Leu Thr Lys Arg Ile Arg Pro Xaa Leu Met Asp Leu Asp Ser Thr Asn
115 120 125

(2) INFORMATION FOR SEQ ID NO:2287:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..461
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502844
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2287:
tacgacctgc tcgggatctc agcggatggg agccccgatg atgttcgggc gtcctacagg 60
cggtctggcg taaagtacca ccagacgctg tccccctcgg cgccgcggcc gagaacacgc 120
gccgcttcac cgaggtgcag gaggcctacg agacgctctc cgacccaagc gcccgctcca 180
gctaacgacg tgcactcgcc cggcgssstct gccgctcgcc ttctcggggc gccgttccca 240
atccccaccg gctactacc accaccagga gcaggagag agatctgggt ggagaaggct 300
ctggggaggac cagatcgacg agctgaagag gaggagcggt gcgaaggatt cagaagagaa 360
cctgtcgtgg ggcgctcgca tgcggagaag ggccgaggcg tcacagcgna gtacctcgca 420
caagcgaccg tgccaaatgc agctgtactc gtacgtagca t
(2) INFORMATION FOR SEQ ID NO:2288:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..137
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502845
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2288:
Tyr Asp Leu Leu Gly Ile Ser Ala Asp Gly Ser Pro Asp Asp Val Arg
1 5 10 15
Ala Ser Tyr Arg Arg Leu Ala Leu Lys Tyr His Pro Asp Val Ser Pro
20 25 30
Pro Ala Pro Arg Pro Arg Thr Arg Ala Ala Ser Ser Arg Cys Arg Arg
35 40 45
Pro Thr Arg Arg Ser Pro Thr Gln Ala Ala Pro Ala Thr Thr Val
50 55 60
His Ser Pro Ala Xaa Ser Ala Ala Arg Leu Leu Arg Ala Pro Phe Pro
65 70 75 80
Ile Pro Pro Arg Leu Leu Pro Pro Pro Gly Ala Gly Arg Glu Ile Trp
85 90 95
Val Glu Lys Val Leu Gly Gly Pro Asp Arg Arg Ala Glu Glu Glu Glu
100 105 110
Arg Gly Glu Gly Phe Arg Arg Glu Pro Val Val Gly Arg Ser His Ala
115 120 125
Glu Lys Gly Arg Gly Val Thr Ala Xaa
130 135
(2) INFORMATION FOR SEQ ID NO:2289:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 503 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..503
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502850
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2289:
atgcgtgcac gccgtgctag ctaggtaact tgcggccaag agcgaggcgg accactacaa 60
gcgggagatg agaaggkagc agggaggagat catcgccgct ccagacaccg aggcckctga 120
gatttgagat atcatgtcac ggtatgggct cgagccgcag agtacggccc tgcgtcgccc 180
gggctcaggc ggaacctca agcttkgcta gacttcatgr tgaggttcga gctgggactg 240

gagagaccgg atcccagaag ggctctgcag acgccttcac gatcgcactg tctctacgtgg 300
tcggcgggct ggctccctctc ctgccctacg tgctcgtctc cgccgcgcag gatgccatgc 360
tcacatccgt cggagtcacg ctggccgcgc tgcttttctt cggtctacgc aaggggcgcct 420
tcacggggga accgkccgctt cgccagtgcc gtccagaccg ctgtcattgg agcgctcgtc 480
tcggcggcgg cgtacssgga tgg

(2) INFORMATION FOR SEQ ID NO:2290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2290:

Cys Val His Gly Val Leu Ala Arg Tyr Leu Ala Ala Lys Ser Glu Ala
1 5 10 15
Asp His Tyr Lys Arg Glu Met Arg Arg Xaa Gln Glu Glu Ile Ile Ala
20 25 30
Val Pro Asp Thr Glu Ala Xaa Glu Ile Gly Asp Ile Met Ser Arg Tyr
35 40 45
Gly Leu Glu Pro Gln Ser Thr Ala Leu Ser Ser Pro Gly Ser Gly Gly
50 55 60
Thr Leu Lys Leu Xaa
65

(2) INFORMATION FOR SEQ ID NO:2291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2291:

Met Gly Ser Ser Arg Arg Val Arg Pro Cys Arg Arg Arg Ala Gln Ala
1 5 10 15
Glu Pro Ser Ser Xaa Ala Arg Leu His Xaa Glu Val Arg Ala Gly Thr
20 25 30
Gly Glu Thr Gly Ser Gln Lys Gly Ser Ala Asp Ala Phe Thr Ile Ala
35 40 45
Leu Ser Tyr Val Val Gly Gly Leu Val Pro Leu Leu Pro Tyr Val Leu
50 55 60
Val Ser Ala Ala Gln Asp Ala Met Leu Thr Ser Val Gly Val Thr Leu
65 70 75 80
Ala Ala Leu Leu Phe Phe Gly Tyr Val Lys Gly Arg Phe Thr Gly Glu
85 90 95
Pro Xaa Val Arg Gln Cys Arg Pro Asp Arg Cys His Trp Ser Ala Arg
100 105 110
Phe Gly Gly Gly Val Xaa Gly Trp
115 120

(2) INFORMATION FOR SEQ ID NO:2292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1502853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2292:

Met	Xaa	Arg	Phe	Glu	Leu	Gly	Leu	Glu	Arg	Pro	Asp	Pro	Arg	Arg	Ala	
1				5				10						15		
Leu	Gln	Thr	Pro	Ser	Arg	Ser	His	Cys	Pro	Thr	Trp	Ser	Ala	Gly	Trp	
			20				25						30			
Ser	Leu	Ser	Cys	Pro	Thr	Cys	Ser	Ser	Pro	Pro	Arg	Arg	Met	Pro	Cys	
			35				40					45				
Ser	His	Pro	Ser	Glu	Ser	Arg	Trp	Pro	Arg	Cys	Phe	Ser	Ser	Ala	Thr	
	50					55					60					
Ser	Arg	Ala	Ala	Ser	Arg	Gly	Asn	Xaa	Pro	Phe	Ala	Ser	Ala	Val	Gln	
	65				70			75						80		
Thr	Ala	Val	Ile	Gly	Ala	Leu	Ala	Ser	Ala	Ala	Ala	Tyr	Xaa	Asp		
				85				90						95		

(2) INFORMATION FOR SEQ ID NO:2293:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..475

(D) OTHER INFORMATION: / Ceres Seq. ID 1502860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2293:

atcccaaaagc	acaagagcac	gcactgcagc	accacttctc	gcgctgctgc	tcatacacaca	60
ccgtagtact	aacactccat	cgccacaatg	gctcccaagg	ttgcgctctt	ccttgccctc	120
agcctctctt	tcgctgccgc	cgcgcatggc	tgcgaaacct	actgtcccgc	cccagtcgtc	180
ccaacgccgc	cgcgtgtgcc	gtcgacacgc	cacggggcgt	gcssatcgac	gcactaaagc	240
tcaagggtgtg	cgccaacgtg	ctggacctcg	tcaaggtcgg	cctaccgccg	cacgagcaat	300
gttgcccgcgt	gctggagggg	ctggtagacc	tcgacggcgc	actgtgcctc	tgacccgccca	360
tcaaggctaa	cgctctcggc	atccacctca	acgtgccctc	tagcctcaac	ctctacctca	420
acaattgcgg	caagatttgc	ccaaaagact	ttacttgccc	caactaatgg	agctg	

(2) INFORMATION FOR SEQ ID NO:2294:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1502861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2294:

Ser	Gln	Ser	Thr	Arg	Ala	Arg	Thr	Ala	Ala	Pro	Leu	Pro	Ala	Leu	Leu	
1				5				10						15		
Leu	Ile	Thr	His	Arg	Ser	Thr	Asn	Thr	Pro	Ser	Pro	Gln	Trp	Leu	Pro	
			20				25						30			
Arg	Leu	Arg	Ser	Ser	Leu	Pro	Ser	Ala	Ser	Ser	Ser	Leu	Pro	Pro	Arg	
			35				40					45				
Met	Ala	Ala	Asn	Pro	Thr	Val	Pro	Ala	Gln	Ser	Ser	Gln	Arg	Arg	Pro	
	50				55					60						
Ser	Cys	Arg	Arg	Thr	Ala	Thr	Gly	Ala	Xaa	Xaa	Arg	Arg	Thr	Lys	Ala	
	65				70			75						80		
Gln	Gly	Val	Arg	Gln	Arg	Ala	Gly	Pro	Arg	Gln	Gly	Arg	Pro	Thr	Pro	

85 90 95
Ala Arg Ala Met Leu Pro Ala Ala Gly Gly Ala Gly Gly Pro Arg Arg
100 105 110
Arg Thr Val Pro Leu His Arg His Gln Gly
115 120

(2) INFORMATION FOR SEQ ID NO:2295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2295:

Pro Lys Ala Gln Glu His Ala Leu Gln His His Phe Leu Arg Cys Cys
1 5 10 15
Ser Ser His Thr Val Val Leu Thr Leu His Arg His Asn Gly Ser Gln
20 25 30
Gly Cys Ala Leu Pro Cys Pro Gln Pro Pro Leu Arg Cys Arg Arg Ala
35 40 45
Trp Leu Arg Thr Leu Leu Ser Arg Pro Ser Arg Pro Asn Ala Ala Arg
50 55 60
Arg Ala Val Ala Gln Pro Arg Ala Leu Xaa Ile Asp Ala Leu Lys Leu
65 70 75 80
Lys Val Cys Ala Asn Val Leu Asp Leu Val Lys Val Gly Leu Pro Gln
85 90 95
His Glu Gln Cys Cys Pro Leu Leu Glu Gly Leu Val Asp Leu Asp Ala
100 105 110
Ala Leu Cys Leu Cys Thr Ala Ile Lys Ala Asn Val Leu Gly Ile His
115 120 125
Leu Asn Val Pro Leu Ser Leu Asn Leu Ile Leu Asn Cys Gly Lys
130 135 140
Ile Cys Pro Lys Asp Phe Thr Cys Pro Asn
145 150

(2) INFORMATION FOR SEQ ID NO:2296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..334
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2296:

cactttcttta agacgagttg tggtagcccg aattatgcag cacttgaggt catatctggt 60
aaactatata ctggtcctga agttgacgctg tggagctgtg gagttattot ttatgctctt 120
ctttgtggca ctctccatt tgacgatgag aatattocaa accttttcaa gaaataaag 180
ggtggaatat atacccttcc tagtcatttg tcaccttcag cgagggactt gattcccaga 240
atgctggttg ttgatccaat gaaaaggatt acaatacgtg aaatccgtga acatgtgtgg 300
ttcaagatcc gacttccgcg ctatttgggt gtgc

(2) INFORMATION FOR SEQ ID NO:2297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..111
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502897
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2297:
His Phe Leu Lys Thr Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu
1 5 10 15
Val Ile Ser Gly Lys Leu Tyr Ala Gly Pro Glu Val Asp Val Trp Ser
 20 25 30
Cys Gly Val Ile Leu Tyr Ala Leu Leu Cys Gly Thr Leu Pro Phe Asp
 35 40 45
Asp Glu Asn Ile Pro Asn Leu Phe Lys Lys Ile Lys Gly Gly Ile Tyr
50 55 60
Thr Leu Pro Ser His Leu Ser Pro Ser Ala Arg Asp Leu Ile Pro Arg
65 70 75 80
Met Leu Val Val Asp Pro Met Lys Arg Ile Thr Ile Arg Glu Ile Arg
 85 90 95
Glu His Val Trp Phe Lys Ile Arg Leu Pro Arg Tyr Leu Ala Val
 100 105 110

(2) INFORMATION FOR SEQ ID NO:2298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2298:

Thr Phe Leu Arg Arg Val Val Val Ala Arg Ile Met Gln His Leu Arg
1 5 10 15
Ser Tyr Leu Val Asn Tyr Met Leu Val Leu Lys Leu Thr Ser Gly Ala
 20 25 30
Val Glu Leu Phe Phe Met Leu Phe Phe Val Ala Leu Ser His Leu Thr
 35 40 45
Met Arg Ile Phe Gln Thr Phe Ser Arg Lys
50 55

(2) INFORMATION FOR SEQ ID NO:2299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2299:

atcagtcctgt tccaccagca cgcgnaccac actcgccgac cgnaaatgaa ccacggcgcc 60
ggcgggagga gcacgagccg gctccgggac cggctggccc ggaatgtccg ccagagcgcc 120
ctgctccgct ccacctgcaa caggcgccgc gccgcatact cctgctctcc ctgctctccc 180
cgctccacgg ccaagctccc gcctccgcct gtggctgcgg cggcctccgc gtgctctccc 240
agccgcgcgc tgctcgccgc cgtcgtcgac ggggaactcgt cgttctccgc ctctcggcg 300
cgcgacctcg cgcgc

(2) INFORMATION FOR SEQ ID NO:2300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..105
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502903
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2300:
Ile Ser Pro Val His Gln His Arg Xaa His Thr Arg Arg Pro Xaa Met
1 5 10 15
Asn His Gly Gly Gly Arg Ser Ser Ser Arg Leu Arg Asp Arg Leu
 20 25 30
Ala Arg Met Phe Arg Pro Ser Ala Leu Leu Arg Ser Thr Cys Asn Thr
 35 40 45
Ala Ala Ala Ala Ser Ser Cys Ser Ser Ser Ser Pro Ala Ser Thr Ala
50 55 60
Lys Pro Pro Pro Pro Pro Val Ala Ala Ala Ala Ser Ala Cys Ser Ser
65 70 75 80
Ser Arg Ala Leu Leu Gly Ala Val Val Asp Gly Asp Ser Ser Phe Leu
 85 90 95
Ala Ser Ser Arg Arg Asp Leu Ala Val
 100 105

(2) INFORMATION FOR SEQ ID NO:2301:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..104
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502904
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2301:
Gln Ser Cys Pro Pro Ala Pro Xaa Pro His Ser Pro Thr Xaa Asn Glu
1 5 10 15
Pro Arg Arg Arg Arg Glu Glu Gln Gln Pro Ala Pro Gly Pro Ala Gly
 20 25 30
Pro Asp Val Pro Pro Glu Arg Ala Ala Pro Leu His Leu Gln His Gly
 35 40 45
Arg Arg Arg Ile Leu Leu Leu Leu Val Ser Arg Val His Gly Gln
50 55 60
Ala Ser Ala Ser Ala Cys Gly Cys Gly Gly Leu Arg Val Leu Leu Gln
65 70 75 80
Pro Arg Ala Ala Arg Arg Arg Arg Arg Gly Leu Val Val Pro Arg
 85 90 95
Leu Leu Ala Ala Arg Pro Arg Arg
 100

(2) INFORMATION FOR SEQ ID NO:2302:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..90
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502905
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2302:

Met Asn His Gly Gly Gly Arg Ser Ser Ser Arg Leu Arg Asp Arg
1 5 10 15
Leu Ala Arg Met Phe Arg Pro Ser Ala Leu Leu Arg Ser Thr Cys Asn
20 25 30
Thr Ala Ala Ala Ala Ser Ser Cys Ser Ser Ser Pro Ala Ser Thr
35 40 45
Ala Lys Pro Pro Pro Pro Val Ala Ala Ala Ala Ser Ala Cys Ser
50 55 60
Ser Ser Arg Ala Leu Leu Gly Ala Val Val Asp Gly Asp Ser Ser Phe
65 70 75 80
Leu Ala Ser Ser Arg Arg Asp Leu Ala Val
85 90

(2) INFORMATION FOR SEQ ID NO:2303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..337
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2303:

aaaacccatt	gtgtgccgcg	cgtcgacgca	gcctccgtcc	tcccccgcat	ccgaatcacg	60
cacgccaacg	tcccaccct	gtcatggcca	cctccagcga	cgcgcgggcg	accagcgggc	120
ctctctccca	tccccaagga	aggcgagcgc	atcatcgcg	ccacgssccg	ccccgacggc	180
acgctccgca	agggcatccg	catccgcgcc	ggttacgtgc	cccaggagga	ggtcgccatc	240
taccagtcca	agggcgccct	aatgaggaa	tcagggcccg	acgtgccgcc	ggggtagcac	300
ccggcgcyta	gtggccgacg	ccaaaccccc	ccccccc			

(2) INFORMATION FOR SEQ ID NO:2304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2304:

Lys Thr His Cys Val Pro Ala Val Asp Ala Ala Ser Val Leu Pro Arg
1 5 10 15
Ile Arg Ile Thr His Ala Asn Val Pro Pro Leu Ser Trp Pro Pro Pro
20 25 30
Ala Thr Ala Arg Arg Pro Ala Ala Leu Leu Ser Ile Pro Lys Glu Gly
35 40 45
Glu Arg Ile Ile Ala Pro Thr Xaa Arg Pro Asp Gly Thr Leu Arg Lys
50 55 60
Ala Ile Arg Ile Arg Ala Gly Tyr Val Pro Glu Glu Val Ala Ile
65 70 75 80
Tyr Gln Ser Lys Gly Ala Leu Met Arg Lys Ser Gly Pro Asp Val Pro
85 90 95
Pro Gly Tyr Asp Pro Ala Xaa Ser Gly Arg Arg Gln Thr Pro Pro Pro
100 105 110

(2) INFORMATION FOR SEQ ID NO:2305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..86
(D) OTHER INFORMATION: / Ceres Seq. ID 1502939
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2305:
Lys Pro Ile Val Cys Pro Pro Ser Thr Gln Pro Pro Ser Ser Pro Ala
1 5 10 15
Ser Glu Ser Arg Thr Pro Thr Ser His Pro Cys His Gly His Leu Gln
20 25 30
Arg Arg Arg Gly Asp Gln Arg Arg Ser Ser Pro Ser Pro Arg Lys Ala
35 40 45
Ser Ala Ser Ser Arg Pro Xaa Xaa Ala Pro Thr Ala Arg Ser Ala Arg
50 55 60
Pro Ser Ala Ser Ala Pro Val Thr Cys Pro Arg Arg Ser Pro Ser
65 70 75 80
Thr Ser Pro Arg Ala Pro
85

(2) INFORMATION FOR SEQ ID NO:2306:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..102
(D) OTHER INFORMATION: / Ceres Seq. ID 1502940
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2306:
Asn Pro Leu Cys Ala Arg Arg Arg Arg Ser Leu Arg Pro Pro His
1 5 10 15
Pro Asn His Ala Arg Gln Arg Pro Thr Pro Val Met Ala Thr Ser Ser
20 25 30
Asp Gly Ala Ala Thr Ser Gly Ala Pro Leu His Pro Gln Gly Arg Arg
35 40 45
Ala His His Arg Ala His Xaa Pro Pro Arg Arg His Ala Pro Gln Gly
50 55 60
His Pro His Pro Arg Arg Leu Arg Ala Pro Gly Gly Gly Arg His Leu
65 70 75 80
Pro Val Gln Gly Arg Pro Asn Glu Glu Val Arg Ala Arg Arg Ala Ala
85 90 95
Gly Val Arg Pro Gly Xaa
100

(2) INFORMATION FOR SEQ ID NO:2307:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 443 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..443
(D) OTHER INFORMATION: / Ceres Seq. ID 1502981
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2307:
aatcggtcaaa tcacgtctac ttgcttcgac acgattctcc agggatacgt cccatctgct
gcgaccaggg cgatggggga ggaggagacc cgcgaggcg acctcccga gccgtgcctg
60
120

gcgacgcgcca tcgcgcctcac ctgcgcgcgc gacgcctgcc gctgcgcgcgc cgtctcccc 180
gccttcgcgcg ccgcgcgcgca ctccgactac gtctgggggcc gcttcgtccc ggaggatacac 240
cgccgcgcgcca tcgcgcctgca tctgcatgcc gccgcgcgcgc accgtgggcc gaggaaggac 300
gcgtaccttg cgctctgcga cgccgcgcgc gccgcgcgtcc ccgtcgacgt cgacgtcgas 360
gccttggtgc agcgtgtggc tggaccaggc cagcgssgcc aagtgcctac gcgtgtcggc 420
gaggagcctc agcctgcctg ggg

(2) INFORMATION FOR SEQ ID NO:2308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1502982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2308:

Asn	Arg	Ser	Ile	Thr	Ser	Thr	Cys	Leu	Gln	Thr	Ile	Leu	Gln	Gly	Tyr
1			5					10					15		
Val	Pro	Ser	Ala	Ala	Thr	Arg	Ala	Met	Gly	Glu	Glu	Glu	Thr	Arg	Ala
			20				25						30		
Gly	Asp	Leu	Pro	Glu	Pro	Cys	Leu	Ala	His	Ala	Ile	Ala	Leu	Thr	Ser
		35					40					45			
Pro	Arg	Asp	Ala	Cys	Arg	Cys	Ala	Ala	Val	Ser	Pro	Ala	Phe	Arg	Ala
		50				55					60				
Ala	Ala	Asp	Ser	Asp	Tyr	Val	Trp	Gly	Arg	Phe	Val	Pro	Glu	Asp	His
		65			70				75					80	
Arg	Arg	Ala	Ile	Ala	Leu	His	Leu	His	Ala	Ala	Gly	Arg	Asp	Arg	Gly
			85					90					95		
Pro	Arg	Lys	Asp	Ala	Tyr	Leu	Ala	Leu	Cys	Asp	Gly	Gly	Gly	Gly	Gly
		100					105					110			
Val	Pro	Val	Asp	Val	Asp	Val	Xaa	Ala	Leu	Val	Gln	Ala	Val	Ala	Gly
		115					120				125				
Pro	Gly	Gln	Xaa	Xaa	Gln	Val	Leu	Arg	Ala	Val	Gly	Glu	Glu	Ala	Gln
		130				135					140				
Pro	Ala	Val													
		145													

(2) INFORMATION FOR SEQ ID NO:2309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1502983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2309:

Ile	Gly	Gln	Ser	Arg	Leu	Leu	Ala	Cys	Arg	Arg	Phe	Ser	Arg	Asp	Thr
1			5					10					15		
Ser	His	Leu	Leu	Arg	Pro	Gly	Arg	Trp	Gly	Arg	Arg	Arg	Pro	Ala	Gln
			20					25					30		
Ala	Thr	Ser	Arg	Ser	Arg	Ala	Trp	Arg	Thr	Pro	Ser	Arg	Ser	Pro	Arg
		35					40					45			
Arg	Ala	Thr	Pro	Ala	Ala	Ala	Pro	Pro	Ser	Pro	Pro	Pro	Ser	Ala	Pro
		50				55					60				
Pro	Pro	Thr	Pro	Thr	Thr	Ser	Gly	Ala	Ala	Ser	Ser	Arg	Arg	Ile	Thr
		65			70				75					80	
Ala	Ala	Pro	Ser	Pro	Cys	Ile	Cys	Met	Pro	Pro	Ala	Gly	Thr	Val	Gly

(2) INFORMATION FOR SEQ ID NO:2310:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME

(B) LOCATION: 1 - 147

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:2310:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:2310:
Val Asp His Val Thr Leu Leu Ala Asp Asp Ser

(2) INFORMATION FOR SEO ID NO:2311:

(A) LENGTH: 335 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

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(ix) FEATURE:
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(A) NAME

(B) LOCATION: 1

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:2311:

ggaaaac gggggcagtt ggtgagttgg gacttgggag co

caatggcggc	ggggggcagc	ggagcggcgg	gcgcggggag	ctgcgcgcgc	ggggggcgcc	
cagtgcgcgc	cgaacgccgc	gaacgcgcgc	gcgcgcgcgc	ctccctctac	gcgggacssgg	120
naggaccctt	ccactccacg	agccggcgct	gtccgatcgt	gagcccatgt	cggaatccat	180
cgtctccctg	gccgcgcgcc	ccgcggcgcc	ckcgccctgc	ttctcctacc	tgcccgctgt	240
ctcccaactg	ccgctcgctg	ccgcggtgct	cgccctcgcc	atcgcgcagt	cttccaaagt	300
ctctaccacc	tggtataaag	agaacccggtg	ggacg			

(2). INFORMATION FOR SEQ ID NO:2312:

(1) SEQUENCE CHARACTERISTICS:

(一) 二、三、四、五、六、七、八、九、十、十一、十二、十三、十四、十五、十六、十七、十八、十九、二十、二十一、二十二、二十三、二十四、二十五、二十六、二十七、二十八、二十九、三十、三十一、三十二、三十三、三十四、三十五、三十六、三十七、三十八、三十九、四十、四十一、四十二、四十三、四十四、四十五、四十六、四十七、四十八、四十九、五十、五十一、五十二、五十三、五十四、五十五、五十六、五十七、五十八、五十九、六十、六十一、六十二、六十三、六十四、六十五、六十六、六十七、六十八、六十九、七十、七十一、七十二、七十三、七十四、七十五、七十六、七十七、七十八、七十九、八十、八十一、八十二、八十三、八十四、八十五、八十六、八十七、八十八、八十九、九十、九十一、九十二、九十三、九十四、九十五、九十六、九十七、九十八、九十九、一百

(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..111
(D) OTHER INFORMATION: / Ceres Seq. ID 1502986
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2312:
Thr Glu Thr Gly Ala Val Gly Glu Leu Gly Leu Gly Ser Arg Arg Cys
1 5 10 15
Arg Gly Asp Pro Val Ala Ala Asp Ala Ala Glu Arg Ala Arg Ala Arg
20 25 30
Ala Ser Leu Tyr Ala Asp Xaa Xaa Gly Pro Phe His Ser Gln Ser Arg
35 40 45
Ala Cys Pro Ile Val Ser Pro Trp Arg Asn Pro Ser Ser Pro Ala Pro
50 55 60
Pro Pro Arg Arg Arg Xaa Arg Pro Arg Ser Pro Thr Trp Pro Cys Ser
65 70 75 80
Pro Thr Ala Arg Ser Ser Pro Arg Cys Ser Pro Ser Pro Ser Arg Ser
85 90 95
Pro Ser Arg Ser Ser Pro Pro Gly Ile Arg Arg Thr Gly Gly Thr
100 105 110

(2) INFORMATION FOR SEQ ID NO:2313:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..56
(D) OTHER INFORMATION: / Ceres Seq. ID 1502987
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2313:
Met Ala Glu Ser Ile Val Ser Gly Ala Ala Ala Pro Pro Gly Xaa
1 5 10 15
Pro Ser Phe Ser Tyr Leu Ala Val Phe Ser Asn Cys Pro Leu Val Ala
20 25 30
Ala Val Leu Ala Phe Ala Ile Ala Gln Ser Ile Lys Val Leu Thr Thr
35 40 45
Trp Tyr Lys Glu Asn Arg Trp Asp
50 55

(2) INFORMATION FOR SEQ ID NO:2314:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 505 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..505
(D) OTHER INFORMATION: / Ceres Seq. ID 1503000
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2314:
gaaggaattc cgcgtcgccg tcaagcaggt gctcgacctg ttccaggaca actacccccga 60
gctcgctcgcg agaaacatct tgatcaacgt gccgttcttg tactacgcgt tcagcacctc 120
gttctaccgc ttctcgacgc agaggacgaa gagcaagttc gtcgttgctc gcccgcccaa 180
ggtcaccgag acctctctca agtatcatcc gatcgaggcc atcccggtga agtacggcgg 240
cctgaagcgc gacggcgaca ccgagttctc cgcggacgac ggccgaggtcg cggaggtcac 300

cgctcaaggga agctccacgg agaccatcga gatcgaagcc actgaggctg atgccacgct 360
gacatggggac ctgacgggtgc tgggggtggga ggtgaactac aaggaggagt tcgtgccggc 420
ggacgagggc tcctacacca tcctcgtcag gaagggcaag aagatggcgt ccggcgagga 480
kcgcggtccgc aactcgttcc gcacc

(2) INFORMATION FOR SEQ ID NO:2315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2315:

Glu Gly Leu Pro Arg Arg Arg Gln Ala Gly Ala Arg Pro Val Pro Gly
1 5 10 15
Gln Leu Pro Arg Ala Arg Arg Glu Lys His Leu Asp Gln Arg Ala Val
20 25 30
Leu Val Leu Arg Val Gln His Pro Val Leu Pro Val Pro Asp Ala Glu
35 40 45
Asp Glu Glu Gln Val Arg Arg Cys Ser Pro Val Gln Gly His Arg Asp
50 55 60
Pro Pro Gln Val His Ser Asp Arg Gly His Pro Gly Glu Val Arg Arg
65 70 75 80
Pro Glu Ala Arg Arg Arg His Arg Val Leu Arg Gly Arg Arg Gly
85 90 95
Arg Gly Gly His Arg Gln Gly Lys Leu His Gly Asp His Arg Asp Arg
100 105 110
Ser His

(2) INFORMATION FOR SEQ ID NO:2316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2316:

Lys Asp Phe Arg Val Ala Val Lys Gln Val Leu Asp Leu Phe Gln Asp
1 5 10 15
Asn Tyr Pro Glu Leu Val Ala Arg Asn Ile Leu Ile Asn Val Pro Phe
20 25 30
Trp Tyr Tyr Ala Phe Ser Thr Leu Phe Tyr Pro Phe Leu Thr Gln Arg
35 40 45
Thr Lys Ser Lys Phe Val Val Ala Arg Pro Ser Lys Val Thr Glu Thr
50 55 60
Leu Leu Lys Tyr Ile Pro Ile Glu Ala Ile Pro Val Lys Tyr Gly Gly
65 70 75 80
Leu Lys Arg Asp Gly Asp Thr Glu Phe Ser Ala Asp Asp Gly Glu Val
85 90 95
Ala Glu Val Thr Val Lys Gly Ser Ser Thr Glu Thr Ile Glu Ile Glu
100 105 110
Ala Thr Glu Ala Asp Ala Thr Leu Thr Trp Asp Leu Thr Val Leu Gly
115 120 125
Trp Glu Val Asn Tyr Lys Glu Glu Phe Val Pro Ala Asp Glu Gly Ser

130 135 140
Tyr Thr Ile Ile Val Arg Lys Gly Lys Lys Met Ala Ser Gly Glu Xaa
145 150 155 160
Ala Val Arg Asn Ser Phe Arg Thr

- 165
(2) INFORMATION FOR SEQ ID NO:2317:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 495 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..495
(D) OTHER INFORMATION: / Ceres Seq. ID 1503010
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2317:

gtcggtccat agcatcgatt cactccgcgc gcgcgcgtgt ctctcgtcgc tcgcccgcgtt 60
cctcgattat ctctccatgg cggccgctca tcccccgctg catccgcgcgc ctcccccggt 120
aggggtcgcg cgaccctccc gcggcassag cggcgcgcgc gctgggtgcc cctgccecat 180
atgcctcgaa gccctcaaa acgaggccta cctcgacact tgettccatt ccttttgcta 240
caagtgtata tggcagtggtg taaggatagt agcgagcaag caccgagaac ctttgtcttc 300
agttagatgt ccactttgta agactgagaa tctatccgtc atacatgctt ttgatggcga 360
atcatttgag cgggtgtaca taaatcagga acytaggaag aggcgttctt tcagatgcac 420
acgagttggt gtcacaattc tataacatga aagagaccac aagcaacatt tctagggtgc 480
agcaataactg ggagc

- (2) INFORMATION FOR SEQ ID NO:2318:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..147
(D) OTHER INFORMATION: / Ceres Seq. ID 1503011
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2318:

Ser Val His Ser Ile Asp Ser Leu Arg Ala Arg Arg Cys Leu Leu Val
1 5 10 15
Val Ala Ala Phe Leu Asp Tyr Leu Ser Met Ala Ala Ala His Pro Pro
20 25 30
Leu His Pro Pro Pro Pro Val Gly Cys Arg Arg Pro Ser Arg Gly
35 40 45
Xaa Ser Gly Ala Thr Ala Gly Cys Pro Cys Pro Ile Cys Leu Glu Ala
50 55 60
Phe Lys Asp Glu Ala Tyr Leu Asp Thr Cys Phe His Ser Phe Cys Tyr
65 70 75 80
Lys Cys Ile Cys Glu Trp Val Arg Ile Val Ala Ser Lys His Ala Glu
85 90 95
Pro Leu Ser Ser Val Arg Cys Pro Leu Cys Lys Thr Glu Asn Leu Ser
100 105 110
Val Ile His Ala Phe Asp Gly Glu Ser Phe Glu Arg Trp Tyr Ile Asn
115 120 125
Gln Glu Xaa Arg Lys Arg Arg Ser Phe Arg Cys Thr Arg Val Gly Val
130 135 140
Thr Ile Leu

- 145
(2) INFORMATION FOR SEQ ID NO:2319:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..122
(D) OTHER INFORMATION: / Ceres Seq. ID 1503012
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2319:
Met Ala Ala His Pro Pro Leu His Pro Pro Pro Pro Val Gly
1 5 10 15
Cys Arg Arg Pro Ser Arg Gly Xaa Ser Gly Ala Thr Ala Gly Cys Pro
20 25 30
Cys Pro Ile Cys Leu Glu Ala Phe Lys Asp Glu Ala Tyr Leu Asp Thr
35 40 45
Cys Phe His Ser Phe Cys Tyr Lys Cys Ile Cys Gln Trp Val Arg Ile
50 55 60
Val Ala Ser Lys His Ala Glu Pro Leu Ser Ser Val Arg Cys Pro Leu
65 70 75 80
Cys Lys Thr Glu Asn Leu Ser Val Ile His Ala Phe Asp Gly Glu Ser
85 90 95
Phe Glu Arg Trp Tyr Ile Asn Gln Glu Xaa Arg Lys Arg Arg Ser Phe
100 105 110
Arg Cys Thr Arg Val Gly Val Thr Ile Leu
115 120

(2) INFORMATION FOR SEQ ID NO:2320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..436
(D) OTHER INFORMATION: / Ceres Seq. ID 1503042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2320:

cttttttcgg aggaggcgga ccaggtaagc agcagcagga accctagcac cgccgcatcc 60
gcagccatgg gtatcgacct cgttgccggt gggaggaaca agaagacca ggcacacgcs 120
cgaagtcoga cgaatgtttat ctcaagctcc ttgtcaagct ctaccgtttc ttggtcagga 180
ggaccaagag caacttcaat gctgtcattc tcaagaggct ctccatgagc aaacacatc 240
gccaccacat ctccatgcgc cgcctgttca agttcatgga aggaaggag aagaacattg 300
ctgtgattgt tggcacagtc acagatgaca agaggatcca agaggttcca gcaatgaagg 360
gaagctcgat gactacatga agttctttga tggctcttct gcttagatgt ttatttgtga 420
ctgctagggg cgatgt

(2) INFORMATION FOR SEQ ID NO:2321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..75
(D) OTHER INFORMATION: / Ceres Seq. ID 1503043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2321:

Leu Phe Ser Glu Glu Ala Asp Gln Val Ser Ser Ser Arg Asn Pro Ser
1 5 10 15
Thr Ala Ala Ser Ala Ala Met Gly Ile Asp Leu Val Ala Gly Gly Arg
20 25 30

Asn Lys Lys Thr Lys Arg Thr Xaa Arg Ser Pro Thr Met Phe Ile Ser
35 40 45
Ser Ser Leu Ser Ser Ser Thr Val Ser Trp Ser Gly Gly Pro Arg Ala
50 55 60
Thr Ser Met Leu Ser Phe Ser Arg Gly Ser Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:2322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1503044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2322:

Met Gly Ile Asp Leu Val Ala Gly Gly Arg Asn Lys Lys Thr Lys Arg
1 5 10 15
Thr Xaa Arg Ser Pro Thr Met Phe Ile Ser Ser Ser Leu Ser Ser Ser
20 25 30
Thr Val Ser Trp Ser Gly Gly Pro Arg Ala Thr Ser Met Leu Ser Phe
35 40 45
Ser Arg Gly Ser Ser
50

(2) INFORMATION FOR SEQ ID NO:2323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51

(D) OTHER INFORMATION: / Ceres Seq. ID 1503045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2323:

Met Ser Lys Thr Asn Arg Pro Pro Ile Ser Met Arg Arg Leu Val Lys
1 5 10 15
Phe Met Glu Gly Lys Glu Lys Asn Ile Ala Val Ile Val Gly Thr Val
20 25 30
Thr Asp Asp Lys Arg Ile Gln Glu Val Pro Ala Met Lys Gly Ser Ser
35 40 45
Met Thr Thr
50

(2) INFORMATION FOR SEQ ID NO:2324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..227

(D) OTHER INFORMATION: / Ceres Seq. ID 1503048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2324:

aggacaggtt gcatttgcat ctgagttcct gatcgttgta ttccagtttc ttccgtgagt 60
tttgtgggat cgcgaggaag aaggatgtcg tgctgcggag gcaactgcgg gtgcggcgcc 120
ggggcassag ccggcggggca gtgcctgccg cagctgaacc gcctcctggs stgccgcgcg 180

tacctgtgtgc ccggcgcgcc ggaccccagc gcggactgct gcagcgc

(2) INFORMATION FOR SEQ ID NO:2325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1503049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2325:

Met	Ser	Cys	Cys	Gly	Gly	Asn	Cys	Gly	Cys	Gly	Ala	Gly	Xaa	Xaa	Ala
1				5				10					15		
Gly	Gly	Gln	Cys	Leu	Pro	Gln	Leu	Asn	Arg	Leu	Leu	Xaa	Cys	Arg	Ala
			20				25					30			
Tyr	Leu	Val	Pro	Gly	Ala	Pro	Asp	Pro	Ser	Ala	Asp	Cys	Cys	Ser	
	35					40					45				

(2) INFORMATION FOR SEQ ID NO:2326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..512

(D) OTHER INFORMATION: / Ceres Seq. ID 1503064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2326:

aattctccc	gcctcccct	cgaccctcc	gactaccgc	gcctctctg	scasstctcc	60
tccgcggcc	ttctgcagc	cgctcgccc	acccccagg	tacagctcg	ctgatggcc	120
gtctctctt	acgcggcgt	ctacctctc	ctcgctctg	ccassgcct	ggcssacatg	180
ctgcctggg	ggctcctcg	cttcgtctg	atccagctc	gctggatgg	ccacgactcg	240
ggccaccac	gcatacggg	ccatccgct	ctggaccgc	tcgtgcagg	gctctccgga	300
aactgcctc	ctggcctcag	catcgctcg	tggaaatga	accacaac	gcaccacatc	360
gcctgcaaca	gcctggacca	tgacccgga	ctccagcaca	tgccgctct	cgctgtctcc	420
cccaagctgt	tcggcaacat	atggtctct	tkctaccag	ggaccctgg	cttcgacgc	480
gcctcgaaat	tcctcatcag	ctaccagcac	tg			

(2) INFORMATION FOR SEQ ID NO:2327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1503065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2327:

Asn	Ser	Pro	Arg	Leu	Pro	Leu	Arg	Pro	Ser	Asp	Tyr	Arg	Arg	Leu	Leu
1				5				10						15	
Xaa	Xaa	Xaa	Ser	Ser	Ala	Gly	Leu	Phe	Glu	Arg	Val	Gly	Pro	Thr	Pro
			20				25					30			
Arg	Val	Gln	Leu	Ala	Leu	Met	Ala	Val	Leu	Phe	Tyr	Ala	Ala	Leu	Tyr
	35					40					45				
Leu	Val	Leu	Ala	Cys	Ala	Xaa	Ala	Ser	Xaa	Xaa	Met	Leu	Ala	Gly	Gly
	50					55					60				
Leu	Ile	Gly	Phe	Val	Trp	Ile	Gln	Ser	Gly	Trp	Met	Gly	His	Asp	Ser

65					70					75					80
Gly	His	His	Arg	Ile	Thr	Gly	His	Pro	Leu	Leu	Asp	Arg	Val	Val	Gln
					85					90					95
Val	Leu	Ser	Gly	Asn	Cys	Leu	Thr	Gly	Leu	Ser	Ile	Ala	Trp	Trp	Lys
					100					105					110
Cys	Asn	His	Asn	Thr	His	His	Ile	Ala	Cys	Asn	Ser	Leu	Asp	His	Asp
					115					120					125
Pro	Asp	Leu	Gln	His	Met	Pro	Leu	Phe	Ala	Val	Ser	Pro	Lys	Leu	Phe
					130					135					140
Gly	Asn	Ile	Trp	Ser	Tyr	Xaa	Tyr	Gln	Arg	Thr	Leu	Ala	Phe	Asp	Ala
					145					150					155
Ala	Ser	Lys	Phe	Leu	Ile	Ser	Tyr	Gln	His						160
					165				170						

(2) INFORMATION FOR SEQ ID NO:2328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2328:

Phe	Ser	Pro	Pro	Pro	Pro	Pro	Thr	Leu	Arg	Leu	Pro	Pro	Pro	Pro	Xaa
1						5				10					15
Xaa	Xaa	Leu	Leu	Arg	Gly	Pro	Leu	Arg	Ala	Arg	Arg	Pro	His	Pro	Gln
						20				25				30	
Gly	Thr	Ala	Arg	Pro	Asp	Gly	Arg	Pro	Leu	Leu	Arg	Gly	Ala	Leu	Pro
						35				40				45	
Arg	Pro	Arg	Leu	Arg	Xaa	Xaa	Leu	Gly	Xaa	His	Ala	Arg	Trp	Gly	Ala
						50				55				60	
His	Arg	Leu	Arg	Leu	Asp	Pro	Val	Arg	Leu	Asp	Gly	Pro	Arg	Leu	Gly
						65				70				75	
Pro	Pro	Pro	His	His	Gly	Pro	Ser	Ala	Pro	Gly	Pro	Arg	Arg	Ala	Gly
						85				90				95	
Ala	Leu	Arg	Lys	Leu	Pro	His	Trp	Pro	Gln	His	Arg	Leu	Val	Glu	Met
						100				105				110	
Gln	Pro	Gln	His	Ala	Pro	His	Arg	Leu	Gln	Gln	Pro	Gly	Pro		
						115				120				125	

(2) INFORMATION FOR SEQ ID NO:2329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2329:

Met	Ala	Val	Leu	Phe	Tyr	Ala	Ala	Leu	Tyr	Leu	Val	Leu	Ala	Cys	Ala
1						5				10				15	
Xaa	Ala	Ser	Xaa	Xaa	Met	Leu	Ala	Gly	Gly	Leu	Ile	Gly	Phe	Val	Trp
						20				25				30	
Ile	Gln	Ser	Gly	Trp	Met	Gly	His	Asp	Ser	Gly	His	His	Arg	Ile	Thr
						35				40				45	
Gly	His	Pro	Leu	Leu	Asp	Arg	Val	Val	Gln	Val	Leu	Ser	Gly	Asn	Cys
						50				55				60	

Leu Thr Gly Leu Ser Ile Ala Trp Trp Lys Cys Asn His Asn Thr His
65 70 75 80
His Ile Ala Cys Asn Ser Leu Asp His Asp Pro Asp Leu Gln His Met
85 90 95
Pro Leu Phe Ala Val Ser Pro Lys Leu Phe Gly Asn Ile Trp Ser Tyr
100 105 110
Xaa Tyr Gln Arg Thr Leu Ala Phe Asp Ala Ala Ser Lys Phe Leu Ile
115 120 125
Ser Tyr Gln His
130

(2) INFORMATION FOR SEQ ID NO:2330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..305
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2330:

catgaagaaa	agaaaggcgg	tattccagacc	tcaagccctg	ctctgaagga	ggagctgcgc	60
aagaggctga	gcggttgctga	agatgatgag	gatttaagct	gggatatcga	ggatgacgat	120
gacaatgcct	gaataccatt	ggtgatatgg	aagtgtcagt	tgkatttcta	cattttgcac	180
cttccattac	tcgtgcaagt	tactgtgatt	tggccaatwa	gattggctat	cottatgcta	240
tggacacgtt	tgtatactgt	aaactctcca	gtttgatgat	atcaagtgcc	aattggctaa	300
gcgcc						

(2) INFORMATION FOR SEQ ID NO:2331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2331:

His	Glu	Glu	Lys	Lys	Gly	Gly	Ile	Gln	Thr	Ser	Ser	Pro	Ala	Leu	Lys
1			5				10							15	
Glu	Glu	Leu	Arg	Lys	Arg	Leu	Ser	Val	Ala	Glu	Asp	Asp	Glu	Asp	Leu
			20				25						30		
Ser	Trp	Asp	Ile	Glu	Asp	Asp	Asp	Asp	Asn	Ala					
			35				40								

(2) INFORMATION FOR SEQ ID NO:2332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2332:

Met	Glu	Val	Ser	Val	Xaa	Phe	Leu	His	Phe	Ala	Pro	Ser	Ile	Thr	Arg
1			5				10						15		
Ala	Ser	Tyr	Cys	Asp	Leu	Ala	Asn	Xaa	Ile	Gly	Tyr	Pro	Tyr	Ala	Met

20 25 30
Asp Thr Phe Val Tyr Cys Lys Leu Ser Ser Leu Met Ile Ser Ser Gly
35 40 45
Asn Trp Leu Ser Ala
50

(2) INFORMATION FOR SEQ ID NO:2333:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 414 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..414
(D) OTHER INFORMATION: / Ceres Seq. ID 1503104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2333:

atccccagaa aacaagacaca gagagagaga gaaccccagc gggcaaacgc ctccctcccc	60
ctgcctccag gccccagatc cggccatccg ggtagctcca gaccttctcc aatggcggtc	120
aagggtctacg tcgtgtttta ctccacctac gggcacgttg ccaagcttgc tgaggagatg	180
aagaaaggcg ccgcttcagt tgaaggcgtg gagggtcaaa tatggcaggt cccggagatt	240
ctgtccgagg aggtgctcgg caagatgggg cgccaccca agaccgacgc gccggtcatc	300
accccgacga gctggcgagg gccgacggcg tctctctcgg gtcccccacg cgggtcggca	360
tgatggcggc gcagatgaag gcctctctcg acgcgaccgg cgggctgtgg cgcg	

(2) INFORMATION FOR SEQ ID NO:2334:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..120
(D) OTHER INFORMATION: / Ceres Seq. ID 1503105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2334:

Ile Pro Arg Lys Gln Ala Gln Arg Glu Arg Glu Pro Gln Arg Ala Asn	
1 5 10 15	
Ala Ser Leu Pro Leu Pro Pro Gly Pro Arg Ser Gly His Pro Gly Ser	
20 25 30	
Ser Arg Pro Ser Pro Met Ala Val Lys Val Tyr Val Val Phe Tyr Ser	
35 40 45	
Thr Tyr Gly His Val Ala Lys Leu Ala Glu Glu Met Lys Lys Gly Ala	
50 55 60	
Ala Ser Val Glu Gly Val Glu Val Lys Val Trp Gln Val Pro Glu Ile	
65 70 75 80	
Leu Ser Glu Glu Val Leu Gly Lys Met Gly Ala Pro Pro Lys Thr Asp	
85 90 95	
Ala Pro Val Ile Thr Pro Gln Ser Trp Arg Arg Pro Thr Ala Ser Ser	
100 105 110	
Ser Gly Ser Pro Arg Gly Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:2335:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide

(B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1503106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2335:

Met	Ala	Val	Lys	Val	Tyr	Val	Val	Phe	Tyr	Ser	Thr	Tyr	Gly	His	Val	
1			5					10					15			
Ala	Lys	Leu	Ala	Glu	Glu	Met	Lys	Lys	Gly	Ala	Ala	Ser	Val	Glu	Gly	
			20					25					30			
Val	Glu	Val	Lys	Val	Trp	Gln	Val	Pro	Glu	Ile	Leu	Ser	Glu	Glu	Val	
			35					40					45			
Leu	Gly	Lys	Met	Gly	Ala	Pro	Pro	Lys	Thr	Asp	Ala	Pro	Val	Ile	Thr	
			50					55				60				
Pro	Gln	Ser	Trp	Arg	Arg	Pro	Thr	Ala	Ser	Ser	Ser	Gly	Ser	Pro	Arg	
							70				75				80	
Gly	Ser	Ala														

(2) INFORMATION FOR SEQ ID NO:2336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1503107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2336:

Met	Ala	Gly	Pro	Gly	Asp	Ser	Val	Arg	Gly	Gly	Ala	Arg	Gln	Asp	Gly	
1			5					10					15			
Arg	Ala	Thr	Gln	Asp	Arg	Arg	Ala	Gly	His	His	Pro	Ala	Glu	Leu	Ala	
			20					25					30			
Glu	Ala	Asp	Gly	Val	Leu	Phe	Gly	Phe	Pro	Thr	Arg	Phe	Gly	Met	Met	
			35					40				45				
Ala	Ala	Gln	Met	Lys	Ala	Phe	Phe	Asp	Ala	Thr	Gly	Gly	Leu	Trp	Arg	
			50					55				60				

(2) INFORMATION FOR SEQ ID NO:2337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 510 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..510

(D) OTHER INFORMATION: / Ceres Seq. ID 1503108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2337:

gtkattgggt	tggtcgcttg	gtttctccct	gcgggaagat	accttcgtt	cggtgtcgcc	60
aactcgccat	tcttgggagg	tcttggtcgg	gaccggtgct	gatggaggag	aggtacagg	120
cgctgaagga	gctggggggc	ggcaacttcg	gcgtggcgag	gctggtcagg	gacaagcggg	180
ccaaggagct	ggtagccgtc	aagtacatcg	agagggggc	gaagattgat	gagaacgtgc	240
agagggagat	catcaatcac	cagtcgtccc	ggcaccctaa	catcgtagcg	ttcaaggagg	300
tttgtctaac	accacacat	cttgctattg	tcattggaata	tgctgtggtg	ggagagctat	360
ttgagaaaa	ctgctcagca	gggcgattca	gtgaagatgw	ktccaggtat	ttcttccaac	420
agctgataac	aggggttcag	ctactgccat	tttatggaaa	tttgtcaccg	tgatctttaa	480
acttkagaac	acctcctctg	atggggatgc				

(2) INFORMATION FOR SEQ ID NO:2338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..156
(D) OTHER INFORMATION: / Ceres Seq. ID 1503109
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2338:
Xaa Trp Val Gly Arg Leu Val Leu Pro Cys Arg Lys Ile Pro Phe Val
1 5 10 15
Arg Cys Arg Gln Leu Ala Ile Leu Gly Arg Ser Trp Ser Gly Pro Val
20 25 30
Leu Met Glu Glu Arg Tyr Glu Ala Leu Lys Glu Leu Gly Ala Gly Asn
35 40 45
Phe Gly Val Ala Arg Leu Val Arg Asp Lys Arg Thr Lys Glu Leu Val
50 55 60
Ala Val Lys Tyr Ile Glu Arg Gly Lys Lys Ile Asp Glu Asn Val Gln
65 70 75 80
Arg Glu Ile Ile Asn His Gln Ser Leu Arg His Pro Asn Ile Val Arg
85 90 95
Phe Lys Glu Val Cys Leu Thr Pro Thr His Leu Ala Ile Val Met Glu
100 105 110
Tyr Ala Ala Gly Gly Glu Leu Phe Glu Lys Ile Cys Ser Ala Gly Arg
115 120 125
Phe Ser Glu Asp Xaa Ser Arg Tyr Phe Phe Gln Gln Leu Ile Ser Gly
130 135 140
Val Gln Leu Leu Pro Phe Tyr Gly Asn Leu Ser Pro
145 150 155
(2) INFORMATION FOR SEQ ID NO:2339:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..123
(D) OTHER INFORMATION: / Ceres Seq. ID 1503110
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2339:
Met Glu Glu Arg Tyr Glu Ala Leu Lys Glu Leu Gly Ala Gly Asn Phe
1 5 10 15
Gly Val Ala Arg Leu Val Arg Asp Lys Arg Thr Lys Glu Leu Val Ala
20 25 30
Val Lys Tyr Ile Glu Arg Gly Lys Lys Ile Asp Glu Asn Val Gln Arg
35 40 45
Glu Ile Ile Asn His Gln Ser Leu Arg His Pro Asn Ile Val Arg Phe
50 55 60
Lys Glu Val Cys Leu Thr Pro Thr His Leu Ala Ile Val Met Glu Tyr
65 70 75 80
Ala Ala Gly Gly Glu Leu Phe Glu Lys Ile Cys Ser Ala Gly Arg Phe
85 90 95
Ser Glu Asp Xaa Ser Arg Tyr Phe Phe Gln Gln Leu Ile Ser Gly Val
100 105 110
Gln Leu Leu Pro Phe Tyr Gly Asn Leu Ser Pro
115 120
(2) INFORMATION FOR SEQ ID NO:2340:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..263
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503132
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2340:
accagccggt gttggtttca gcttggtattc ccactctgtc gcacagcgtc gcccgctgcgc 60
gctgagatcc taggaagaaa tggagctctc tcgcaagctc ttcaaggccg tcctccctcgt 120
catgctgctg ctgctgtccg cagaggtcgg gccggtggcg gtggcggagg cgcggacgtg 180
ccagtcgcaq agccacaggt tccggggccc ctgcctccgc cggtcacaact gcgcacaagt 240
ctgcaggacc gaggggttcc ccg
(2) INFORMATION FOR SEQ ID NO:2341:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..87
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503133
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2341:
Thr Ser Arg Cys Trp Phe Gln Leu Val Phe Pro Leu Cys Arg Thr Ala
1 5 10 15
Ser Pro Val Ala Ala Glu Ile Leu Gly Arg Asn Gly Ala Leu Ser Gln
20 25 30
Ala Leu His Gly Arg Pro Pro Arg His Ala Ala Ala Val Arg Arg
35 40 45
Gly Arg Ala Gly Gly Gly Gly Gly Ala Asp Val Pro Val Ala Glu
50 55 60
Pro Gln Val Pro Gly Pro Leu Pro Pro Pro Val Gln Leu Arg Gln Arg
65 70 75 80
Leu Gln Asp Arg Gly Val Pro
85
(2) INFORMATION FOR SEQ ID NO:2342:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..61
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503134
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2342:
Met Glu Leu Ser Arg Lys Leu Phe Thr Ala Val Leu Leu Val Met Leu
1 5 10 15
Leu Leu Leu Ser Ala Glu Val Gly Pro Val Ala Val Ala Glu Ala Arg
20 25 30
Thr Cys Gln Ser Gln Ser His Arg Phe Arg Gly Pro Cys Leu Arg Arg
35 40 45
Ser Asn Cys Ala Asn Val Cys Arg Thr Glu Gly Phe Pro
50 55 60
(2) INFORMATION FOR SEQ ID NO:2343:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..47
(D) OTHER INFORMATION: / Ceres Seq. ID 1503135
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2343:
Met Leu Leu Leu Leu Ser Ala Glu Val Gly Pro Val Ala Val Ala Glu
1 5 10 15
Ala Arg Thr Cys Gln Ser Gln Ser His Arg Phe Arg Gly Pro Cys Leu
20 25 30
Arg Arg Ser Asn Cys Ala Asn Val Cys Arg Thr Glu Gly Phe Pro
35 40 45

(2) INFORMATION FOR SEQ ID NO:2344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..342

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2344:

tccaccacgc	cttcacatc	ccctccaggc	ccaccaccac	catggcctct	ctttcccttt	60
cttccccgcg	cgcgcctccc	ggccgcgcgc	tgccgcgcgc	gtgctggacg	accgacgaga	120
ccctcgcgct	cgcgssggtc	ctacaccgcg	ccgcgcctcg	cgtcggcccg	gagcacctga	180
cctccaccga	ctgggcgcgc	gtagccgcgc	cgccccgtcc	aagaccgcga	gcagtgcgcg	240
cacaagatcg	agaagctccg	cgcacgccto	cgtccaacc	gccgacgccc	atgcccgctt	300
ctctgacgcc	atggatctcc	tcgacggccc	tttcccgcgc	ct		

(2) INFORMATION FOR SEQ ID NO:2345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..113

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2345:

Pro	Pro	Pro	Leu	His	His	Pro	Leu	Gln	Ala	His	His	His	Gly	Leu
1			5					10					15	
Ser	Phe	Pro	Phe	Phe	Pro	Arg	Pro	Arg	Leu	Arg	Pro	Pro	Arg	Ala
			20					25					30	
Ala	Val	Leu	Asp	Asp	Arg	Arg	Asp	Pro	Arg	Ala	Arg	Xaa	Gly	Pro
			35					40					45	
Pro	Arg	Pro	Pro	Arg	Arg	Arg	Pro	Gly	Ala	Pro	Asp	Leu	His	Arg
			50					55				60		
Gly	Arg	Arg	Ser	Arg	Gly	Ala	Pro	Ser	Lys	Thr	Ala	Ser	Ser	Ala
			65					70						80
Thr	Arg	Ser	Arg	Ser	Ser	Ala	Asp	Ala	Ser	Gly	Pro	Thr	Ala	Asp
								85						95
His	Ala	Arg	Phe	Leu	Asp	Ala	Met	Asp	Leu	Leu	Asp	Gly	Pro	Phe
								100						110
Ala														

(2) INFORMATION FOR SEQ ID NO:2346:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..113
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503138
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2346:
His His Arg Phe Thr Ile Pro Ser Arg Pro Thr Thr Met Ala Ser
1 5 10 15
Pro Ser Pro Ser Ser Pro Ala Arg Ala Ser Gly Arg Arg Val Pro Pro
 20 25 30
Pro Cys Trp Thr Thr Asp Glu Thr Leu Ala Leu Xaa Val Leu His
 35 40 45
Arg Ala Arg Leu Ala Val Gly Arg Glu His Leu Thr Ser Thr Asp Trp
 50 55 60
Ala Ala Val Ala Ala Ala Pro Arg Pro Arg Pro Pro Ala Val Pro Pro
65 70 75 80
Gln Asp Arg Glu Ala Pro Pro Thr Pro Pro Val Gln Pro Pro Thr Pro
 85 90 95
Met Pro Ala Ser Ser Thr Pro Trp Ile Ser Ser Thr Ala Leu Ser Pro
 100 105 110
Pro

(2) INFORMATION FOR SEQ ID NO:2347:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..100
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503139
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2347:
Met Ala Ser Pro Ser Ser Ser Pro Ala Arg Ala Ser Gly Arg Arg
1 5 10 15
Val Pro Pro Pro Cys Trp Thr Thr Asp Glu Thr Leu Ala Leu Xaa
 20 25 30
Val Leu His Arg Ala Arg Leu Ala Val Gly Arg Glu His Leu Thr Ser
 35 40 45
Thr Asp Trp Ala Ala Val Ala Ala Ala Pro Arg Pro Arg Pro Pro Ala
 50 55 60
Val Pro Pro Gln Asp Arg Glu Ala Pro Pro Thr Pro Pro Val Gln Pro
65 70 75 80
Pro Thr Pro Met Pro Ala Ser Ser Thr Pro Trp Ile Ser Ser Thr Ala
 85 90 95
Leu Ser Pro Pro
 100

(2) INFORMATION FOR SEQ ID NO:2348:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..536
(D) OTHER INFORMATION: / Ceres Seq. ID 1503144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2348:
attacacacc agcctcttga tgcaggtttt agtgcattg tggaatcatg caaggkcctc 60
agkcggtttt ctgtttcagg tccttctcac ggacagtgtg tttaaatcca tcggggcaca 120
tgetgaccgt ctgtgagatgc tctcgattgc cttcgccggg aacagtgatt tgggcctcca 180
ttacatccta tcgggctgca agagcttgaa gaagctagag attagggact gccatttgg 240
tgacaagccc ttgctggcaa acgctgcaa gctggagaca atgcgatccc tttggatgtc 300
gacgtgtcta atgaccttgg ggcgatgagg cagcttgccg gcaagatgcc cgtcttagt 360
gtggaggtca tgaatgatcc tcgacgagga ttccccctgg acctcttaac agatgagagc 420
cctgttgaga cgtgttatgt ctaccggaca atttcaggtc caakgtccka cacaccagct 480
tgtgtccaga ttctctaagg ggcagctgtg gtcacaaa g tactatgga agcatc

(2) INFORMATION FOR SEQ ID NO:2349:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..123
(D) OTHER INFORMATION: / Ceres Seq. ID 1503145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2349:
Leu His Thr Ser Leu Leu Met Gln Val Leu Val Pro Leu Trp Asn His
1 5 10 15
Ala Arg Xaa Ser Xaa Gly Phe Leu Phe Gln Val Leu Leu Thr Asp Ser
20 25 30
Val Phe Lys Ser Ile Gly Ala His Ala Asp Arg Leu Glu Met Leu Ser
35 40 45
Ile Ala Phe Ala Gly Asn Ser Asp Leu Gly Leu His Tyr Ile Leu Ser
50 55 60
Gly Cys Lys Ser Leu Lys Lys Leu Glu Ile Arg Asp Cys Pro Phe Gly
65 70 75 80
Asp Lys Pro Leu Leu Ala Asn Ala Ala Lys Leu Glu Thr Met Arg Ser
85 90 95
Leu Trp Met Ser Thr Cys Ser Met Thr Leu Gly Ala Cys Gly Ser Leu
100 105 110
Arg Ala Arg Cys Pro Val Leu Val Trp Arg Ser
115 120

(2) INFORMATION FOR SEQ ID NO:2350:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..117
(D) OTHER INFORMATION: / Ceres Seq. ID 1503146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2350:
Met Gln Val Leu Val Pro Leu Trp Asn His Ala Arg Xaa Ser Xaa Gly
1 5 10 15
Phe Leu Phe Gln Val Leu Leu Thr Asp Ser Val Phe Lys Ser Ile Gly
20 25 30
Ala His Ala Asp Arg Leu Glu Met Leu Ser Ile Ala Phe Ala Gly Asn
35 40 45
Ser Asp Leu Gly Leu His Tyr Ile Leu Ser Gly Cys Lys Ser Leu Lys
50 55 60

Lys Leu Glu Ile Arg Asp Cys Pro Phe Gly Asp Lys Pro Leu Leu Ala
65 70 75 80
Asn Ala Ala Lys Leu Glu Thr Met Arg Ser Leu Trp Met Ser Thr Cys
85 90 95
Ser Met Thr Leu Gly Ala Cys Gly Ser Leu Arg Ala Arg Cys Pro Val
100 105 110
Leu Val Trp Arg Ser
115

(2) INFORMATION FOR SEQ ID NO:2351:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1503147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2351:

Met Leu Ser Ile Ala Phe Ala Gly Asn Ser Asp Leu Gly Leu His Tyr
1 5 10 15
Ile Leu Ser Gly Cys Lys Ser Leu Lys Lys Leu Glu Ile Arg Asp Cys
20 25 30
Pro Phe Gly Asp Lys Pro Leu Leu Ala Asn Ala Ala Lys Leu Glu Thr
35 40 45
Met Arg Ser Leu Trp Met Ser Thr Cys Ser Met Thr Leu Gly Ala Cys
50 55 60
Gly Ser Leu Arg Ala Arg Cys Pro Val Leu Val Trp Arg Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:2352:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1503148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2352:

atcaatgcgc gggtcaggct ctggaagcca atggtggagg agatgtacgt ggaggagatg 60
aaggccgagg gcaggacggc gggggccagc agcaggtagg cgtcgcgkcg ccaacaaccc 120
taaccctagc agcgccggcc acgcctccga ggcggcgtga ggacg

(2) INFORMATION FOR SEQ ID NO:2353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..32

(D) OTHER INFORMATION: / Ceres Seq. ID 1503149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2353:

Ile Asn Ala Arg Val Arg Leu Trp Lys Pro Met Val Glu Glu Met Tyr
1 5 10 15
Val Glu Glu Met Lys Ala Glu Gly Arg Thr Ala Gly Ala Ser Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO:2354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..54

(D) OTHER INFORMATION: / Ceres Seq. ID 1503150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2354:

```
Gln Cys Ala Gly Gln Ala Leu Glu Ala Asn Gly Gly Gly Asp Val Arg
1          5          10          15
Gly Gly Asp Glu Gly Arg Gly Gln Asp Gly Gly Gly Gln Gln Val
20          25          30
Gly Val Ala Xaa Pro Thr Thr Leu Thr Leu Ala Ala Pro Ala Thr Pro
35          40          45
Pro Arg Arg Arg Glu Asp
50
```

(2) INFORMATION FOR SEQ ID NO:2355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..453

(D) OTHER INFORMATION: / Ceres Seq. ID 1503151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2355:

```
ctctccagcg gctccagcca atccggcaat cccgctcccc cagctcgctg ctccgccgct 60
ctctcccgcc ctcgcccatg ggccttcccc ctccgcctcc cagtcgccgg cgatctccgc 120
ctcgacctgg agcatggctt cctccgtac gtcctcccc gactccgcc cctccccgcc 180
ggcgaggctc cgttcgttgt tctgcgccgc gggcggtacc acggttgcgt cggtcggctg 240
cctcggttcc ttctccggcc tcgcgccgt ctggaatctc ctctccctcg gcgtgagaa 300
ctcaagcttt gacatcggtt tgtttgatt gatgccctg gaaggatagt tgcgatcgca 360
catgggagac gcgttcttaa acttaacagg cctccggatc aaaggaaagc actgctcgct 420
gggcttacca cacagctgct gaagcatggg agg
```

(2) INFORMATION FOR SEQ ID NO:2356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1503152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2356:

```
Leu Ser Ser Gly Ser Ser Gln Ser Gly Asn Pro Ala Pro Pro Ala Arg
1          5          10          15
Cys Ser Pro Ala Leu Leu Arg Pro Pro Pro Trp Xaa Leu Pro Leu Arg
20          25          30
Leu Pro Val Ala Gly Asp Leu Arg Leu Asp Leu Glu His Gly Phe Pro
35          40          45
Pro Tyr Val Pro Pro Arg Thr Pro Pro Leu Pro Arg Gly Gln Ala Pro
```

Leu	Gln	Arg	Leu	Gln	Pro	Ile	Arg	Gln	Ser	Arg	Ser	Pro	Ser	Ser	Leu
1			5					10						15	
Leu	Ala	Arg	Ser	Pro	Pro	Pro	Ser	Ala	Met	Xaa	Pro	Ser	Pro	Pro	Pro
			20					25					30		
Pro	Arg	Arg	Arg	Arg	Ser	Pro	Pro	Arg	Pro	Gly	Ala	Trp	Leu	Pro	Ser
			35				40					45			
Val	Arg	Pro	Ser	Pro	His	Ser	Ala	Pro	Pro	Pro	Arg	Ala	Gly	Ser	Val
			50			55					60				
Arg	Arg	Ser	Arg	Pro	Arg	Gly	Gly	Pro	Arg	Leu	His	Arg	Ser	Ala	Ala
65					70				75					80	
Ser	Gly	Pro	Ser	Pro	Ala	Ser	Arg	Pro	Ser	Arg	Ile	Ser	Ser	Pro	Ser
			85					90						95	
Ala	Leu	Arg	Thr	Gln	Ala	Leu	Xaa	Ile	Gly	Cys	Leu	Asp			
			100					105							

(2) INFORMATION FOR SEQ ID NO:2359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..455
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2359:

aaaggatgca	ctggttccag	ttcaacctcc	ctgagctgtg	atgggaaatcg	cattcccctct	60
ataattccta	taaatagggg	ccctcccgct	cccatcacaa	tcacccatca	ctogctatat	120
tccattccca	agtcccgcgt	cttggtattcc	cgacgacgag	ctcggagctt	cttcttccct	180
gctcgggtgt	cgccgcaaca	gctgcgcgca	tgtctgcgcg	gaaccagctc	gccgctctgg	240
tcagcaacat	gtacgccacg	ggtttgcctg	acgatcagtt	ccagcagctc	cagctsstcc	300
aggaccocag	cgccocctgac	tttctgtctc	gaggtcgctca	cgctcttctg	tcaggacggc	360
gagcggatca	tcgaagagct	ggccaaactg	ctggagaagc	ccaactgga	ttttgacagg	420
gttgacgcct	ytgtgcatca	gctcaaggga	agcag			

(2) INFORMATION FOR SEQ ID NO:2360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2360:

Lys	Gly	Cys	Thr	Gly	Ser	Ser	Ser	Thr	Ser	Leu	Ser	Cys	Asp	Gly	Asn
1				5				10					15		
Arg	Ile	Pro	Ser	Ile	Ile	Pro	Ile	Asn	Arg	Gly	Pro	Pro	Ala	Pro	Ile
			20					25					30		
Thr	Ile	Thr	His	His	Ser	Leu	Tyr	Ser	His	Ser	Lys	Ser	Pro	Leu	Leu
			35				40					45			
Asp	Ser	Arg	Arg	Arg	Ala	Arg	Ser	Phe	Phe	Phe	Pro	Ala	Arg	Cys	Ser
			50			55					60				
Pro	Gln	Gln	Leu	Pro	Pro	Cys	Leu	Pro	Arg	Thr	Ser	Ser	Pro	Leu	Trp
			65			70			75				80		
Ser	Ala	Thr	Cys	Thr	Pro	Arg	Val	Cys	Leu	Thr	Ile	Ser	Ser	Ser	Ser
			85					90					95		
Ser	Ser	Xaa	Ser	Arg	Thr	Pro	Ala	Pro	Leu	Thr	Phe	Val	Ser	Glu	Val
			100				105					110			
Val	Thr	Leu	Phe	Cys	Gln	Asp	Gly	Glu	Arg	Ile	Ile	Glu	Glu	Leu	Ala
			115			120						125			
Lys	Leu	Leu	Glu	Lys	Pro	Asn	Val	Asp	Phe	Asp	Arg	Val	Asp	Ala	Xaa
			130			135					140				
Val	His	Gln	Leu	Lys	Gly	Ser									
			145		150										

(2) INFORMATION FOR SEQ ID NO:2361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..461

(D) OTHER INFORMATION: / Ceres Seq. ID 1503170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2361:

ctatggactt	cggtgaaggt	ttgcctcgct	cacagcatgc	tgattgcac	ctggttattg	60
tggaacaaat	ctctaataat	ggccacttcc	ttccactcag	tcattccctat	actgctcaact	120
cggttgctca	cagctctctg	ttcaatgttt	acaagatcca	tggtctttct	tcagttatta	180
tttcggatcg	tgacctagtg	ttcaccagcc	agttttggca	acaaccgttt	cgtcttgcgg	240
gcattgagct	taagccgagt	tcttcttacc	atccccaaac	cgacggacag	accgaacaag	300
tcaatcaatg	cttggaaca	tatctgcgct	gcttcgcaaa	tgctgcccc	acgaatgga	360
aagagtgggt	gcctgtgggc	gagtactggt	acaacaccag	cctccactct	gcactggggc	420
gtgcaccatt	tgaggttctt	tatggccgcc	aaccgcgtac	c		

(2) INFORMATION FOR SEQ ID NO:2362:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1503171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2362:

Met	Asp	Phe	Val	Glu	Gly	Leu	Pro	Arg	Ser	Gln	His	Ala	Asp	Cys	Ile	
1			5					10						15		
Leu	Val	Ile	Val	Asp	Lys	Phe	Ser	Lys	Tyr	Gly	His	Phe	Leu	Pro	Leu	
			20					25						30		
Ser	His	Pro	Tyr	Thr	Ala	His	Ser	Val	Ala	His	Ser	Phe	Leu	Phe	Asn	
			35					40						45		
Val	Tyr	Lys	Ile	His	Gly	Leu	Ser	Ser	Val	Ile	Ile	Ser	Asp	Arg	Asp	
			50					55						60		
Leu	Val	Phe	Thr	Ser	Gln	Phe	Trp	Gln	Gln	Pro	Phe	Arg	Leu	Ala	Gly	
			65					70						75		
Ile	Glu	Leu	Lys	Pro	Ser	Ser	Ser	Tyr	His	Pro	Gln	Thr	Asp	Gly	Gln	
			85					90						95		
Thr	Glu	Gln	Val	Asn	Gln	Cys	Leu	Glu	Thr	Tyr	Leu	Arg	Cys	Phe	Ala	
			100					105						110		
Asn	Val	Cys	Pro	Thr	Lys	Trp	Lys	Glu	Trp	Leu	Pro	Val	Gly	Glu	Tyr	
			115					120						125		
Trp	Tyr	Asn	Thr	Ser	Leu	His	Ser	Ala	Leu	Gly	Arg	Ala	Pro	Phe	Glu	
			130					135						140		
Val	Leu	Tyr	Gly	Arg	Gln	Pro	Arg	Thr								
			145					150								

(2) INFORMATION FOR SEQ ID NO:2363:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1503172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2363:

Met	Asp	Phe	Val	Glu	Gly	Leu	Pro	Arg	Ser	Gln	His	Ala	Asp	Cys	Ile	
1			5					10						15		
Leu	Val	Ile	Val	Asp	Lys	Phe	Ser	Lys	Tyr	Gly	His	Phe	Leu	Pro	Leu	
			20					25						30		
Ser	His	Pro	Tyr	Thr	Ala	His	Ser	Val	Ala	His	Ser	Phe	Leu	Phe	Asn	
			35					40						45		

Val Tyr Lys Ile His Gly Leu Ser Ser Val Ile Ile Ser Asp Arg Asp
50 55 60
Leu Val Phe Thr Ser Gln Phe Trp Gln Gln Pro Phe Arg Leu Ala Gly
65 70 75 80
Ile Glu Leu Lys Pro Ser Ser Ser Tyr His Pro Gln Thr Asp Gly Gln
85 90 95
Thr Glu Gln Val Asn Gln Cys Leu Glu Thr Tyr Leu Arg Cys Phe Ala
100 105 110
Asn Val Cys Pro Thr Lys Trp Lys Glu Trp Leu Pro Val Gly Glu Tyr
115 120 125
Trp Tyr Asn Thr Ser Leu His Ser Ala Leu Gly Arg Ala Pro Phe Glu
130 135 140
Val Leu Tyr Gly Arg Gln Pro Arg Thr
145 150

(2) INFORMATION FOR SEQ ID NO:2364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..456
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2364:

acacttcgat	cagtgctgcc	aacaagtagc	tagacgatga	gcagaggagc	tgagaagaag	60
aattggcgcg	cgtctcggtc	ttctctctcc	tcctcttctt	caccgacgtc	gtcgtngggg	120
cgccagcagg	tcctatggcgg	ggttctaccg	ctaccgcctc	tcctactcga	cctccggcaw	180
kgacagaacc	cagccgcgcg	cagcaccacg	tgacccgaca	caacaacaag	gcgacaagag	240
cagcagcaag	aagaagagga	ggagatcatc	catcgccggc	agcatcacgt	gcgcggggctc	300
catctgcagt	accaagagaga	gctcgggtcat	gagccgggac	gcgcgcggcg	cctccagcag	360
gtcgcctcagg	gcaccctacg	tgcagctcga	cgtaacgac	gcctctgcgc	ccgcatctc	420
cgccacgtcg	tccttcaact	cggagaccac	cgtggc			

(2) INFORMATION FOR SEQ ID NO:2365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2365:

Met Ser Arg Gly Ala Glu Lys Lys Asn Trp Pro Pro Ser Arg Ser Ser
1 5 10 15
Ser Ser Ser Ser Ser Pro Thr Ser Ser Xaa Gly Arg Gln Gln Val
20 25 30
His Gly Gly Val Leu Pro Leu Pro Val Leu His Ser His Leu Arg Xaa
35 40 45
Xaa Gln Asn Pro Ala Ala Ala Ser Thr Ser Cys Thr Asp Thr Thr Thr
50 55 60
Arg Arg Gln Glu Gln Gln Gln Glu Glu Glu Tyr Gln His Arg
65 70 75 80
Pro Glu His His Val Arg Gly Leu His Leu Gln Tyr Gln Gly Glu Leu
85 90 95
Gly His Glu Pro Gly Pro Pro Arg Arg Leu Gln Gln Val Ala Gln Gly
100 105 110
Thr Leu Arg Arg Arg Arg Arg Gln Arg Arg Leu Cys Arg Arg His Leu

115 120 125
Arg His Val Val Leu Gln Leu Gly Asp His Arg Gly
130 135 140

(2) INFORMATION FOR SEQ ID NO:2366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2366:

```
Met Ala Gly Phe Tyr Arg Tyr Pro Ser Ser Thr Arg Thr Ser Gly Xaa
1      5      10      15
Asp Arg Thr Gln Pro Pro Pro Ala Pro Ala Ala Pro Thr Gln Gln
      20      25      30
Gly Asp Lys Ser Ser Ser Lys Lys Lys Arg Arg Ser Ile Ser Ile Gly
      35      40      45
Arg Ser Ile Thr Cys Ala Gly Ser Ile Cys Ser Thr Lys Glu Ser Ser
      50      55      60
Val Met Ser Arg Asp Arg Arg Gly Ala Ser Ser Arg Ser Leu Arg Ala
      65      70      75      80
Pro Tyr Val Asp Val Asp Val Asn Asp Ala Ser Ala Ala Ala Ile Ser
      85      90      95
Ala Thr Ser Ser Phe Asn Ser Glu Thr Thr Val
      100     105
```

(2) INFORMATION FOR SEQ ID NO:2367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..512
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2367:

```
atgcatgctg aaactgtggc aaattggaac cacttattca gttggtgttt tgcaaatcca 60
gatttgggtg aattactgac tctcaactgc cctgtgaca gagcaatggt gctgctgatg 120
taccaaaattg agttgagact gctcaattgg gcctgggacg acgagtgtgt cttcaacctg 180
tgtctacttc gattacacag tgttgttcat agcagcctag ccaatgctta taaactctgg 240
ttgataacag tgattcacgg aacacactca attggccaag atcatttttg gaataacgtg 300
gataggggtg tgggtgtgtg aattaaggat agatgctgtg caagattggc aaagctagtt 360
ttatctgcta cactgacaca agattctggc aagctttctc aacttgaatt gcaccatcca 420
ttgtgtgtga atactcagtc aagcggcttg aggacaagcg gattttcaag cgggtggggaa 480
tatcagcata tcattctctc ctcaagtcaa ag
```

(2) INFORMATION FOR SEQ ID NO:2368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2368:

Met	His	Ala	Glu	Thr	Val	Ala	Asn	Trp	Asn	His	Leu	Phe	Ser	Trp	Cys
1			5						10					15	
Phe	Ala	Asn	Ser	Asp	Leu	Gly	Glu	Leu	Leu	Thr	Leu	Asn	Cys	Pro	Ala
			20					25					30		
Asp	Arg	Ala	Met	Val	Leu	Leu	Met	Tyr	Gln	Ile	Glu	Leu	Arg	Leu	Leu
			35				40					45			
Asn	Trp	Ala	Trp	Ala	Asp	Glu	Cys	Val	Phe	Asn	Leu	Cys	Leu	Leu	Arg
			50				55				60				
Leu	His	Ser	Val	Val	His	Ser	Ser	Leu	Ala	Asn	Ala	Tyr	Lys	Ser	Trp
					70				75					80	
Leu	Ile	Thr	Val	Ile	His	Arg	Thr	His	Ser	Ile	Gly	Gln	Asp	His	Phe
				85				90						95	
Trp	His	Asn	Val	Asp	Arg	Gly	Val	Val	Cys	Gly	Ile	Lys	Asp	Arg	Cys
			100					105					110		
Cys	Ala	Arg	Leu	Ala	Lys	Leu	Val	Leu	Ser	Ala	Thr	Leu	Thr	Gln	Asp
			115				120						125		
Ser	Gly	Lys	Leu	Ser	Gln	Leu	Glu	Leu	His	His	Pro	Leu	Leu	Leu	Asn
			130				135				140				
Thr	Gln	Ser	Ser	Gly	Leu	Arg	Thr	Ser	Arg	Ile	Ser	Ser	Gly	Gly	Glu
					150					155					160
Tyr	Gln	His	Ile	Ile	Phe	Ser	Ser	Ser	Gln						
				165					170						

(2) INFORMATION FOR SEQ ID NO:2369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2369:

Met	His	Ala	Glu	Thr	Val	Ala	Asn	Trp	Asn	His	Leu	Phe	Ser	Trp	Cys
1			5						10					15	
Phe	Ala	Asn	Ser	Asp	Leu	Gly	Glu	Leu	Leu	Thr	Leu	Asn	Cys	Pro	Ala
			20					25					30		
Asp	Arg	Ala	Met	Val	Leu	Leu	Met	Tyr	Gln	Ile	Glu	Leu	Arg	Leu	Leu
			35				40					45			
Asn	Trp	Ala	Trp	Ala	Asp	Glu	Cys	Val	Phe	Asn	Leu	Cys	Leu	Leu	Arg
			50				55				60				
Leu	His	Ser	Val	Val	His	Ser	Ser	Leu	Ala	Asn	Ala	Tyr	Lys	Ser	Trp
					70				75					80	
Leu	Ile	Thr	Val	Ile	His	Arg	Thr	His	Ser	Ile	Gly	Gln	Asp	His	Phe
				85				90						95	
Trp	His	Asn	Val	Asp	Arg	Gly	Val	Val	Cys	Gly	Ile	Lys	Asp	Arg	Cys
			100					105					110		
Cys	Ala	Arg	Leu	Ala	Lys	Leu	Val	Leu	Ser	Ala	Thr	Leu	Thr	Gln	Asp
			115				120						125		
Ser	Gly	Lys	Leu	Ser	Gln	Leu	Glu	Leu	His	His	Pro	Leu	Leu	Leu	Asn
			130				135				140				
Thr	Gln	Ser	Ser	Gly	Leu	Arg	Thr	Ser	Arg	Ile	Ser	Ser	Gly	Gly	Glu
					150					155					160
Tyr	Gln	His	Ile	Ile	Phe	Ser	Ser	Ser	Gln						
				165					170						

(2) INFORMATION FOR SEQ ID NO:2370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..135
(D) OTHER INFORMATION: / Ceres Seq. ID 1503203
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2370:
Met Val Leu Leu Met Tyr Gln Ile Glu Leu Arg Leu Leu Asn Trp Ala
1 5 10 15
Trp Ala Asp Glu Cys Val Phe Asn Leu Cys Leu Leu Arg Leu His Ser
20 25 30
Val Val His Ser Ser Leu Ala Asn Ala Tyr Lys Ser Trp Leu Ile Thr
35 40 45
Val Ile His Arg Thr His Ser Ile Gly Gln Asp His Phe Trp His Asn
50 55 60
Val Asp Arg Gly Val Val Cys Gly Ile Lys Asp Arg Cys Cys Ala Arg
65 70 75 80
Leu Ala Lys Leu Val Leu Ser Ala Thr Leu Thr Gln Asp Ser Gly Lys
85 90 95
Leu Ser Gln Leu Glu Leu His His Pro Leu Leu Asn Thr Gln Ser
100 105 110
Ser Gly Leu Arg Thr Ser Arg Ile Ser Ser Gly Gly Glu Tyr Gln His
115 120 125
Ile Ile Phe Ser Ser Ser Gln
130 135
(2) INFORMATION FOR SEQ ID NO:2371:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..345
(D) OTHER INFORMATION: / Ceres Seq. ID 1503237
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2371:
tctcgcgcga ctccacccca ctgcgccgcg ccgctgccac cgcgcttgc tgcgcgagcc 60
gccatggggg cgtacaagta cgtatcggaa ctatggagga ggaagcagtc ggaactgatg 120
gcggctacgg cgcgcgcggc ggcggctgga gggactgatg tgtgggccca tctcggcttc 180
ggccgagtta tcttatctat ctatagtatc gtgtaccgt tgcgtctgt caccgtgtta 240
gtgtccgctt tacctttgga ttagggtgtt gtaccctgt tgttccctt gggtgtctcc 300
gctatgaac gagacgaag aagaatgagc aaggttttg ttcgc
(2) INFORMATION FOR SEQ ID NO:2372:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..87
(D) OTHER INFORMATION: / Ceres Seq. ID 1503238
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2372:
Ser Pro Arg Thr Pro Pro His Ser Pro Pro Pro Leu Pro Pro Pro Leu
1 5 10 15
Ala Ala Ala Ala Ala Met Gly Ala Tyr Lys Tyr Val Ser Glu Leu Trp
20 25 30
Arg Arg Lys Gln Ser Asp Val Met Ala Ala Thr Ala Ala Ala Ala

35 40 45
Ala Gly Thr Asp Val Trp Ala His Pro Gly Phe Gly Arg Val Ile
50 55 60
Leu Ser Ile Tyr Ser Ile Val Leu Pro Phe Ala Ser Val Thr Val Leu
65 70 75 80
Val Ser Val Leu Pro Leu Asp

(2) INFORMATION FOR SEQ ID NO:2373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2373:

Ser Ala His Ser Thr Pro Leu Ala Ala Ala Thr Ala Ala Cys
1 5 10 15
Cys Arg Ser Arg His Gly Gly Val Gln Val Arg Ile Gly Thr Met Glu
20 25 30
Glu Glu Ala Val Gly Arg Asp Gly Gly Tyr Gly Gly Gly Gly Gly
35 40 45
Trp Arg Asp
50

(2) INFORMATION FOR SEQ ID NO:2374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2374:

Met Gly Ala Tyr Lys Tyr Val Ser Glu Leu Trp Arg Arg Lys Gln Ser
1 5 10 15
Asp Val Met Ala Ala Thr Ala Ala Ala Ala Gly Thr Asp
20 25 30
Val Trp Ala His Pro Gly Phe Gly Arg Val Ile Leu Ser Ile Tyr Ser
35 40 45
Ile Val Leu Pro Phe Ala Ser Val Thr Val Leu Val Ser Val Leu Pro
50 55 60
Leu Asp
65

(2) INFORMATION FOR SEQ ID NO:2375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..400
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2375:

cccgtaaataa tcacgacgctg gtggtgactg gtgagtccac agtccacact ccccaactcca 60
ttttctacca tcacactgac acgttcatag ctactgtagt ttcagctagt aacgtacgac 120
ggactaatct cgatctggga gcgagagagga ggacgacgat aatgaagatg agctccgtgc 180
ccgcggcass cgggtgatgg tgggtgggtgt gctgctctct gcggcgcgcg cgactgtgtgc 240
ggggcaggcg cttgtgccgg gcgtgatgat cttcggcgac tcgggtggtg acgcaggcaa 300
caacaaccgg ctacgcagcg tgggtgcgag cgacttcccg cccctacggcc gcgacttccc 360
ggcgacgcac gcgcccacgg gntnnctgc aacggcaagg

(2) INFORMATION FOR SEQ ID NO:2376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2376:

Met Val Val Val Val Leu Leu Ser Ala Ala Ala Thr Val Thr Gly
1 5 10 15
Gln Ala Leu Val Pro Gly Val Met Ile Phe Gly Asp Ser Val Val Asp
20 25 30
Ala Gly Asn Asn Asn Arg Leu Ala Thr Leu Val Arg Ala Asp Phe Pro
35 40 45
Pro Tyr Gly Arg Asp Phe Pro Ala Thr His Ala Pro Thr Xaa Xaa Pro
50 55 60
Ala Thr Ala Ser
65

(2) INFORMATION FOR SEQ ID NO:2377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2377:

Met Ile Phe Gly Asp Ser Val Val Asp Ala Gly Asn Asn Asn Arg Leu
1 5 10 15
Ala Thr Leu Val Arg Ala Asp Phe Pro Pro Tyr Gly Arg Asp Phe Pro
20 25 30
Ala Thr His Ala Pro Thr Xaa Xaa Pro Ala Thr Ala Ser
35 40 45

(2) INFORMATION FOR SEQ ID NO:2378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2378:

ctctttctcc ccagtagcaa cgaccgcgcg tcctccgcn cgcactaaa cctactcca 60
tgtaccacagg tctgcgtcgg gccccccggc gatgagaacc cgctcagtcc aaagatggct 120

cgctgctggaat tgatggaaca kgacttaagc aaactggatg tgacgaagct tcaccccctg 180
tcacctggaag ttatctcacc ccaagcaaca atcaatatgg gtaccattgg ccatgtggct 240
kcatggaaaag tccactgttg ttaaagctat atctggtgtt cagactgttc ggttcaagaa 300
tgagctggaa cgtaacatta ctataaagct gggttacgct aatgcacaaa tctacaaatg 360
tgaggatgac agatgtccgc gaccaatgtg ctacaaggcc tatggaagcg gaaaakaaga 420
tagccctcta tgtgatgtgc ctggatttga aaacactaga atg

(2) INFORMATION FOR SEQ ID NO:2379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1503276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2379:

Leu Phe Leu Pro Ser Ser Asn Asp Arg Ala Ser Ser Ala Xaa Ala Leu
1 5 10 15
Asn Pro Thr Pro Cys Thr Gln Val Cys Val Gly Pro Pro Gly Asp Glu
20 25 30
Asn Pro Ser Val Pro Lys Met Ala Arg Arg Gly Leu Met Glu Xaa Asp
35 40 45
Leu Ser Lys Leu Asp Val Thr Lys Leu His Pro Leu Ser Pro Glu Val
50 55 60
Ile Ser Arg Gln Ala Thr Ile Asn Met Gly Thr Ile Gly His Val Ala
65 70 75 80
Xaa Trp Lys Val His Cys Cys
85

(2) INFORMATION FOR SEQ ID NO:2380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1503277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2380:

Met Ala Arg Arg Gly Leu Met Glu Xaa Asp Leu Ser Lys Leu Asp Val
1 5 10 15
Thr Lys Leu His Pro Leu Ser Pro Glu Val Ile Ser Arg Gln Ala Thr
20 25 30
Ile Asn Met Gly Thr Ile Gly His Val Ala Xaa Trp Lys Val His Cys
35 40 45
Cys

(2) INFORMATION FOR SEQ ID NO:2381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1503278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2381:
Met Trp Xaa His Gly Lys Ser Thr Val Val Lys Ala Ile Ser Gly Val
1 5 10 15
Gln Thr Val Arg Phe Lys Asn Glu Leu Glu Arg Asn Ile Thr Ile Lys
20 25 30
Leu Gly Tyr Ala Asn Ala Lys Ile Tyr Lys Cys Glu Asp Asp Arg Cys
35 40 45
Pro Arg Pro Met Cys Tyr Lys Ala Tyr Gly Ser Gly Lys Xaa Asp Ser
50 55 60
Pro Leu Cys Asp Val Pro Gly Phe Glu Asn Thr Arg Met
65 70 75

(2) INFORMATION FOR SEQ ID NO:2382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2382:

ttgttgatga	tttagtgcaa	tctgggggaa	ctcttagaga	atgccagaad	agttctagct	60
ttgcatggcg	ctgcaaaagt	cagtgcttat	gtgactcatg	ctgtgtttcc	taagcagtc	120
tatgaacgtt	tcatggcgct	tattcttctg	gggccagggt	acagatttgc	ttactcttgg	180
atcacggact	catgcccaca	cacagtaaaa	gctattggcg	aaagacctcc	atttgaggtt	240
ctgagctctg	ctggctcaat	tgcagatgct	cttcagatat	gaagctacac	tggtagatgg	300
gcattggcgt	ggattgttga	tgcccaccag	attgaaactt	gtactatgag	gtggaaatgt	360
cccgttttcc	ctaaatgtaa	gagttgtgtt	ccagttcctg	gaaaagcaaa	taatgtgtag	420
taagttaaag	tacttgaagg	ttccataaac	agccctgtgg	ctt		

(2) INFORMATION FOR SEQ ID NO:2383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2383:

Val Asp Asp Leu Val Gln Ser Gly Gly Thr Leu Arg Glu Cys Gln Xaa
1 5 10 15
Ser Ser Ser Phe Ala Trp Arg Cys Lys Ser Gln Cys Leu Cys Asp Ser
20 25 30
Cys Cys Val Ser
35

(2) INFORMATION FOR SEQ ID NO:2384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2384:

Met Leu Cys Phe Leu Ser Ser His Met Asn Val Ser Trp Arg Leu Val
1 5 10 15
Leu Leu Gly Gln Val Thr Asp Leu Leu Thr Ser Gly Ser Arg Thr His
20 25 30
Ala His Thr Gln
35

(2) INFORMATION FOR SEQ ID NO:2385:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1503282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2385:

Met Ala Ser Ser Ser Ala Gly Pro Gly Asp Arg Phe Ala Tyr Phe Trp
1 5 10 15
Ile Thr Asp Ser Cys Pro His Thr Val Lys Ala Ile Gly Gln Arg Pro
20 25 30
Pro Phe Glu Val Leu Ser Leu Ala Gly Ser Ile Ala Asp Ala Leu Gln
35 40 45
Ile

(2) INFORMATION FOR SEQ ID NO:2386:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 509 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..509

(D) OTHER INFORMATION: / Ceres Seq. ID 1503297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2386:

cacaggggtgc	tgatgtgata	gagaaagctc	cagatggcac	tccagctggt	ggtggcttgc	60
tttatgttgt	tgttcatgaa	gcccaagatc	ttgaggggaa	gcaccataca	aaccatgatg	120
caaaaataat	tttcaaaggc	gaggagaaga	aaactaaggt	catcaagaag	aataggggatc	180
caagatggga	ggatgagttt	gagttogtgt	gtgaggagcc	tctctgtaat	gataaaactgc	240
atgttgaaat	cataagtaaa	gccccgaagc	agggctgata	catggcaagg	aaactttggg	300
ctatattgat	attagccttg	cagacgtgat	cagcaacaag	cggattaatg	aaaagtacca	360
ttctcatagac	tcgaaaaatg	gtcagatcca	gacgagttg	cagtggaaga	cttcctagac	420
aggaagggwc	cagaatgcct	tgatgttctt	ctattcagtt	tcgctatata	tggtattgag	480
gattgaggtc	atgtagataa	tttcttttt				

(2) INFORMATION FOR SEQ ID NO:2387:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1503298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2387:

Gln Gly Ala Asp Val Ile Glu Lys Ala Pro Asp Gly Thr Pro Ala Gly
1 5 10 15

Gly Gly Leu Leu Tyr Val Val Val His Glu Ala Gln Asp Leu Glu Gly
20 25 30
Lys His His Thr Asn Pro Tyr Ala Lys Ile Ile Phe Lys Gly Glu Glu
35 40 45
Lys Lys Thr Lys Val Ile Lys Lys Asn Arg Asp Pro Arg Trp Glu Asp
50 55 60
Glu Phe Glu Phe Val Cys Glu Glu Pro Pro Val Asn Asp Lys Leu His
65 70 75 80
Val Glu Val Ile Ser Lys Ala Pro Lys Gln Gly
85 90

(2) INFORMATION FOR SEQ ID NO:2388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..482
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2388:

tacatcgtga	tattaagtct	agcaacatct	tgcttgatgg	cagtttcgag	gcccggtgat	60
cagactttgg	acttgcgaag	cttttagagg	atgaagaatc	acatattact	acaatagttg	120
caggaacatt	tggtcacctt	gcaccagagt	atatgcaatt	tggcagagca	cgcagaagac	180
tgatgtctac	agttttgggg	ttttggtact	cgaaatactc	agtggaagac	ggcctactga	240
tgcatctctc	attgagaagg	gactaaacat	tgttggatgg	ttaaattttc	ttgctagtga	300
gaaccgggag	agggaaattg	tcgacctgaa	ctgtgaagga	gtgcagactg	agaccttaga	360
tgccctgtct	tctcttgcca	agcaatgtgt	tagctcctcg	ccagagagag	gccgacaagt	420
cacaggggtg	tacatatgct	gggagtcgga	tgtaattaca	ccgtgcccta	gcgacttcta	480
tg						

(2) INFORMATION FOR SEQ ID NO:2389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2389:

His Arg Asp Ile Lys Ser Ser Asn Ile Leu Leu Asp Gly Ser Phe Glu	
1 5 10 15	
Ala Arg Val Ser Asp Phe Gly Leu Ala Lys Leu Leu Glu Asp Glu Glu	
20 25 30	
Ser His Ile Thr Thr Ile Val Ala Gly Thr Phe Gly Tyr Leu Ala Pro	
35 40 45	
Glu Tyr Met Gln Phe Gly Arg Ala Pro Arg Arg Leu Met Ser Thr Val	
50 55 60	
Leu Gly Phe Trp Tyr Ser Lys Tyr Ser Val Glu Ser Gly Leu Leu Met	
65 70 75 80	
His Pro Ser Leu Arg Arg Asp	
85	

(2) INFORMATION FOR SEQ ID NO:2390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..448
(D) OTHER INFORMATION: / Ceres Seq. ID 1503305

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2390:

aagcagcaac	atataaagct	cagagcctca	gagcgccass	caagtcttgc	ggtcgcgaa	60
agcaacgc	caagatgggtg	aagctcgcat	tcggaagcgt	cggcgactcc	ttcagcgta	120
cctccatcaa	ggcctacgt	gcggagtcca	tcgccaccct	cctctctgct	ttcgccggcg	180
tggtttccgc	catcgcccttc	gggcaactga	cgaatggcgg	cgcgctggac	cctgcgggac	240
tggtggcgat	cgcgggtggcg	cacgcgctgg	cctctctctg	ggcgctctcc	gtggccgcga	300
acacctccgg	cggccacactg	aaccgcgcg	tgacgttcgg	cctggccgctg	ggcgccacat	360
tcaccgtctc	caccggcctc	ttctactgtg	tgggcccacg	tgctggggcg	gtccgtggcg	420
tgccctggctc	ctcagggttcg	tgaccac				

- (2) INFORMATION FOR SEQ ID NO:2391:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..149
(D) OTHER INFORMATION: / Ceres Seq. ID 1503306

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2391:

Ser	Ser	Asn	Ile	Ser	Ser	Ser	Glu	Pro	Gln	Ser	Ala	Xaa	Gln	Val	Leu
1		5						10					15		
Arg	Ser	Arg	Arg	Ala	Thr	Gln	Gln	Asp	Gly	Glu	Ala	Arg	Ile	Arg	Lys
		20						25				30			
Arg	Arg	Arg	Leu	Leu	Gln	Arg	His	Leu	His	Gln	Gly	Leu	Arg	Xaa	Gly
		35					40					45			
Val	His	Arg	His	Pro	Pro	Leu	Arg	Leu	Arg	Arg	Arg	Gly	Phe	Arg	His
		50				55					60				
Arg	Leu	Arg	Ala	Thr	Asp	Glu	Trp	Arg	Arg	Ala	Gly	Pro	Cys	Gly	Thr
		65			70					75				80	
Gly	Gly	Asp	Arg	Gly	Gly	Ala	Arg	Ala	Gly	Pro	Leu	Arg	Gly	Arg	Leu
		85							90					95	
Arg	Gly	Arg	Glu	His	Leu	Arg	Arg	Pro	Pro	Glu	Pro	Arg	Arg	Asp	Val
		100						105					110		
Arg	Pro	Gly	Arg	Gly	Arg	His	Ile	His	Arg	Pro	His	Arg	Pro	Leu	Leu
		115				120						125			
Leu	Gly	Gly	Pro	Ser	Cys	Trp	Ala	Arg	Pro	Trp	Arg	Ala	Trp	Leu	Leu
		130				135						140			
Arg	Phe	Val	Thr	His											
		145													

- (2) INFORMATION FOR SEQ ID NO:2392:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..146
(D) OTHER INFORMATION: / Ceres Seq. ID 1503307

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2392:

Ala	Ala	Thr	Tyr	Gln	Ala	Gln	Ser	Leu	Arg	Ala	Pro	Xaa	Lys	Ser	Cys
1								5					10		15
Gly	Arg	Glu	Glu	Gln	Arg	Asn	Lys	Met	Val	Lys	Leu	Ala	Phe	Gly	Ser

20	25	30
Val Gly Asp Ser Phe Ser	Val Thr Ser Ile Lys Ala Tyr Xaa Ala Glu	
35	40	45
Phe Ile Ala Thr Leu Leu	Phe Val Phe Ala Gly Val Gly Ser Ala Ile	
50	55	60
Ala Phe Gly Gln Leu Thr	Asn Gly Gly Ala Leu Asp Pro Ala Gly Leu	
65	70	75
Val Ala Ile Ala Val Ala	His Ala Leu Ala Leu Phe Val Gly Val Ser	
85	90	95
Val Ala Ala Asn Thr Ser	Gly Gly His Leu Asn Pro Ala Val Thr Phe	
100	105	110
Gly Leu Ala Val Gly Gly	Thr Phe Thr Val Leu Thr Gly Leu Phe Tyr	
115	120	125
Trp Val Gly Pro Ala Ala	Gly Arg Val Arg Gly Val Pro Gly Ser Ser	
130	135	140
Gly Ser		

(2) INFORMATION FOR SEQ ID NO:2393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2393:

Met Val Lys Leu Ala Phe Gly Ser Val Gly Asp Ser Phe Ser Val Thr	
1	15
Ser Ile Lys Ala Tyr Xaa Ala Glu Phe Ile Ala Thr Leu Leu Phe Val	
20	30
Phe Ala Gly Val Gly Ser Ala Ile Ala Phe Gly Gln Leu Thr Asn Gly	
35	45
Gly Ala Leu Asp Pro Ala Gly Leu Val Ala Ile Ala Val Ala His Ala	
50	60
Leu Ala Leu Phe Val Gly Val Ser Val Ala Ala Asn Thr Ser Gly Gly	
65	80
His Leu Asn Pro Ala Val Thr Phe Gly Leu Ala Val Gly Gly Thr Phe	
85	95
Thr Val Leu Thr Gly Leu Phe Tyr Trp Val Gly Pro Ala Ala Gly Arg	
100	110
Val Arg Gly Val Pro Gly Ser Ser Gly Ser	
115	120

(2) INFORMATION FOR SEQ ID NO:2394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..464
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2394:

gtggcctcgt ctcttcccc acttcggcct cggcagttcc gacttccgcg tgcggcgccg	60
agcctgtccc cgcttcgcat ctgcgaattc ggccttcgc cgctgcgatt ccttagcagc	120
tcctcgccgcg ctccacccac ccctgcgcgc gcgagatgga gctcaagccc ggcattgcgg	180
cgtcgtcac cgcgcgccgc tcggcgcacg ggaaagcact ttgtattgct tttgcaagga	240

ggggttttatt tgtgactgtc gttgatttct cagaggaaaa tggagagaa gttgctacat 300
tagttcaaaa agaaaaatagc aaatttcacg gagatcttag aattccatct tcaatatttg 360
ttaagtgtga tgtttagaat gcagataatc ttgctgtgtg ttttgagaag catgtacaga 420
catacaatgg actagatata tgcataaact gtgctggaat tgct

(2) INFORMATION FOR SEQ ID NO:2395:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..87
(D) OTHER INFORMATION: / Ceres Seq. ID 1503323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2395:

Trp	Pro	Arg	Leu	Leu	Pro	His	Phe	Gly	Leu	Gly	Ser	Ser	Asp	Phe	Arg	
1				5					10					15		
Val	Pro	Ala	Gly	Ala	Ser	Ser	Arg	Phe	Ala	Ser	Arg	Thr	Ser	Arg	Leu	
			20					25					30			
Arg	Arg	Cys	Asp	Ser	Leu	Ala	Ala	Pro	Arg	Pro	Leu	His	Pro	Pro	Leu	
			35				40					45				
Arg	Arg	Arg	Asp	Gly	Ala	Gln	Ala	Arg	His	Val	Gly	Ala	Arg	His	Arg	
			50				55				60					
Arg	Arg	Leu	Arg	His	Arg	Glu	Ser	Thr	Leu	Tyr	Cys	Phe	Cys	Lys	Glu	
			65			70				75					80	
Gly	Phe	Ile	Cys	Asp	Cys	Arg										
						85										

(2) INFORMATION FOR SEQ ID NO:2396:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..103
(D) OTHER INFORMATION: / Ceres Seq. ID 1503324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2396:

Met	Glu	Leu	Lys	Pro	Gly	Met	Ser	Ala	Leu	Val	Thr	Gly	Gly	Ala	Ser	
1				5					10					15		
Gly	Ile	Gly	Lys	Ala	Leu	Cys	Ile	Ala	Phe	Ala	Arg	Arg	Gly	Leu	Phe	
			20					25					30			
Val	Thr	Val	Val	Asp	Phe	Ser	Glu	Asn	Gly	Arg	Glu	Val	Ala	Thr		
			35				40					45				
Leu	Val	Gln	Lys	Glu	Asn	Ser	Lys	Phe	His	Gly	Asp	Leu	Arg	Ile	Pro	
			50				55				60					
Ser	Ser	Ile	Phe	Val	Lys	Cys	Asp	Val	Ser	Asn	Ala	Asp	Asn	Leu	Ala	
			65			70				75				80		
Ala	Cys	Phe	Glu	Lys	His	Val	Gln	Thr	Tyr	Asn	Gly	Leu	Asp	Ile	Cys	
				85					90					95		
Ile	Asn	Cys	Ala	Gly	Ile	Ala										
						100										

(2) INFORMATION FOR SEQ ID NO:2397:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1503325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2397:

```
Met Ser Ala Leu Val Thr Gly Gly Ala Ser Gly Ile Gly Lys Ala Leu
1      5      10      15
Cys Ile Ala Phe Ala Arg Arg Gly Leu Phe Val Thr Val Val Asp Phe
      20      25      30
Ser Glu Glu Asn Gly Arg Glu Val Ala Thr Leu Val Gln Lys Glu Asn
      35      40      45
Ser Lys Phe His Gly Asp Leu Arg Ile Pro Ser Ser Ile Phe Val Lys
      50      55      60
Cys Asp Val Ser Asn Ala Asp Asn Leu Ala Ala Cys Phe Glu Lys His
      65      70      75      80
Val Gln Thr Tyr Asn Gly Leu Asp Ile Cys Ile Asn Cys Ala Gly Ile
      85      90      95
```

Ala

(2) INFORMATION FOR SEQ ID NO:2398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..489

(D) OTHER INFORMATION: / Ceres Seq. ID 1503330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2398:

```
tgtagagagt ttcaggtgct cagcaacaag gataggatct gatgtgggag tcgcatttgt 60
ctgaggcaatt ggggacatgc actcgtctga agaaacttga tcttagggac aacttgtttg 120
gtgttgatgc agggttagct ctacgcgaaa cccttccaaa actacctgat ctgtttgagc 180
tttatctcag tgactctcaat cttgagaaca aggttactat agcaattgca aaagccctca 240
aacagtcagc actgcagttg gaggtccttg aaattgctgg aatgaaata aatgccaaag 300
cagccccaga tttggctgaa tgtctagcag taatgcagtc actcaagaag ctgaccttgg 360
ctgaaaatga actgaaggac aatggtgctg tgataattgc aaaatcattg gaagatggcc 420
actcagatct caaggaaact gatgtgagca cgaacatgct gcagagggtt ggagctcgggt 480
gctttacgac
```

(2) INFORMATION FOR SEQ ID NO:2399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1503331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2399:

```
Met Val Glu Ser His Leu Ser Glu Ala Leu Gly Thr Cys Thr Arg Leu
1      5      10      15
Lys Lys Leu Asp Leu Arg Asp Asn Leu Phe Gly Val Asp Ala Gly Leu
      20      25      30
Ala Leu Ser Glu Thr Leu Pro Lys Leu Pro Asp Leu Val Glu Leu Tyr
      35      40      45
Leu Ser Asp Leu Asn Leu Glu Asn Lys Gly Thr Ile Ala Ile Ala Lys
      50      55      60
Ala Leu Lys Glu Ser Ala Leu Gln Leu Glu Val Leu Glu Ile Ala Gly
```

65		70		75		80									
Asn	Glu	Ile	Asn	Ala	Lys	Ala	Ala	Pro	Asp	Leu	Ala	Glu	Cys	Leu	Ala
			85						90					95	
Val	Met	Gln	Ser	Leu	Lys	Lys	Leu	Thr	Leu	Ala	Glu	Asn	Glu	Leu	Lys
			100					105					110		
Asp	Asn	Gly	Ala	Val	Ile	Ile	Ala	Lys	Ser	Leu	Glu	Asp	Gly	His	Ser
		115						120					125		
Asp	Leu	Lys	Glu	Leu	Asp	Val	Ser	Thr	Asn	Met	Leu	Gln	Arg	Val	Gly
		130					135					140			
Ala	Arg	Cys	Phe	Thr											

(2) INFORMATION FOR SEQ ID NO:2400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..449
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2400:

tctcttcttc	caatcattgg	tggttgtgct	ctagctgctg	tcacagagct	gaactttaat	60
atgggttgat	ttatgggtgc	catgatatcc	aaccttgcat	ttgttttccg	caacatcttc	120
tcgaagaggg	catgaagggg	aagtcogtca	gtggcatgaa	ttactacgct	tgccgtgcaa	180
ttatgtccct	ggtcatactg	actccatttg	ctatagctat	ggaaggccct	caaatgtggg	240
ctgctgttg	gc aaaaggct	cttcagaaag	ttggacccaa	tggtgtctgg	tggattgctg	300
ccacagagcgt	gttctaccac	ttatataaac	aggtgtccta	catgtctctc	gacagattt	360
ctccattgac	attcagcatt	ggcaatacaa	tgaagcgat	atcagtgatt	gtttcatcaa	420
tcattatctt	ccacactcct	gtccgcgct				

(2) INFORMATION FOR SEQ ID NO:2401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2401:

Met	Lys	Gly	Lys	Ser	Val	Ser	Gly	Met	Asn	Tyr	Tyr	Ala	Cys	Leu	Ser
1			5					10					15		
Ile	Met	Ser	Leu	Val	Ile	Leu	Thr	Pro	Phe	Ala	Ile	Ala	Met	Glu	Gly
			20					25					30		
Pro	Gln	Met	Trp	Ala	Ala	Gly	Trp	Gln	Lys	Ala	Leu	Ala	Glu	Val	Gly
			35				40					45			
Pro	Asn	Val	Val	Trp	Trp	Ile	Ala	Ala	Gln	Ser	Val	Phe	Tyr	His	Leu
		50				55				60					
Tyr	Asn	Gln	Val	Ser	Tyr	Met	Ser	Leu	Asp	Gln	Ile	Ser	Pro	Leu	Thr
		65				70				75				80	
Phe	Ser	Ile	Gly	Asn	Thr	Met	Lys	Arg	Ile	Ser	Val	Ile	Val	Ser	Ser
			85					90					95		
Ile	Ile	Ile	Phe	His	Thr	Pro	Val	Arg	Ala						
			100					105							

(2) INFORMATION FOR SEQ ID NO:2402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..98
(D) OTHER INFORMATION: / Ceres Seq. ID 1503334
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2402:
Met Asn Tyr Tyr Ala Cys Leu Ser Ile Met Ser Leu Val Ile Leu Thr
1 5 10 15
Pro Phe Ala Ile Ala Met Glu Gly Pro Gln Met Trp Ala Ala Gly Trp
20 25 30
Gln Lys Ala Leu Ala Glu Val Gly Pro Asn Val Val Trp Trp Ile Ala
35 40 45
Ala Gln Ser Val Phe Tyr His Leu Tyr Asn Gln Val Ser Tyr Met Ser
50 55 60
Leu Asp Gln Ile Ser Pro Leu Thr Phe Ser Ile Gly Asn Thr Met Lys
65 70 75 80
Arg Ile Ser Val Ile Val Ser Ser Ile Ile Phe His Thr Pro Val
85 90 95
Arg Ala

(2) INFORMATION FOR SEQ ID NO:2403:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..89
(D) OTHER INFORMATION: / Ceres Seq. ID 1503335
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2403:
Met Ser Leu Val Ile Leu Thr Pro Phe Ala Ile Ala Met Glu Gly Pro
1 5 10 15
Gln Met Trp Ala Ala Gly Trp Gln Lys Ala Leu Ala Glu Val Gly Pro
20 25 30
Asn Val Val Trp Trp Ile Ala Ala Gln Ser Val Phe Tyr His Leu Tyr
35 40 45
Asn Gln Val Ser Tyr Met Ser Leu Asp Gln Ile Ser Pro Leu Thr Phe
50 55 60
Ser Ile Gly Asn Thr Met Lys Arg Ile Ser Val Ile Val Ser Ser Ile
65 70 75 80
Ile Ile Phe His Thr Pro Val Arg Ala
85

(2) INFORMATION FOR SEQ ID NO:2404:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..233
(D) OTHER INFORMATION: / Ceres Seq. ID 1503336
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2404:
aacacataga gcgctgagga cgttggtcat cagtcacac ctatctaact agctagctag 60
cttgaacaag acggtacgta gcaagaaacg agctccgctg cgagagaaa ctaaggggacc 120
tagctagcta tcatgtcttg gaccctacgt gagaacgcgc tgttcgagcg sctctggcca 180

cctacgaccg ggacacgccc aggcgggtggg agctcgtggc cgcgcggtg ggc

(2) INFORMATION FOR SEQ ID NO:2405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2405:

Met	Ser	Trp	Thr	Tyr	Arg	Glu	Asn	Ala	Leu	Phe	Glu	Xaa	Leu	Trp	Pro
1				5					10					15	
Pro	Thr	Thr	Gly	Thr	Arg	Pro	Gly	Gly	Gly	Ser	Ser	Trp	Pro	Pro	Arg
			20				25						30		

Trp

(2) INFORMATION FOR SEQ ID NO:2406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2406:

actttccatt	gaggatgcta	cagtattgaa	gtccttoagc	caacctctoc	atcgtaacaa	60
gaaggtagat	ttcattgaac	agttcaatga	aaagctctctg	gtcaagcagg	aaggggagaa	120
tcttcaaatt	cttgatgtaa	ggaacttcca	attgacagaa	gtgagcagaa	ctgagtttat	180
gactccatct	gcctttat	ttctgtatga	gctgcaactg	ttcctgacgt	tccggaatcg	240
atcagtagca	gtttggaact	ttcgaggatga	actggtoaca	tcatttgaag	atcacotgtt	300
gtggcaccct	gactgcaaca	caaacaacat	atacattaca	agtgatcaag	atcttattat	360
ttcatactgc	aaggctgact	caactgattc	ctcttcagaa	gaaaatgctg	gctctataaa	420
cataagcagc	atactgaccg	gcaaatgctt	ggcaaaaaata	aacctgtgaa	attcgcgc	

(2) INFORMATION FOR SEQ ID NO:2407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2407:

Leu	Ser	Ile	Glu	Asp	Gly	Thr	Val	Leu	Lys	Ser	Phe	Ser	His	Leu	Leu
1				5					10					15	
His	Arg	Asn	Lys	Lys	Val	Asp	Phe	Ile	Glu	Lys	Gln	Phe	Asn	Glu	Lys
				20				25					30		
Leu	Val	Lys	Gln	Glu	Gly	Glu	Asn	Leu	Gln	Ile	Leu	Asp	Val	Arg	Asn
				35				40					45		
Phe	Gln	Leu	Thr	Glu	Val	Ser	Arg	Thr	Glu	Phe	Met	Thr	Pro	Ser	Ala
				50				55					60		
Phe	Ile	Phe	Leu	Tyr	Glu	Leu	Gln	Leu	Phe	Leu	Thr	Phe	Arg	Asn	Arg
				70				75					80		

Ser Val Ala Val Trp Asn Phe Arg Gly Glu Leu Val Thr Ser Phe Glu
85 90 95
Asp His Leu Leu Trp His Pro Asp Cys Asn Asn Ile Tyr Ile
100 105 110
Thr Ser Asp Gln Asp Leu Ile Ile Ser Tyr Cys Lys Ala Asp Ser Thr
115 120 125
Asp Ser Ser Ser Glu Glu Asn Ala Gly Ser Ile Asn Ile Ser Ser Ile
130 135 140
Leu Thr Gly Lys Cys Leu Ala Lys Ile Asn Pro Gly Asn Ser Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:2408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1503344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2408:

Met Thr Pro Ser Ala Phe Ile Phe Leu Tyr Glu Leu Gln Leu Phe Leu
1 5 10 15
Thr Phe Arg Asn Arg Ser Val Ala Val Trp Asn Phe Arg Gly Glu Leu
20 25 30
Val Thr Ser Phe Glu Asp His Leu Leu Trp His Pro Asp Cys Asn Thr
35 40 45
Asn Asn Ile Tyr Ile Thr Ser Asp Gln Asp Leu Ile Ile Ser Tyr Cys
50 55 60
Lys Ala Asp Ser Thr Asp Ser Ser Ser Glu Glu Asn Ala Gly Ser Ile
65 70 75 80
Asn Ile Ser Ser Ile Leu Thr Gly Lys Cys Leu Ala Lys Ile Asn Pro
85 90 95
Gly Asn Ser Arg
100

(2) INFORMATION FOR SEQ ID NO:2409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..260

(D) OTHER INFORMATION: / Ceres Seq. ID 1503345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2409:

agagttgttg attgcaggga aaccgccaat tggcaaggat gaagcttggt accgccttg 60
ttgtgctgct cttttctctc ctcccgcact cgtccaccgc ggaggacttc gattcttct 120
acctgtgcc aacgtggccg ggcctgttct gcgacacgcg gcagggttgc tgettcccg 180
acggcgcggg caagccggab sncgttttcg catccacggg ctgtggccaa ctacgccaa 240
tgccgcggcc gccaccacg

(2) INFORMATION FOR SEQ ID NO:2410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2410:

Glu Leu Leu Ile Ala Gly Lys Pro Pro Ile Gly Lys Asp Glu Ala Cys
1 5 10 15
Asp Arg Leu Arg Cys Ala Ala Leu Phe Ser Pro Pro Arg Leu Val His
20 25 30
Arg Gly Gly Leu Arg Phe Leu Leu Pro Cys Pro Thr Val Ala Gly Leu
35 40 45
Val Leu Arg His Ala Ala Gly Leu Leu Leu Pro Gly Arg Arg Gly Gln
50 55 60
Ala Gly Xaa Arg Phe Gly Ile His Gly Leu Trp Pro Thr Thr Pro Xaa
65 70 75 80
Ala Ala Ala Ala Thr Thr
85

(2) INFORMATION FOR SEQ ID NO:2411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2411:

Met Lys Leu Val Thr Ala Phe Val Val Leu Leu Phe Ser Leu Leu Pro
1 5 10 15
Asp Ser Ser Thr Ala Glu Asp Phe Asp Phe Phe Tyr Leu Val Gln Gln
20 25 30
Trp Pro Gly Ser Phe Cys Asp Thr Arg Gln Gly Cys Cys Phe Pro Asp
35 40 45
Gly Ala Gly Lys Pro Xaa Xaa Val Ser Ala Ser Thr Gly Cys Gly Gln
50 55 60
Leu Arg Gln Xaa Pro Arg Pro Pro Pro Pro
65 70

(2) INFORMATION FOR SEQ ID NO:2412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2412:

aatctactaa aaaaactctc caactgcggc aattgccaac cgccagcacc agcgccgcgc 60
ccccgntcc cccgcggcg cctcgagaa ttgattgct tggcgcgctg acccgccgcg 120
gccgtccgcg agcagcagcg acccccctcg cgggccatga cctctgctca ttccaagc

(2) INFORMATION FOR SEQ ID NO:2413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..36
(D) OTHER INFORMATION: / Ceres Seq. ID 1503352
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2413:
Asn Leu Leu Lys Lys Leu Ser Asn Cys Gly Asn Cys Gln Pro Pro Ala
1 5 10 15
Pro Ala Pro Pro Pro Xaa Leu Pro Arg Arg Arg Leu Gly Glu Leu Asp
20 25 30
Trp Leu Gly Ala
35

(2) INFORMATION FOR SEQ ID NO:2414:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..58
(D) OTHER INFORMATION: / Ceres Seq. ID 1503353
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2414:
Ser Thr Lys Lys Thr Leu Gln Leu Arg Gln Leu Pro Thr Ala Ser Thr
1 5 10 15
Ser Ala Ala Ala Pro Xaa Pro Pro Pro Ala Pro Arg Arg Ile Gly Leu
20 25 30
Ala Gly Arg Val Thr Arg Arg Arg Arg Pro Arg Ala Ala Ala Thr Pro
35 40 45
Leu Ala Gly His Asp Leu Cys Ser Phe Gln
50 55

(2) INFORMATION FOR SEQ ID NO:2415:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 492 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..492
(D) OTHER INFORMATION: / Ceres Seq. ID 1503354
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2415:
atacagaaat ggtagggttc ttccggcgct ctgctgcac tgatcaactgt cgtttgtcta 60
caacaaatgg atcagttcac catgaactga tttagcgaca ccatgggcaga ccaagaagtg 120
cgatcagggt ctgcagcagc acggcaaggg gaaggaccag ggactattac ataccagggtg 180
ctgggcatcg caattcaatc cacacctcag cagatcaagg aggcctacag gaaactccag 240
aagcaacacc atccagacat cgccggctac aaggggccacg actacacgct gctgctgaac 300
gaggcgtaga aggttctgat gcgggatggt tccaggtcca ggcacgccga tggaaagggc 360
aggagtaggg tggggctcagg agccgggttac accgtggacg gatacagttc ttgggaaggg 420
cccgtagaag gccaaagctc ctctgtggac gagaacaagt gcataggatg ccgggagatg 480
gtgcaccatg cc

(2) INFORMATION FOR SEQ ID NO:2416:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1503355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2416:

Thr Glu Met Val Gly Phe Phe Gly Ala Ser Ala Ala Ser Asp His Cys
1 5 10 15
Arg Leu Leu Thr Thr Asn Gly Ser Val His His Glu Leu Ile Arg Arg
20 25 30
His His Gly Arg Pro Arg Ser Ala Ile Arg Cys Cys Ser Thr Ala
35 40 45
Arg Gly Arg Thr Arg Asp Tyr Tyr Ile Pro Gly Ala Gly His Arg Asn
50 55 60
Ser Ile His Thr Ser Ala Asp Gln Gly Gly Leu Gln Glu Thr Pro Glu
65 70 75 80
Ala Thr Pro Ser Arg His Arg Arg Leu Gln Gly Pro Arg Leu His Ala
85 90 95
Ala Ala Glu Arg Gly Val Gln Gly Ser Asp Ala Gly Cys Phe Gln Phe
100 105 110
Gln Ala Arg Arg Trp Lys Gly Gln Glu
115 120

(2) INFORMATION FOR SEQ ID NO:2417:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1503356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2417:

Met Val Gly Phe Phe Gly Ala Ser Ala Ala Ser Asp His Cys Arg Leu
1 5 10 15
Leu Thr Thr Asn Gly Ser Val His His Glu Leu Ile Arg Arg His His
20 25 30
Gly Arg Pro Arg Ser Ala Ile Arg Cys Cys Ser Ser Thr Ala Arg Gly
35 40 45
Arg Thr Arg Asp Tyr Tyr Ile Pro Gly Ala Gly His Arg Asn Ser Ile
50 55 60
His Thr Ser Ala Asp Gln Gly Gly Leu Gln Glu Thr Pro Glu Ala Thr
65 70 75 80
Pro Ser Arg His Arg Arg Leu Gln Gly Pro Arg Leu His Ala Ala Ala
85 90 95
Glu Arg Gly Val Gln Gly Ser Asp Ala Gly Cys Phe Gln Phe Gln Ala
100 105 110
Arg Arg Trp Lys Gly Gln Glu
115

(2) INFORMATION FOR SEQ ID NO:2418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1503357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2418:

Met Ala Asp Gln Glu Val Arg Ser Gly Ala Ala Ala Ala Arg Gln Gly
1 5 10 15
Glu Gly Pro Gly Thr Ile Thr Tyr Gln Val Leu Gly Ile Ala Ile Gln

20 25 30
Ser Thr Pro Gln Gln Ile Lys Glu Ala Tyr Arg Lys Leu Gln Lys Gln
35 40 45
His His Pro Asp Ile Ala Gly Tyr Lys Gly His Asp Tyr Thr Leu Leu
50 55 60
Leu Asn Glu Ala Tyr Lys Val Leu Met Arg Asp Val Ser Ser Ser Arg
65 70 75 80
His Ala Asp Gly Arg Gly Arg Ser Arg Val Gly Ser Gly Ala Gly Tyr
85 90 95
Thr Val Asp Gly Tyr Ser Ser Trp Glu Gly Pro Val Arg Ser Gln Ala
100 105 110
Leu Phe Val Asp Glu Asn Lys Cys Ile Gly Cys Arg Glu Cys Val His
115 120 125
His Ala
130

(2) INFORMATION FOR SEQ ID NO:2419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..462
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2419:

acatgcaaa tataacacag accagatcaa acccaagttc aggcttcccg aatcattcag 60
caagccacta ttgagtgcgc atccatctat catctcccgc gatcttgaac caaatgactg 120
tttcatcata ttgcgcatcag atggattgtg ggagcacctc agcaatcaag aagcggttga 180
gattgttcac agccatcaac gtgctggaag cgcaagaaga ctcatataag ccgctctaca 240
agaagcagcg cgnaaastga gatgcgttac tcggatctta caaagatcga taagaaagtt 300
cgcaggcatt tccatgatga cattactgtc atcgttatt ttataaacta tgacctatta 360
ttgaaaggtg ctccgcagga caaccctct ccatcagatg tgccctagat tattgacagt 420
gagctagttc acccatgtgt attcaagctc ctgcgtgcag cc

(2) INFORMATION FOR SEQ ID NO:2420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2420:

His Ala Lys Tyr Asn Thr Asp Gln Ile Lys Pro Lys Phe Arg Leu Pro
1 5 10 15
Glu Ser Phe Ser Lys Pro Leu Leu Ser Ala Asp Pro Ser Ile Ile Ser
20 25 30
Arg Asp Leu Glu Pro Asn Asp Cys Phe Ile Ile Phe Ala Ser Asp Gly
35 40 45
Leu Trp Glu His Leu Ser Asn Gln Glu Ala Val Glu Ile Val His Ser
50 55 60
His Gln Arg Ala Gly Ser Ala Arg Arg Leu Ile Lys Ala Ala Leu Gln
65 70 75 80
Glu Ala Ala Xaa Xaa Xaa Arg Cys Val Thr Arg Ile Leu Gln Arg Ser
85 90 95
Ile Arg Lys Phe Ala Gly Ile Ser Met Met Thr Leu Leu Ser Ser Ser
100 105 110

Tyr Leu

(2) INFORMATION FOR SEQ ID NO:2421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..346
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2421:

tttccgtgcc gccaccagc cccttaacnc tctgtcctct agccgtctcg cgcgacacag	60
cctccatttc tctccgcagc gcggtgcggc tagctcaacc atggcggact ccaaggccac	120
ctcgccggtc accctccgca ctcckaagtt catgaccaac cggggccccc tgctggcccg	180
cwaacaattt gtgcttgagg ttatccaccc cggccgcgcc aacgtctcca aggcggagtt	240
gaagggaaga ggccttgccaa gatgtacgag gtgaaggacc ccaacacccat ctctgctctc	300
aagtccgca ccaacttcgg tggaggcaag tccactggct tgggcc	

(2) INFORMATION FOR SEQ ID NO:2422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2422:

Phe Arg Ala Ala Thr Gln Pro Leu Asn Xaa Arg Ser Ser Ser Arg Leu	
1 5 10 15	
Ala Gln His Ser Leu His Phe Ser Ser Asp Gly Gly Ala Ala Ser Ser	
20 25 30	
Thr Met Ala Asp Ser Lys Ala Thr Ser Ala Val Thr Leu Arg Thr Xaa	
35 40 45	
Lys Phe Met Thr Asn Arg Gly Pro Xaa Leu Ala Arg Xaa Gln Phe Val	
50 55 60	
Leu Glu Val Ile His Pro Gly Arg Ala Asn Val Ser Lys Ala Glu Leu	
65 70 75 80	
Lys Gly Arg Gly Leu Pro Arg Cys Thr Arg	
85 90	

(2) INFORMATION FOR SEQ ID NO:2423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2423:

Ser Val Pro Pro Pro Ser Pro Leu Xaa Leu Val Pro Leu Ala Val Ser	
1 5 10 15	
Arg Ser Thr Ala Ser Ile Ser Pro Pro Thr Ala Val Arg Leu Ala Gln	
20 25 30	
Pro Trp Arg Thr Pro Arg Pro Pro Arg Ser Pro Ser Ala Leu Xaa	

35 40 45

Ser Ser
50

(2) INFORMATION FOR SEQ ID NO:2424:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..57
(D) OTHER INFORMATION: / Ceres Seq. ID 1503403
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2424:
Met Ala Asp Ser Lys Ala Thr Ser Ala Val Thr Leu Arg Thr Xaa Lys
1 5 10 15
Phe Met Thr Asn Arg Gly Pro Xaa Leu Ala Arg Xaa Gln Phe Val Leu
20 25 30
Glu Val Ile His Pro Gly Arg Ala Asn Val Ser Lys Ala Glu Leu Lys
35 40 45
Gly Arg Gly Leu Pro Arg Cys Thr Arg
50 55

(2) INFORMATION FOR SEQ ID NO:2425:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 487 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..487
(D) OTHER INFORMATION: / Ceres Seq. ID 1503422
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2425:
tatgaaaaat caagatctcc tgggaggttc tttgacctag tttatcatga aaatgcccggt 60
gtttctactcc atgatgagag catataccga tttgaatgtt gctcgagtcc gacaagggttg 120
tctattcagc tgatggaata tggtcacgaa aagccagaag tgactgcagt atcaattgaa 180
ccaaattttt ctctgtatct ttttagcgag tacttgtgta gtacgccaga caagaaatta 240
tctgaagcgc tctaccttgg aaggaataag cggaatatatt caaataatga tgaaccttca 300
gattctttga aggcfaatgga tggatatcaat gttgtgaatg gtcttgaatg caagatatcc 360
tgcaagacct cgaaagtctc atatgtcctt gatactgaag atttcttgtt ccggtctcgg 420
aagagaagga aaattttgcg gggcggaagt gtgcccgacc gtttgcatg ttcatacata 480
tctgctg

(2) INFORMATION FOR SEQ ID NO:2426:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..162
(D) OTHER INFORMATION: / Ceres Seq. ID 1503423
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2426:
Tyr Glu Lys Ser Arg Ser Pro Gly Arg Phe Asp Leu Val Tyr His
1 5 10 15
Glu Asn Ala Arg Val Leu Leu His Asp Glu Ser Ile Tyr Arg Phe Glu
20 25 30
Cys Cys Ser Ser Pro Thr Arg Leu Ser Ile Gln Leu Met Glu Tyr Gly

35	40	45
His Glu Lys Pro Glu Val Thr Ala Val Ser Ile Glu Pro Asn Phe Ser		
50	55	60
Ser Tyr Leu Phe Ser Glu Tyr Leu Cys Ser Thr Pro Asp Lys Lys Leu		
65	70	75
Ser Glu Gly Val Tyr Leu Gly Arg Asn Lys Arg Lys Tyr Ser Asn Asn		
85	90	95
Asp Glu Pro Ser Asp Ser Leu Lys Ala Met Asp Gly Ile Asn Val Val		
100	105	110
Asn Gly Leu Glu Cys Lys Ile Ser Cys Lys Thr Ser Lys Val Ser Tyr		
115	120	125
Val Leu Asp Thr Glu Asp Phe Leu Phe Arg Leu Arg Lys Arg Arg Lys		
130	135	140
Ile Leu Arg Gly Gly Asn Val Pro Asp Arg Leu Gln Ile Ser Ser Ile		
145	150	155
Ser Ala		160

(2) INFORMATION FOR SEQ ID NO:2427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2427:

Met Glu Tyr Gly His Glu Lys Pro Glu Val Thr Ala Val Ser Ile Glu	
1	5
Pro Asn Phe Ser Ser Tyr Leu Phe Ser Glu Tyr Leu Cys Ser Thr Pro	10
20	25
Asp Lys Lys Leu Ser Glu Gly Val Tyr Leu Gly Arg Asn Lys Arg Lys	30
35	40
Tyr Ser Asn Asn Asp Glu Pro Ser Asp Ser Leu Lys Ala Met Asp Gly	45
50	55
Ile Asn Val Val Asn Gly Leu Glu Cys Lys Ile Ser Cys Lys Thr Ser	60
65	70
Lys Val Ser Tyr Val Leu Asp Thr Glu Asp Phe Leu Phe Arg Leu Arg	75
85	90
Lys Arg Arg Lys Ile Leu Arg Gly Gly Asn Val Pro Asp Arg Leu Gln	95
100	105
Ile Ser Ser Ile Ser Ala	110
115	

(2) INFORMATION FOR SEQ ID NO:2428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..439
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2428:

acacctactt cataagctg gcttctccc	cgacggccct catcgccctc aactcgcgc	60
tgaaagtccc caagtttgag ttctgtgcga	acgcgamscg tgcgtgttcg attaccctaaa	120
gccagtgacc cagcagacca cagccacgtc	agtcaaggtg ccggcggsca tctgtgcag	180
ctatgcccaag tccaaatcca gggcaaggaa	ggacgcagag agcaaggcca aggcgaaaagc	240

agagagactct tccagtgctt ctacttcgat gcaggtggac ggcgcttcgt ctgctgggtgc 300
tgctgcagag aagaaggccc cggagccaga gcctacgttc cagatcctga cgaaccggc 360
ccgggtcggt ccagccagg agaagttcat aaagttcctg gaagacagca ggtacaagcc 420
ggtgaaggct gcccccctg

(2) INFORMATION FOR SEQ ID NO:2429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..41
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2429:

Thr Tyr Phe Ile Ser Leu Ala Phe Ser Pro Thr Ala Leu Ile Gly Leu
1 5 10 15
Asn Ser Asp Leu Lys Val Pro Lys Phe Glu Phe Leu Ser Asn Ala Xaa
20 25 30
Arg Arg Cys Ser Ile Thr Pro Ser Gln
35 40

(2) INFORMATION FOR SEQ ID NO:2430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..55
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2430:

Met Pro Ser Pro Asn Pro Gly Gln Gly Arg Thr Gln Arg Ala Arg Pro
1 5 10 15
Arg Arg Lys Gln Arg Thr Leu Pro Val Leu Leu Leu Arg Cys Arg Trp
20 25 30
Thr Ala Leu Leu Leu Val Leu Leu Gln Arg Arg Arg Pro Arg Ser
35 40 45
Gln Ser Leu Arg Ser Arg Ser
50 55

(2) INFORMATION FOR SEQ ID NO:2431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2431:

Met Gln Val Asp Gly Ala Ser Ala Ala Gly Ala Ala Ala Glu Lys Lys
1 5 10 15
Ala Pro Glu Pro Glu Pro Thr Phe Gln Ile Leu Thr Asn Pro Ala Arg
20 25 30
Val Val Pro Ala Gln Glu Lys Phe Ile Lys Phe Leu Glu Asp Ser Arg
35 40 45
Tyr Lys Pro Val Lys Ala Ala Pro Ser

50 55

(2) INFORMATION FOR SEQ ID NO:2432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1503443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2432:

actggcggtg	aacagcgaga	acctaaccag	gacagcgac	acgactcgcc	taacctccgg	60
acagccacgt	ctttccccc	tctccggagc	aaccttccc	atggcgacgc	gacctccccc	120
ccagctgccc	ccgggtccac	cgccaccacc	tccgtctcgc	gtctccggcc	actgcgccct	180
tctcttcgcg	gccttcgctt	ctggccagca	ccagtgggcg	ccgcgcggt	gtgcctttct	240
cgattgtctt	ggggccaggc	tgtcgtccct	tgcccggcat	acgctgtcga	gccgcgcgcc	300
ggccctcgcc	gccctcctca	gagcccccct	ctccatcccc	gcacggttgg	caagagaggg	360
tgtaagttt	gcaggataga	gcaaggatct	tctttgccgt	tctgttctgg	atgcatctgt	420
ttttctgggg	aagtgccttg	gatggaaagta	acaactcggg	aggcaagaag	c	

(2) INFORMATION FOR SEQ ID NO:2433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1503444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2433:

Thr	Gly	Gly	Glu	Gln	Arg	Glu	Pro	Lys	Gln	Asp	Ser	Glu	His	Asp	Ser
1				5					10					15	
Pro	Asn	Leu	Arg	Thr	Ala	Thr	Ser	Phe	Pro	Thr	Leu	Arg	Thr	Asn	Leu
			20					25						30	
Pro	Asp	Gly	Asp	Ala	Thr	Ser	Pro	Pro	Ala	Ala	Pro	Ala	Ser	Thr	Ala
			35					40						45	
Thr	Thr	Ser	Val	Ser	Arg	Leu	Arg	Pro	Leu	Arg	Pro	Phe	Leu	Pro	Arg
			50					55						60	
Leu	Arg	Phe	Trp	Pro	Ala	Pro	Val	Ala	Ala	Ala	Pro	Xaa	Cys	Leu	Ser
65				70					75					80	
Arg	Leu	Leu	Trp	Ala	Gln	Ala	Val	Val	Pro	Cys	Pro	Ala	Tyr	Ala	Val
				85					90					95	
Glu	Pro	Pro	Pro	Gly	Pro	Arg	Arg	Pro	Pro	Gln	Ser	Pro	Leu	Leu	His
				100					105					110	
Pro	Arg	Thr	Val	Gly	Lys	Arg	Gly	Cys	Gln	Val	Cys	Arg	Ile	Glu	Gln
				115				120						125	
Gly	Ser	Ser	Leu	Pro	Phe	Cys	Ser	Gly	Cys	His	Cys	Phe	Ser	Gly	Glu
				130				135						140	
Val	Leu	Gly	Met	Glu	Val	Thr	Thr	Arg	Glu	Ala	Arg	Ser			
145					150									155	

(2) INFORMATION FOR SEQ ID NO:2434:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..125
(D) OTHER INFORMATION: / Ceres Seq. ID 1503445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2434:

Leu	Ala	Val	Asn	Ser	Glu	Asn	Leu	Asn	Arg	Thr	Thr	Arg	
1			5					10				15	
Leu	Thr	Ser	Gly	Gln	Pro	Arg	Leu	Ser	Pro	Leu	Ser	Gly	Arg
			20				25				30		Thr
Pro	Met	Ala	Thr	Arg	Pro	Pro	Leu	Gln	Leu	Pro	Pro	Arg	Pro
		35					40				45		Pro
Pro	Pro	Pro	Ser	Arg	Val	Ser	Gly	His	Cys	Ala	Leu	Ser	Phe
		50				55					60		Arg
Phe	Ala	Ser	Gly	Gln	His	Gln	Trp	Arg	Pro	Arg	Xaa	Cys	Ala
65					70					75			Phe
Asp	Cys	Ser	Gly	Pro	Arg	Leu	Ser	Ser	Leu	Ala	Arg	His	Thr
			85						90				Leu
Ser	Arg	Arg	Arg	Ala	Leu	Ala	Ala	Leu	Leu	Arg	Ala	Pro	Ser
			100					105					Ile
Pro	Ala	Arg	Leu	Ala	Arg	Glu	Ala	Val	Lys	Phe	Ala	Gly	
			115				120					125	

(2) INFORMATION FOR SEQ ID NO:2435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..92
(D) OTHER INFORMATION: / Ceres Seq. ID 1503446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2435:

Met	Ala	Thr	Arg	Pro	Pro	Leu	Gln	Leu	Pro	Pro	Arg	Pro	Pro	Pro
1				5				10					15	
Pro	Pro	Ser	Arg	Val	Ser	Gly	His	Cys	Ala	Leu	Ser	Phe	Arg	Ala
			20					25				30		Phe
Ala	Ser	Gly	Gln	His	Gln	Trp	Arg	Pro	Arg	Xaa	Cys	Ala	Phe	Leu
		35					40				45			Asp
Cys	Ser	Gly	Pro	Arg	Leu	Ser	Ser	Leu	Ala	Arg	His	Thr	Leu	Ser
		50				55					60			Ser
Arg	Arg	Arg	Ala	Leu	Ala	Ala	Leu	Leu	Arg	Ala	Pro	Ser	Ser	Ile
				70					75					Pro
Ala	Arg	Leu	Ala	Arg	Glu	Ala	Val	Lys	Phe	Ala	Gly			
			85						90					

(2) INFORMATION FOR SEQ ID NO:2436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..445
(D) OTHER INFORMATION: / Ceres Seq. ID 1503476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2436:

gaaactcact	cgccatcgcc	gggcatcgcg	ggcatcgac	acaaacgcaa	ctgacagcca		60
tgccacagaa	gtcgcgcgcca	ccgacggcgg	sggtcgtcgt	cgctctgtgt	gcgctcgccct		120
tgctggccgc	cgccgagaac	tgcgggtgcg	cgtcgggccc	gtgctgcagc	cggttcgggt		180
actcggggac	gggcgaggac	tactgcggcg	ccgggtgcc	gtcggggccc	tgcgacgtgc		240
cggagaccaa	caacgcgtcc	gtggccagca	tcgtgacgcc	ggccttcttc	gacgcgctcc		300

tcgcgcagcgc cgccgcctcgc tgcgaggcca acggtctcta caccgcgcac gccttcctcgc 360
ccgcgcgcgcgc ctactaccgc gcgttcggcc gcaccggcac cgtcgacgac tccaagcgcgc 420
agatcgcgcgc ctctctcgcgc aacgc

(2) INFORMATION FOR SEQ ID NO:2437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2437:

Lys Leu Thr Arg His Arg Arg Ala Ser Arg Ala Ser His Thr Asn Ala
1 5 10 15
Thr Cys Ser His Gly Thr Glu Ala Arg Ala Thr Asp Gly Xaa Gly Arg
20 25 30
Arg Arg Pro Ala Gly Ala Arg Leu Val Gly Arg Arg Ala Glu Leu Arg
35 40 45
Val Arg Val Gly Pro Val Leu Gln Pro Val Arg Val Leu Arg Asp Gly
50 55 60
Arg Gly Leu Leu Arg Arg Arg Val Pro Val Gly Pro Leu Arg Arg Ala
65 70 75 80
Gly Asp Gln Gln Arg Val Arg Gly Gln His Arg Asp Ala Gly Leu Leu
85 90 95
Arg Arg Ala Pro Arg Ala Gly Arg Arg Leu Val Arg Gly Gln Arg Leu
100 105 110
Leu His Pro Arg Arg Leu Pro Arg Arg Arg Leu Leu Pro Gly Val
115 120 125
Arg Pro His Arg His Arg Arg Arg Leu Gln Ala Arg Asp Arg Arg Leu
130 135 140
Leu Arg Gln Arg
145

(2) INFORMATION FOR SEQ ID NO:2438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2438:

Asn Ser Leu Ala Ile Ala Gly His Arg Thr Gln Thr Gln
1 5 10 15
Pro Ala Ala Met Ala Gln Lys Leu Ala Pro Pro Thr Ala Xaa Val Val
20 25 30
Val Val Leu Leu Ala Leu Ala Leu Ser Ala Ala Ala Gln Asn Cys Gly
35 40 45
Cys Ala Ser Gly Leu Cys Cys Ser Arg Phe Gly Tyr Cys Gly Thr Gly
50 55 60
Glu Asp Tyr Cys Gly Ala Gly Cys Gln Ser Gly Pro Cys Asp Val Pro
65 70 75 80
Glu Thr Asn Asn Ala Ser Val Ala Ser Ile Val Thr Pro Ala Phe Phe
85 90 95
Asp Ala Leu Leu Ala Gln Ala Ala Ala Ser Cys Glu Ala Asn Gly Phe
100 105 110

Tyr Thr Arg Asp Ala Phe Leu Ala Ala Ala Gly Tyr Tyr Pro Ala Phe
115 120 125
Gly Arg Thr Gly Thr Val Asp Asp Ser Lys Arg Glu Ile Ala Ala Phe
130 135 140
Phe Gly Asn
145

(2) INFORMATION FOR SEQ ID NO:2439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1503479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2439:

Met	Ala	Gln	Lys	Leu	Ala	Pro	Pro	Thr	Ala	Xaa	Val	Val	Val	Val	Leu
1				5					10					15	
Leu	Ala	Leu	Ala	Leu	Ser	Ala	Ala	Ala	Gln	Asn	Cys	Gly	Cys	Ala	Ser
				20				25					30		
Gly	Leu	Cys	Cys	Ser	Arg	Phe	Gly	Tyr	Cys	Gly	Thr	Gly	Glu	Asp	Tyr
				35				40					45		
Cys	Gly	Ala	Gly	Cys	Gln	Ser	Gly	Pro	Cys	Asp	Val	Pro	Glu	Thr	Asn
				50				55				60			
Asn	Ala	Ser	Val	Ala	Ser	Ile	Val	Thr	Pro	Ala	Phe	Phe	Asp	Ala	Leu
				65				70						80	
Leu	Ala	Gln	Ala	Ala	Ala	Ser	Cys	Glu	Ala	Asn	Gly	Phe	Tyr	Thr	Arg
				85				90						95	
Asp	Ala	Phe	Leu	Ala	Ala	Ala	Gly	Tyr	Tyr	Pro	Ala	Phe	Gly	Arg	Thr
				100				105					110		
Gly	Thr	Val	Asp	Asp	Ser	Lys	Arg	Glu	Ile	Ala	Ala	Phe	Gly	Asn	
				115				120					125		

(2) INFORMATION FOR SEQ ID NO:2440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..511

(D) OTHER INFORMATION: / Ceres Seq. ID 1503480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2440:

caaatgccaag	agcagcaact	gttaaagtgt	gaaaaacagt	gtgccgagca	cataatgctt	60
gtggacttgg	gaaggaatga	tgttggcaag	gtatccaaac	caggatcagt	gaaggtggag	120
aagtgtgatga	acattgagag	atactcccat	gttatgcaca	tcagctcaac	ggttagtggg	180
cagttggatg	atcatctcca	gagttgggat	gccttgagag	ctgccttgcc	cgttggaaca	240
gtcagtggtg	caccaaaggt	gaagcccatg	gagttgattg	ataagttgga	agttacgagg	300
cgaggaccat	atagtggtgg	tctaggagga	atatogtttg	atggtgacat	gcaaatggca	360
ctttctctcc	gcaccatcgt	atttctcaaca	gcgccgagcc	acaacacgat	gtactcatat	420
aaagacgcag	ataggcgctcg	gggagtggtt	cgctcatctt	caggctggtg	caggcattgt	480
tgccgcagct	agcccgagatg	acgaacaacg	t			

(2) INFORMATION FOR SEQ ID NO:2441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..163
(D) OTHER INFORMATION: / Ceres Seq. ID 1503481
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2441:
Gln Met Gln Glu Gln Gln Leu Leu Ser Asp Glu Lys Gln Cys Ala Glu
1 5 10 15
His Ile Met Leu Val Asp Leu Gly Arg Asn Asp Val Gly Lys Val Ser
20 25 30
Lys Pro Gly Ser Val Lys Val Glu Lys Leu Met Asn Ile Glu Arg Tyr
35 40 45
Ser His Val Met His Ile Ser Ser Thr Val Ser Gly Gln Leu Asp Asp
50 55 60
His Leu Gln Ser Trp Asp Ala Leu Arg Ala Ala Leu Pro Val Gly Thr
65 70 75 80
Val Ser Gly Ala Pro Lys Val Lys Ala Met Glu Leu Ile Asp Lys Leu
85 90 95
Glu Val Thr Arg Arg Gly Pro Tyr Ser Gly Leu Gly Gly Ile Ser
100 105 110
Phe Asp Gly Asp Met Gln Ile Ala Leu Ser Leu Arg Thr Ile Val Phe
115 120 125
Ser Thr Ala Pro Ser His Asn Thr Met Tyr Ser Tyr Lys Asp Ala Asp
130 135 140
Arg Arg Arg Gly Val Gly Arg Ser Ser Ser Gly Trp Cys Arg His Cys
145 150 155 160
Cys Arg Gln

(2) INFORMATION FOR SEQ ID NO:2442:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1503482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2442:
Met Gln Glu Gln Gln Leu Leu Ser Asp Glu Lys Gln Cys Ala Glu His
1 5 10 15
Ile Met Leu Val Asp Leu Gly Arg Asn Asp Val Gly Lys Val Ser Lys
20 25 30
Pro Gly Ser Val Lys Val Glu Lys Leu Met Asn Ile Glu Arg Tyr Ser
35 40 45
His Val Met His Ile Ser Ser Thr Val Ser Gly Gln Leu Asp Asp His
50 55 60
Leu Gln Ser Trp Asp Ala Leu Arg Ala Ala Leu Pro Val Gly Thr Val
65 70 75 80
Ser Gly Ala Pro Lys Val Lys Ala Met Glu Leu Ile Asp Lys Leu Glu
85 90 95
Val Thr Arg Arg Gly Pro Tyr Ser Gly Leu Gly Gly Ile Ser Phe
100 105 110
Asp Gly Asp Met Gln Ile Ala Leu Ser Leu Arg Thr Ile Val Phe Ser
115 120 125
Thr Ala Pro Ser His Asn Thr Met Tyr Ser Tyr Lys Asp Ala Asp Arg
130 135 140
Arg Arg Gly Val Gly Arg Ser Ser Ser Gly Trp Cys Arg His Cys Cys

145 150 155 160
Arg Gln

(2) INFORMATION FOR SEQ ID NO:2443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2443:

```
Met Leu Val Asp Leu Gly Arg Asn Asp Val Gly Lys Val Ser Lys Pro
1      5      10      15
Gly Ser Val Lys Val Glu Lys Leu Met Asn Ile Glu Arg Tyr Ser His
20      25      30
Val Met His Ile Ser Ser Thr Val Ser Gly Gln Leu Asp Asp His Leu
35      40      45
Gln Ser Trp Asp Ala Leu Arg Ala Ala Leu Pro Val Gly Thr Val Ser
50      55      60
Gly Ala Pro Lys Val Lys Ala Met Glu Leu Ile Asp Lys Leu Glu Val
65      70      75      80
Thr Arg Arg Gly Pro Tyr Ser Gly Gly Leu Gly Gly Ile Ser Phe Asp
85      90      95
Gly Asp Met Gln Ile Ala Leu Ser Leu Arg Thr Ile Val Phe Ser Thr
100      105      110
Ala Pro Ser His Asn Thr Met Tyr Ser Tyr Lys Asp Ala Asp Arg Arg
115      120      125
Arg Gly Val Gly Arg Ser Ser Ser Gly Trp Cys Arg His Cys Cys Arg
130      135      140
Gln
145
```

(2) INFORMATION FOR SEQ ID NO:2444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2444:

```
aatcaacacc agaagctctc gatccaccc aggaagaaga gaggaatggc gtccgaggag      60
gagggagctg tgatcgccctg ccacaccaag gccgacttcg acgcccacat ggccaaggcc      120
aaggaggccg gcaagctggt gatcattgac ttcacggcct cctggtgcgg cccctgcccgt      180
ttcatcgccg cactgttctg cgagcagccc aagaagtcca cccaggctgt gttcctgaag      240
gtggacgtgg acgagctgaa ggaagttgcc gcggcctacg atgtcgaggc gatgccgacc      300
ttocacttcg tcaagaacgg ggtgacggtg gagaccgtcg tcggtgccag gaaggagaac      360
ctctctggcc agatcgagaa gcactgcgcc gcggccgtgt ctgctgcctc tgcgtagaga      420
ggatggacca gcacgtacgt gcgggtggtg gtggtcttgt cgtttcagtt tgggcttctg      480
agcgtgtggt ctgggtggtc gattgtgaac tggag
```

(2) INFORMATION FOR SEQ ID NO:2445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..138
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503485
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2445:
Asn Gln His Gln Lys Leu Ser Ile Pro Pro Arg Lys Lys Arg Gly Met
1 5 10 15
Ala Ser Glu Glu Glu Gly Val Val Ile Ala Cys His Thr Lys Ala Asp
 20 25 30
Phe Asp Ala His Met Ala Lys Ala Lys Glu Ala Gly Lys Leu Val Ile
 35 40 45
Ile Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro
 50 55 60
Leu Phe val Glu His Ala Lys Lys Phe Thr Gln Ala Val Phe Leu Lys
65 70 75 80
Val Asp val Asp Glu Leu Lys Glu val Ala Ala Tyr Asp Val Glu
 85 90 95
Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Val Thr Val Glu Thr
 100 105 110
Val Val Gly Ala Arg Lys Glu Asn Leu Leu Ala Gln Ile Glu Lys His
 115 120 125
Cys Ala Ala Ala Val Ser Ala Ala Ser Ala
 130 135

(2) INFORMATION FOR SEQ ID NO:2446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1503486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2446:

Met Ala Ser Glu Glu Glu Gly Val Val Ile Ala Cys His Thr Lys Ala
1 5 10 15
Asp Phe Asp Ala His Met Ala Lys Ala Lys Glu Ala Gly Lys Leu Val
 20 25 30
Ile Ile Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala
 35 40 45
Pro Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Ala Val Phe Leu
 50 55 60
Lys Val Asp Val Asp Glu Leu Lys Glu Val Ala Ala Tyr Asp Val
65 70 75 80
Glu Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Val Thr Val Glu
 85 90 95
Thr val Val Gly Ala Arg Lys Glu Asn Leu Leu Ala Gln Ile Glu Lys
 100 105 110
His Cys Ala Ala Val Ser Ala Ala Ser Ala
 115 120

(2) INFORMATION FOR SEQ ID NO:2447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..102
(D) OTHER INFORMATION: / Ceres Seq. ID 1503487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2447:

```
Met Ala Lys Ala Lys Glu Ala Gly Lys Leu Val Ile Ile Asp Phe Thr
1      5      10      15
Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro Leu Phe Val Glu
20     25     30
His Ala Lys Lys Phe Thr Gln Ala Val Phe Leu Lys Val Asp Val Asp
35     40     45
Glu Leu Lys Glu Val Ala Ala Tyr Asp Val Glu Ala Met Pro Thr
50     55     60
Phe His Phe Val Lys Asn Gly Val Thr Val Glu Thr Val Val Gly Ala
65     70     75     80
Arg Lys Glu Asn Leu Leu Ala Gln Ile Glu Lys His Cys Ala Ala Ala
85     90     95
Val Ser Ala Ala Ser Ala
100
```

(2) INFORMATION FOR SEQ ID NO:2448:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 522 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..522
(D) OTHER INFORMATION: / Ceres Seq. ID 1503492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2448:

```
aacctctagc tgattgatct ctggtttacc actctttcct tccctccttc aattctaaat 60
accacaaatc aaagttgctt tgcgatgggt agcagcagca tggacacgac gagtgcacaaa 120
cgtgcgctcat ccattgctggc tctaaccctt ggcaaggcca cgatcctcgc ccttgccacc 180
gccttccccc agcagntgtc atgcaggact acgtcgtcga cggcttcagt aagaacacca 240
tcgtgtacgt gctggagaac atggtggagg acacccggcg gaggaggctg ctggctgccg 300
acgacggtgg agaggactgc gagggtgggt tcattcctdc gttcggggcg gggatcacgt 360
tcgagggcat cctcgccagg aacttgcagg caaccgcgcg cgcttcagcc cagccctgat 420
caccctctgt tgggttgctt ttctgtctgc tctgcacctc tgctcccggt tgattgtctg 480
tttgagggag aatgctgagc atcaacattg ctcatgagca tc
```

(2) INFORMATION FOR SEQ ID NO:2449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..72
(D) OTHER INFORMATION: / Ceres Seq. ID 1503493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2449:

```
Met Gln Asp Tyr Val Val Asp Gly Phe Met Lys Asn Thr Ile Val Tyr
1      5      10      15
Val Leu Glu Asn Met Val Glu Asp Thr Arg Arg Arg Leu Leu Ala
20     25     30
Ala Asp Asp Gly Gly Glu Asp Cys Glu Trp Gly Leu Ile Leu Xaa Phe
35     40     45
Gly Pro Gly Ile Thr Phe Glu Gly Ile Leu Ala Arg Asn Leu Gln Ala
50     55     60
Thr Ala Arg Ala Ser Ala Gln Pro
65     70
```

(2) INFORMATION FOR SEQ ID NO:2450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2450:

Met	Lys	Asn	Thr	Ile	Val	Tyr	Val	Leu	Glu	Asn	Met	Val	Glu	Asp	Thr
1				5				10					15		
Arg	Arg	Arg	Arg	Leu	Leu	Ala	Ala	Asp	Asp	Gly	Gly	Glu	Asp	Cys	Glu
				20				25				30			
Trp	Gly	Leu	Ile	Leu	Xaa	Phe	Gly	Pro	Gly	Ile	Thr	Phe	Glu	Gly	Ile
				35				40				45			
Leu	Ala	Arg	Asn	Leu	Gln	Ala	Thr	Ala	Arg	Ala	Ser	Ala	Gln	Pro	
				50				55				60			

(2) INFORMATION FOR SEQ ID NO:2451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2451:

Met	Val	Glu	Asp	Thr	Arg	Arg	Arg	Arg	Leu	Ala	Ala	Asp	Asp	Gly	
1				5				10				15			
Gly	Glu	Asp	Cys	Glu	Trp	Gly	Leu	Ile	Leu	Xaa	Phe	Gly	Pro	Gly	Ile
				20				25				30			
Thr	Phe	Glu	Gly	Ile	Leu	Ala	Arg	Asn	Leu	Gln	Ala	Thr	Ala	Arg	Ala
				35				40				45			
Ser	Ala	Gln	Pro												
				50											

(2) INFORMATION FOR SEQ ID NO:2452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..465
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2452:

atgtcgacac	tctacaccca	cctcctgtgc	gagccacggg	tctccccact	agtgcacagg	60
ctttctctct	cacgggtgac	cctccccccc	cagcgacagg	cctgcgaggc	tgcgacactg	120
cagcatgcc	gagccatct	atctcttct	cgctccagc	tagacctccc	ccgtgcctac	180
gcccatccct	ggtgcggccg	cgctgcccc	tcattgcggc	aacatcgaca	tcctccctct	240
ctccagtag	cggtgcac	tgcaggatc	aaccccttcc	tcacgcccag	ttcatctgt	300
tgtggcgagg	gcgcgcctcc	tcccgcagc	ctggccttgc	gtcgggacag	tcctccgagc	360
ccagcgtccc	ctctcccaaa	gatgacgag	gaggcgctgc	ctccccagc	tcacgagagc	420
gcaasscagg	gaccataccc	acgcctccct	ccctcctggt	cgcgcg		

(2) INFORMATION FOR SEQ ID NO:2453:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 155 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..155
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503497
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2453:
Met Ser Thr Leu Tyr Thr His Pro Pro Val Glu Pro Arg Val Ser Pro
1 5 10 15
Leu Val Gln Pro Leu Ser Pro Pro Arg Val Thr Pro Pro Pro Gln Arg
 20 25 30
Thr Ala Cys Glu Ala Ala Thr Leu Gln His Ala Arg Arg His Leu Ser
 35 40 45
Leu Pro Arg Val Gln Leu Asp Leu Pro Arg Ala Tyr Ala His Pro Trp
50 55 60
Cys Gly Arg Ala Ala Pro Ser Cys Gly Gln His Arg His Pro Ser Pro
65 70 75 80
Leu Pro Val Pro Ala Ala Thr Ala Gly Ile Asn Pro Phe Leu Thr Pro
 85 90 95
Ser Ser Ser Ala Cys Gly Gly Gly Ala Pro Pro Pro Arg Thr Leu Ala
 100 105 110
Leu Arg Arg Thr Ala Pro Pro Thr Pro Ala Ser Pro Pro Pro Lys Met
 115 120 125
Thr Ser Glu Ala Xaa Pro Pro Pro Ala Pro Ala Ser Ala Xaa Gln Gly
130 135 140
Pro Tyr Pro Arg Leu Pro Pro Ser Trp Ser Arg
145 150 155
(2) INFORMATION FOR SEQ ID NO:2454:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 155 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..155
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503498
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2454:
Met Ser Thr Leu Tyr Thr His Pro Pro Val Glu Pro Arg Val Ser Pro
1 5 10 15
Leu Val Gln Pro Leu Ser Pro Pro Arg Val Thr Pro Pro Pro Gln Arg
 20 25 30
Thr Ala Cys Glu Ala Ala Thr Leu Gln His Ala Arg Arg His Leu Ser
 35 40 45
Leu Pro Arg Val Gln Leu Asp Leu Pro Arg Ala Tyr Ala His Pro Trp
50 55 60
Cys Gly Arg Ala Ala Pro Ser Cys Gly Gln His Arg His Pro Ser Pro
65 70 75 80
Leu Pro Val Pro Ala Ala Thr Ala Gly Ile Asn Pro Phe Leu Thr Pro
 85 90 95
Ser Ser Ser Ala Cys Gly Gly Gly Ala Pro Pro Pro Arg Thr Leu Ala
 100 105 110
Leu Arg Arg Thr Ala Pro Pro Thr Pro Ala Ser Pro Pro Pro Lys Met
 115 120 125
Thr Ser Glu Ala Xaa Pro Pro Pro Ala Pro Ala Ser Ala Xaa Gln Gly
130 135 140

Pro Tyr Pro Arg Leu Pro Pro Ser Trp Ser Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:2455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2455:

```
Val Asp Thr Leu His Pro Pro Ser Cys Arg Ala Thr Gly Leu Pro Thr
1 5 10 15
Ser Ala Thr Ala Phe Ser Ser Thr Gly Asp Pro Ser Pro Pro Ala His
20 25 30
Gly Leu Arg Gly Cys Asp Thr Ala Ala Cys Pro Thr Pro Ser Ile Ser
35 40 45
Ser Ser Arg Pro Ala Arg Pro Pro Cys Leu Arg Pro Ser Leu Val
50 55 60
Arg Pro Arg Cys Pro Leu Met Arg Pro Thr Ser Thr Ser Leu Pro Ser
65 70 75 80
Pro Ser Thr Gly Cys Asn Cys Arg His Gln Pro Leu Pro His Ala Gln
85 90 95
Phe Ile Cys Leu Trp Arg Arg Arg Ala Ser Ser Pro His Ala Gly Leu
100 105 110
Ala Ser Asp Ser Ser Ser Asp Ala Ser Val Pro Ser Ser Lys Asp Asp
115 120 125
Glu
```

(2) INFORMATION FOR SEQ ID NO:2456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..470
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2456:

```
ttctcattga aaagcttatc gtaaaagkttg ttctacctga agggctcaag gatatacgaag 60
tttcagctcc ccttccaaca cagcagcagc aagagggttaa gtattcacac cttagcattg 120
tcggaaagacc agttgtgtgc ttggagaaac ctgatgttat tccagagcat aatttgtatt 180
tccagggttta ctacagattc aacaacatat ccttgcctag agagccgttg atgctgatta 240
ctgggtttctt cctcctgttt gtggcctgta ttgtttacat gcgtactgat atgtcaatat 300
ccaagagctc tccttctctac ttggccaagc tgcaatggga tgaggtgcaa gcaactgttc 360
agaaaatcca gggtatcttc gagcaatgct tagcagttca tgataaactg gaggcctcat 420
tgccggattt gtctaggaca ggagacattc agtcttgcaa ggcagctcgt
```

(2) INFORMATION FOR SEQ ID NO:2457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1503508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2457:

```
Leu Ile Glu Lys Leu Ile Val Lys Xaa Val Leu Pro Glu Gly Ser Lys
1      5      10      15
Asp Ile Glu Val Ser Ala Pro Leu Pro Thr Gln Gln Gln Glu Val
20     25     30
Lys Tyr Ser His Leu Asp Ile Val Gly Arg Pro Val Val Val Leu Glu
35     40     45
Lys Pro Asp Val Ile Pro Glu His Asn Leu Tyr Phe Gln Val Tyr Tyr
50     55     60
Arg Phe Asn Asn Ile Ser Leu Leu Arg Glu Pro Leu Met Leu Ile Thr
65     70     75     80
Gly Phe Phe Leu Leu Phe Val Ala Cys Ile Val Tyr Met Arg Thr Asp
85     90     95
Met Ser Ile Ser Lys Ser Ser Pro Ser Tyr Leu Ala Lys Leu Gln Trp
100    105    110
Asp Glu Val Gln Ala Thr Val Gln Lys Ile Gln Gly Ile Phe Glu Gln
115    120    125
Cys Leu Ala Val His Asp Lys Leu Glu Ala Ser Leu Arg Asp Leu Ser
130    135    140
Arg Thr Gly Asp Ile Gln Ser Cys Lys Ala Ala Arg
145    150    155
```

(2) INFORMATION FOR SEQ ID NO:2458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1503509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2458:

```
Met Leu Ile Thr Gly Phe Phe Leu Leu Phe Val Ala Cys Ile Val Tyr
1      5      10      15
Met Arg Thr Asp Met Ser Ile Ser Lys Ser Ser Pro Ser Tyr Leu Ala
20     25     30
Lys Leu Gln Trp Asp Glu Val Gln Ala Thr Val Gln Lys Ile Gln Gly
35     40     45
Ile Phe Glu Gln Cys Leu Ala Val His Asp Lys Leu Glu Ala Ser Leu
50     55     60
Arg Asp Leu Ser Arg Thr Gly Asp Ile Gln Ser Cys Lys Ala Ala Arg
65     70     75     80
```

(2) INFORMATION FOR SEQ ID NO:2459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1503510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2459:

```
ttggatttga caaagatgcc aggagaagcc tcttcacccat gattaacaac ctgcccactg
tttatgaagt tgtgacgggg gttgctaaga agcaatcgaa agcccccaac ggcagcagca
```

60
120

aaagcagcaa gcctaactct aaaccatcaa aactgaccaa ttctaacagt aagcccgcga 180
mscagcccac cc

(2) INFORMATION FOR SEQ ID NO:2460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2460:

Gly Phe Asp Lys Asp Ala Arg Arg Arg Leu Phe Thr Met Ile Asn Asn
1 5 10 15
Leu Pro Thr Val Tyr Glu Val Val Thr Gly Val Ala Lys Lys Gln Ser
20 25 30
Lys Ala Pro Asn Gly Ser Ser Lys Ser Ser Lys Pro Asn Ser Lys Pro
35 40 45
Ser Lys Leu Thr Asn Ser Asn Ser Lys Pro Ala Xaa Gln Pro Thr
50 55 60

(2) INFORMATION FOR SEQ ID NO:2461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2461:

Met Ile Asn Asn Leu Pro Thr Val Tyr Glu Val Val Thr Gly Val Ala
1 5 10 15
Lys Lys Gln Ser Lys Ala Pro Asn Gly Ser Ser Lys Ser Ser Lys Pro
20 25 30
Asn Ser Lys Pro Ser Lys Leu Thr Asn Ser Asn Ser Lys Pro Ala Xaa
35 40 45
Gln Pro Thr
50

(2) INFORMATION FOR SEQ ID NO:2462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..287
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2462:

ctcgagcctg acccttaacg cttcgtctgc gccgccgccg ccgccgccgc tacgccccgc 60
acctcgcttc atttcgtgtc gccaaagatga cgaagcgcac taagaaggca ggaattgttg 120
gcaaatatgg aaccaggatg ggtgctagct tgcgtaassa atcaagaaga tggagggtatc 180
tcagcattcc aattactttt gcgagttctg tgggaagttt gctgtgaaga ggaagaatat 240
agcaaggttt ttgttcgcag ctatttttgt ccaatgatat tgatatt

(2) INFORMATION FOR SEQ ID NO:2463:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..46
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503523
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2463:
Met Thr Lys Arg Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr
1 5 10 15
Arg Tyr Gly Ala Ser Leu Arg Xaa Xaa Ser Arg Arg Trp Arg Tyr Leu
 20 25 30
Ser Ile Pro Ile Thr Phe Ala Ser Ser Val Gly Ser Leu Leu
 35 40 45
(2) INFORMATION FOR SEQ ID NO:2464:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..53
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503524
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2464:
Met Glu Pro Gly Met Val Leu Ala Cys Val Xaa Asn Gln Glu Asp Gly
1 5 10 15
Gly Ile Ser Ala Phe Gln Leu Leu Leu Arg Val Leu Trp Glu Val Cys
 20 25 30
Cys Glu Glu Glu Arg Met Ser Lys Val Phe Val Arg Ser Tyr Phe Cys
 35 40 45
Pro Met Ile Leu Ile
 50
(2) INFORMATION FOR SEQ ID NO:2465:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..49
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503525
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2465:
Met Val Leu Ala Cys Val Xaa Asn Gln Glu Asp Gly Gly Ile Ser Ala
1 5 10 15
Phe Gln Leu Leu Leu Arg Val Leu Trp Glu Val Cys Cys Glu Glu Glu
 20 25 30
Arg Met Ser Lys Val Phe Val Arg Ser Tyr Phe Cys Pro Met Ile Leu
 35 40 45
Ile
 50
(2) INFORMATION FOR SEQ ID NO:2466:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 498 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1.498
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503526
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2466:
ctagttagaga gaaaggaaga gaagggggcg gagaagcacg tacgtcgtac atcgcccacc 60
gcocctttgcc tgcctctgcc tgcctctgcc tgcataatcta acagccggag ccggagccgg 120
agccggagcc gaagccggcg ccgacaatcg ttccaactga tatggctacg acgccaccag 180
gattcacggg caacctgaag aaagcacttg caggtctgag aagaatcagt ttagatgggt 240
tgccatggcg cgtatttgat gctaagggtc aggtgctcgg gcgattggct tcccaaatag 300
ctgtttgtgt tcaaggcaag gataaaccca cctatgcacc acatgtagaa aatggagaca 360
tgtgcattgt acttaattga aaggatatca gtgtttacag gaaggaaaat gacagataag 420
atttactatt ggcatacagg gtatgtttgc catttgaagg aaaggaggct caaggaccag 480
atggagaaag acccaact
(2) INFORMATION FOR SEQ ID NO:2467:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1.65
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503527
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2467:
Leu Val Glu Arg Lys Glu Glu Lys Gly Ala Glu Lys His Val Arg Arg
1 5 10 15
Thr Ser Pro Thr Ala Leu Cys Leu Ala Ser Pro Arg Leu Ala Cys Ile
20 25 30
Ser Asn Ser Arg Ser Arg Ser Arg Ser Arg Arg Arg Arg Arg
35 40 45
Gln Ser Phe Gln Leu Ile Trp Leu Arg Arg His Gln Asp Ser Arg Ala
50 55 60
Thr
65
(2) INFORMATION FOR SEQ ID NO:2468:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1.85
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503528
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2468:
Met Ala Thr Thr Pro Pro Gly Phe Thr Gly Asn Leu Lys Lys Ala Leu
1 5 10 15
Ala Gly Leu Arg Arg Ile Ser Leu Asp Gly Leu Arg Trp Arg Val Phe
20 25 30
Asp Ala Lys Gly Gln Val Leu Gly Arg Leu Ala Ser Gln Ile Ala Val
35 40 45
Val Leu Gln Gly Lys Asp Lys Pro Thr Tyr Ala Pro His Val Glu Asn
50 55 60
Gly Asp Met Cys Ile Val Leu Asn Ala Lys Asp Ile Ser Val Tyr Arg
65 70 75 80
Lys Glu Asn Asp Arg

85

(2) INFORMATION FOR SEQ ID NO:2469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2469:

Met	Glu	Thr	Cys	Ala	Leu	Tyr	Leu	Met	Gln	Arg	Ile	Ser	Val	Phe	Thr
1			5					10					15		
Gly	Arg	Lys	Met	Thr	Asp	Lys	Ile	Tyr	Trp	His	Thr	Gly	Tyr	Val	
			20				25					30			
Gly	His	Leu	Lys	Glu	Arg	Arg	Leu	Lys	Asp	Gln	Met	Glu	Lys	Asp	Pro
			35				40					45			
Thr															

(2) INFORMATION FOR SEQ ID NO:2470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2470:

ataa	ccaagg	ataa	ccagag	tgtg	ctggtt	tatt	gcttct	catg	gggttg	tgt	aatt	tttcg	ttt		60
gttt	tactgc	ttat	gaagac	cgtat	cagtg	gggag	gagga	ggtt	cagtc	gc	agag	ttccag			120
ctagt	gtttcc	ggct	gatcaa	gggt	ctcata	ttata	aaact	ttac	agccat	cgtg	ggaatc				180
ctaata	gcaaa	tcct	tgcat	gacg	gttctg	gacat	ctttg	tttg	catcct	tgcc	ttcatg				240
cccact	ggat	gggt	tttgct	cctg	attgcc	caag	ctatca	ggct	gtgat	tcaaaa	gatc				300
gggctg	tggtg	ggct	gatcaa	ggct	cttgcc	cggg	gctacg	agat	ccataat	gggg	cttctc				360
ctgtt	caacgc	ccatt	gtctt	cttg	gcctgg	ttcc	gcttcg	tg	tccgag	gtt	ccagacc	agg			420
atgct	gttca	accag	gcctt	cagc	agaggt	ctgc	agatc	tccc	gtatcc	tg	ggagg				

(2) INFORMATION FOR SEQ ID NO:2471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503551

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2471:

Ile	Thr	Lys	Asp	Asn	Gln	Ser	Val	Leu	Val	Tyr	Cys	Phe	Ser	Trp	Val
1				5				10					15		
Val	Ile	Phe	Val	Val	Leu	Leu	Val	Met	Lys	Thr	Val	Ser	Val	Gly	Arg
				20				25					30		
Arg	Arg	Phe	Ser	Ala	Glu	Phe	Gln	Leu	Val	Phe	Arg	Leu	Ile	Lys	Gly
				35			40				45				
Leu	Ile	Phe	Ile	Thr	Phe	Thr	Ala	Ile	Val	Val	Ile	Leu	Ile	Ala	Ile
				50			55				60				

Pro Gly Met Thr Val Leu Asp Ile Phe Val Cys Ile Leu Ala Phe Met
65 70 75 80
Pro Thr Gly Trp Gly Leu Leu Leu Ile Ala Gln Ala Ile Arg Pro Val
85 90 95
Ile Gln Lys Ile Gly Leu Trp Gly Ser Ile Lys Ala Leu Ala Arg Gly
100 105 110
Tyr Glu Ile Leu Met Gly Leu Leu Leu Phe Thr Pro Ile Ala Phe Leu
115 120 125
Ala Trp Phe Pro Phe Val Ser Glu Phe Gln Thr Arg Met Leu Phe Asn
130 135 140
Gln Ala Phe Ser Arg Gly Ser Ala Asp Leu Pro Tyr Pro Gly Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:2472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2472:

Met Gly Cys Asn Phe Arg Cys Phe Thr Arg Tyr Glu Asp Arg Ile Ser
1 5 10 15
Gly Glu Glu Glu Val Gln Cys Arg Val Pro Ala Ser Val Pro Ala Asp
20 25 30
Gln Gly Ser His Ile Tyr Asn Phe Tyr Ser His Arg Gly Gly Asn Pro Asn
35 40 45
Ser Asn Pro Trp His Asp Gly Ser Gly His Leu Cys Leu His Pro Cys
50 55 60
Leu His Ala His Trp Met Gly Phe Ala Pro Asp Cys Pro Ser Tyr Gln
65 70 75 80
Ala Cys Asp Ser Lys Asp Arg Ala Val Gly Val Asp Gln Gly Ser Cys
85 90 95
Pro Gly Leu Arg Asp Pro Asn Gly Ala Ser Pro Val His Ala His Cys
100 105 110
Phe Pro Cys Leu Val Pro Val Arg Val Pro Asp Gln Asp Ala
115 120 125
Val Gln Pro Gly Leu Gln Gln Arg Phe Cys Arg Ser Pro Val Ser Trp
130 135 140
Glu
145

(2) INFORMATION FOR SEQ ID NO:2473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2473:

Met Lys Thr Val Ser Val Gly Arg Arg Arg Phe Ser Ala Glu Phe Gln
1 5 10 15
Leu Val Phe Arg Leu Ile Lys Gly Leu Ile Phe Ile Thr Phe Thr Ala
20 25 30
Ile Val Val Ile Leu Ile Ala Ile Pro Gly Met Thr Val Leu Asp Ile

35 40 45
Phe Val Cys Ile Leu Ala Phe Met Pro Thr Gly Trp Gly Leu Leu Leu
50 55 60
Ile Ala Gln Ala Ile Arg Pro Val Ile Gln Lys Ile Gly Leu Trp Gly
65 70 75 80
Ser Ile Lys Ala Leu Ala Arg Gly Tyr Glu Ile Leu Met Gly Leu Leu
85 90 95
Leu Phe Thr Pro Ile Ala Phe Leu Ala Trp Phe Pro Phe Val Ser Glu
100 105 110
Phe Gln Thr Arg Met Leu Phe Asn Gln Ala Phe Ser Arg Gly Ser Ala
115 120 125
Asp Leu Pro Tyr Pro Gly Arg
130 135

(2) INFORMATION FOR SEQ ID NO:2474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..420
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2474:

caggctctag	ctccggcctc	cgccggcgtc	tctcacctcc	gctcccccttc	ctgcccccca	60
tggcgaaggc	gacgccccta	gccgaggccg	ggccgcctct	cacgtcccca	ctccacatg	120
ggcgcaenca	cggaggccct	gacccacgtc	ctgaccaccc	cgccccacgc	gcgcctcact	180
cactcgagcg	tcttctctcg	ctcccgcgtc	ccgtgcccg	cgcggggcct	cggtccacc	240
acgtcgatcc	cgccgctctc	ctgcccgcny	gcctcgctcc	tccgctgggc	tctcgctctc	300
gtgttctctc	cgccgcgcgc	agcctctgcc	tcccgcctcc	gtcctggcgg	tcccgggtgc	360
ctctccagcg	tcccgcgcgc	cggttgtgcc	ctccggcgcc	atcgagccgg	gcgcgccgag	420

(2) INFORMATION FOR SEQ ID NO:2475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2475:

Gly	Pro	Ser	Ser	Gly	Leu	Arg	Arg	Arg	Leu	Ser	Pro	Pro	Leu	Pro	Phe
1				5					10					15	
Pro	Ala	Pro	Met	Ala	Lys	Ala	Thr	Pro	Val	Ala	Glu	Ala	Gly	Pro	Pro
				20				25					30		
Leu	Thr	Ser	Pro	Leu	Pro	His	Gly	Arg	Xaa	His	Gly	Gly	Pro	Asp	Pro
				35			40				45				
Arg	Pro	Asp	Pro	Pro	Val	Pro	Arg	Ala	Val	Thr	Pro	Leu	Ala	Ala	Leu
				50			55				60				
Pro	Arg	Leu	Pro	Arg	Pro	Val	Pro	Ala	Ala	Gly	Pro	Arg	Leu	His	His
				65			70			75				80	
Val	Val	Pro	Ala	Ala	Pro	Leu	Pro	Xaa	Xaa	Leu	Ala	Pro	Pro	Leu	Gly
				85				90					95		
Ser	Arg	Leu	Arg	Val	Pro	Pro	Ala	Arg	Ala	Ser	Leu	Cys	Leu	Pro	Pro
				100			105				110				
Ser	Ser	Trp	Arg	Ser	Arg	Cys	Pro	Phe	Gln	Ala	Pro	Arg	Arg	Arg	Ser
				115			120				125				

Cys Pro Pro Arg Pro Ser Ser Arg Ala Pro Glu
130 135

(2) INFORMATION FOR SEQ ID NO:2476:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1503556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2476:

Met Ala Lys Ala Thr Pro Val Ala Glu Ala Gly Pro Pro Leu Thr Ser
1 5 10 15
Pro Leu Pro His Gly Arg Xaa His Gly Gly Pro Asp Pro Arg Pro Asp
20 25 30
Pro Pro Val Pro Arg Ala Val Thr Pro Leu Ala Ala Leu Pro Arg Leu
35 40 45
Pro Arg Pro Val Pro Ala Ala Gly Pro Arg Leu His His Val Val Pro
50 55 60
Ala Ala Pro Leu Pro Xaa Xaa Leu Ala Pro Pro Leu Gly Ser Arg Leu
65 70 75 80
Arg Val Pro Pro Ala Arg Ala Ser Leu Cys Leu Pro Pro Ser Ser Trp
85 90 95
Arg Ser Arg Cys Pro Phe Gln Ala Pro Arg Arg Arg Ser Cys Pro Pro
100 105 110
Arg Pro Ser Ser Arg Ala Pro Glu
115 120

(2) INFORMATION FOR SEQ ID NO:2477:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1503557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2477:

Met Gly Ala Xaa Thr Glu Ala Leu Thr His Val Leu Thr His Pro Ser
1 5 10 15
His Ala Pro Ser Leu His Ser Gln Leu Leu Ala Ser Arg Val Pro
20 25 30
Cys Pro Pro Arg Gly Leu Gly Ser Thr Thr Ser Tyr Pro Pro Leu Leu
35 40 45
Cys Pro Xaa Ala Ser Leu Leu Arg Trp Ala Leu Ala Ser Val Phe Leu
50 55 60
Pro Arg Ala Arg Ala Ser Ala Ser Arg Pro Arg Pro Gly Gly Pro Gly
65 70 75 80
Ala Pro Ser Arg Leu Pro Ala Ala Gly Arg Ala Leu Arg Gly His Arg
85 90 95
Ala Gly Arg Pro Ser
100

(2) INFORMATION FOR SEQ ID NO:2478:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 418 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..418
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503569
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2478:
ttctggtctc tcttgetttc tcattgatcaa gcgtgtgtcc tctgtctcgt ccttgtccag 60
gcaccacaag gcaaaagaag ctccaggtgag aatgttgtga tgggtgatcc actggaagct 120
aagcgccatg ctgctaaaca aatgcaagaa attagggcca aagaaaaagct gaagaggcgc 180
cgtaacagcag aagcgcattca cggggcattg gcagtgcata gactcacggc tggattgcta 240
gtggaggctc agacaggaaa ggacatctta gggcagctag ctggatatct gacggctatt 300
tctagtttat ttgggcaata acactggacc atggttggag atttattttt cactgtccac 360
ggccaggaga ggtcttatct gaattctatt tgatggatcc acccaatttt ttggggag
(2) INFORMATION FOR SEQ ID NO:2479:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..106
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503570
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2479:
Phe Trp Leu Leu Leu Pro His Asp Gln Ala Cys Val Leu Cys Ser
1 5 10 15
Val Leu Val Gln Ala Pro Gln Gly Lys Arg Ser Ser Gly Glu Asn Val
20 25 30
Val Met Val Asp Pro Leu Glu Ala Lys Arg Leu Ala Ala Lys Gln Met
35 40 45
Gln Glu Ile Arg Ala Lys Glu Lys Leu Lys Arg Arg Gln Ala Glu
50 55 60
Ala Ile Asn Gly Ala Leu Ala Val Ile Gly Leu Thr Ala Gly Leu Leu
65 70 75 80
Val Glu Ala Gln Thr Gly Lys Asp Ile Leu Gly Gln Leu Ala Gly Tyr
85 90 95
Leu Thr Ala Ile Ser Ser Leu Phe Gly Gln
100 105
(2) INFORMATION FOR SEQ ID NO:2480:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..73
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503571
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2480:
Met Val Asp Pro Leu Glu Ala Lys Arg Leu Ala Ala Lys Gln Met Gln
1 5 10 15
Glu Ile Arg Ala Lys Glu Lys Leu Lys Arg Arg Arg Gln Ala Glu Ala
20 25 30
Ile Asn Gly Ala Leu Ala Val Ile Gly Leu Thr Ala Gly Leu Leu Val
35 40 45
Glu Ala Gln Thr Gly Lys Asp Ile Leu Gly Gln Leu Ala Gly Tyr Leu
50 55 60
Thr Ala Ile Ser Ser Leu Phe Gly Gln

65 70
(2) INFORMATION FOR SEQ ID NO:2481:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..59
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503572
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2481:
Met Gln Glu Ile Arg Ala Lys Glu Lys Leu Lys Arg Arg Gln Ala
1 5 10 15
Glu Ala Ile Asn Gly Ala Leu Ala Val Ile Gly Leu Thr Ala Gly Leu
 20 25 30
Leu Val Glu Ala Gln Thr Gly Lys Asp Ile Leu Gly Gln Leu Ala Gly
 35 40 45
Tyr Leu Thr Ala Ile Ser Ser Leu Phe Gly Gln
50 55

(2) INFORMATION FOR SEQ ID NO:2482:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 438 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..438
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503585
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2482:
cagaggatat caatatttgg tggtagaattc ccatacgggc atacagctga tgttcaaagt 60
gtgtccatca actcatcaat acaaatatgt ttgtctctgg ctcatgtgat acaactgtga 120
ggctgtggga tatcagaatt gcaagtcgag ctgttcgaac ctacctgga catgaggatg 180
atgttaacag tgtgaagttt ttccctgatg gccatagggt ttgtactggc tcagattatg 240
gcacatgtag attatttgat atgagaacag ggcatacaact tcaggtgtac agtaggggagc 300
ctgatagaaa tagtaatgaa ctacctactg ttacatctat tgcattttca atatacaggaa 360
ggctactttt tgtctggttac tccaatgggtg actgttatgt gtgggacacm ttctcgccga 420
ggtggtactt aatttggg

(2) INFORMATION FOR SEQ ID NO:2483:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..117
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503586
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2483:
Met Phe Val Ser Gly Ser Cys Asp Thr Thr Val Arg Leu Trp Asp Ile
1 5 10 15
Arg Ile Ala Ser Arg Ala Val Arg Thr Tyr His Gly His Glu Asp Asp
 20 25 30
Val Asn Ser Val Lys Phe Phe Pro Asp Gly His Arg Phe Gly Thr Gly
 35 40 45
Ser Asp Tyr Gly Thr Cys Arg Leu Phe Asp Met Arg Thr Gly His Gln
50 55 60

Leu Gln Val Tyr Ser Arg Glu Pro Asp Arg Asn Ser Asn Glu Leu Pro
65 70 75 80
Thr Val Thr Ser Ile Ala Phe Ser Ile Ser Gly Arg Leu Leu Phe Ala
85 90 95
Gly Tyr Ser Asn Gly Asp Cys Tyr Val Trp Asp Xaa Phe Ser Pro Arg
100 105 110
Trp Tyr Leu Ile Trp
115

(2) INFORMATION FOR SEQ ID NO:2484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..59
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2484:

Met Arg Thr Gly His Gln Leu Gln Val Tyr Ser Arg Glu Pro Asp Arg
1 5 10 15
Asn Ser Asn Glu Leu Pro Thr Val Thr Ser Ile Ala Phe Ser Ile Ser
20 25 30
Gly Arg Leu Leu Phe Ala Gly Tyr Ser Asn Gly Asp Cys Tyr Val Trp
35 40 45
Asp Xaa Phe Ser Pro Arg Trp Tyr Leu Ile Trp
50 55

(2) INFORMATION FOR SEQ ID NO:2485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..506
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2485:

ttcgccgcgc	cgcgccctcg	agaagagata	gaggcgccgc	ctgcatcgac	cccgccacc	60
ccccgcctgc	ctccccgcgc	accgatggg	ttgatcgat	ggcgtagaag	aggatcctga	120
aggagttgaa	ggacctgcag	aaggaccgcg	ccacctcctg	cagcgertoc	tgttggtgag	180
gacatgttcc	attggcaagc	gaccatcatg	gggccttcgg	acagcccatt	tgacaggtggg	240
gtattcttgg	tgaacattca	cttccaccgc	gattaccctt	tcaagccacc	aaaggtgtct	300
ttccgcacca	aggttttcca	cccgaacatc	aacagcaacg	gcagcatttg	ccttgacatt	360
cttaaggaac	agtggagtcg	tgctttaact	atctcaaaag	ttctctgtgc	aatctgetca	420
ctgctcacgg	acccaaccc	tgatgatcct	ctgtccctg	agattgetca	catgtacaat	480
tcattcggtg	gaaaacctgg	aacgtg				

(2) INFORMATION FOR SEQ ID NO:2486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2486:

Met	Phe	His	Trp	Gln	Ala	Thr	Ile	Met	Gly	Pro	Ser	Asp	Ser	Pro	Phe
1				5					10					15	
Ala	Gly	Gly	Val	Phe	Leu	Val	Asn	Ile	His	Phe	Pro	Pro	Asp	Tyr	Pro
			20					25					30		
Phe	Lys	Pro	Pro	Lys	Val	Ser	Phe	Arg	Thr	Lys	Val	Phe	His	Pro	Asn
		35					40					45			
Ile	Asn	Ser	Asn	Gly	Ser	Ile	Cys	Leu	Asp	Ile	Leu	Lys	Glu	Gln	Trp
	50					55					60				
Ser	Pro	Ala	Leu	Thr	Ile	Ser	Lys	Val	Leu	Leu	Ser	Ile	Cys	Ser	Leu
	65				70					75				80	
Leu	Thr	Asp	Pro	Asn	Pro	Asp	Asp	Pro	Leu	Val	Pro	Glu	Ile	Ala	His
			85					90					95		
Met	Tyr	Asn	Ser	Phe	Val	Gly	Lys	Pro	Gly	Thr					
			100					105							

(2) INFORMATION FOR SEQ ID NO:2487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2487:

Met	Gly	Pro	Ser	Asp	Ser	Pro	Phe	Ala	Gly	Gly	Val	Phe	Leu	Val	Asn
1				5					10				15		
Ile	His	Phe	Pro	Pro	Asp	Tyr	Pro	Phe	Lys	Pro	Pro	Lys	Val	Ser	Phe
			20					25				30			
Arg	Thr	Lys	Val	Phe	His	Pro	Asn	Ile	Asn	Ser	Asn	Gly	Ser	Ile	Cys
		35					40					45			
Leu	Asp	Ile	Leu	Lys	Glu	Gln	Trp	Ser	Pro	Ala	Leu	Thr	Ile	Ser	Lys
	50					55					60				
Val	Leu	Leu	Ser	Ile	Cys	Ser	Leu	Leu	Thr	Asp	Pro	Asn	Pro	Asp	Asp
	65				70					75				80	
Pro	Leu	Val	Pro	Glu	Ile	Ala	His	Met	Tyr	Asn	Ser	Phe	Val	Gly	Lys
			85					90						95	
Pro	Gly	Thr													

(2) INFORMATION FOR SEQ ID NO:2488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..383
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2488:

gtacgagcgg	acgcacgacg	agcttgactt	cgaattcctc	gggaactgtc	gcggcaagga	60
gtggcgctg	cagaccaacg	tgtacggcaa	cggcagcacg	gcggccggcc	gggaggagcg	120
ctacggcctc	tggttcgacc	ccacggagga	cttcaccgcc	tacgccatcc	actggaccgc	180
cgacaggatc	atattctaca	tcgacgacac	gccaatcatg	gagatgggtc	ggacggagtc	240
aatgggcgcg	cagttcccg	ccaagcccat	gtcgtgtgac	gccaccatct	gggacggctc	300
cagctggggc	acctcggggg	gccgctacaa	ggtggactac	aagtacgcgc	cctacgtcgc	360
cgagttcgcc	gacctcgcc	tcc				

(2) INFORMATION FOR SEQ ID NO:2489:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..127
(D) OTHER INFORMATION: / Ceres Seq. ID 1503592
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2489:
Tyr Glu Arg Thr His Asp Glu Leu Asp Phe Glu Phe Leu Gly Asn Val
1 5 10 15
Arg Gly Lys Glu Trp Arg Val Gln Thr Asn Val Tyr Gly Asn Gly Ser
20 25 30
Thr Ala Ala Gly Arg Glu Glu Arg Tyr Gly Leu Trp Phe Asp Pro Thr
35 40 45
Glu Asp Phe His Arg Tyr Ala Ile His Trp Thr Arg Asp Arg Ile Ile
50 55 60
Phe Tyr Ile Asp Asp Thr Pro Ile Met Glu Met Val Arg Thr Glu Ser
65 70 75 80
Met Gly Ala Gln Phe Pro Ser Lys Pro Met Ser Leu Tyr Ala Thr Ile
85 90 95
Trp Asp Gly Ser Ser Trp Ala Thr Ser Gly Gly Arg Tyr Lys Val Asp
100 105 110
Tyr Lys Tyr Ala Pro Tyr Val Ala Glu Phe Ala Asp Leu Ala Leu
115 120 125

(2) INFORMATION FOR SEQ ID NO:2490:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..127
(D) OTHER INFORMATION: / Ceres Seq. ID 1503593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2490:

Thr Ser Gly Arg Thr Thr Ser Leu Thr Ser Ser Ser Gly Thr Cys
1 5 10 15
Ala Ala Arg Ser Gly Ala Cys Arg Pro Thr Cys Thr Ala Thr Ala Ala
20 25 30
Arg Arg Pro Ala Gly Arg Ser Ala Thr Ala Ser Gly Ser Thr Pro Arg
35 40 45
Arg Thr Ser Thr Ala Thr Pro Ser Thr Gly Pro Ala Thr Gly Ser Tyr
50 55 60
Ser Thr Ser Thr Thr Arg Gln Ser Trp Arg Trp Cys Gly Arg Ser Gln
65 70 75 80
Trp Ala Arg Ser Ser Arg Pro Ser Pro Cys Arg Cys Thr Pro Pro Ser
85 90 95
Gly Thr Ala Pro Ala Gly Pro Pro Arg Gly Ala Ala Thr Arg Trp Thr
100 105 110
Thr Ser Thr Arg Pro Thr Ser Pro Ser Pro Thr Ser Arg Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:2491:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..365

(D) OTHER INFORMATION: / Ceres Seq. ID 1503594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2491:

actgaacatt	ctgcgtgaag	attggaagcc	tgttctcaac	atcaacaccg	ttatttatgg	60
cctgaattott	ctttttacgc	aaccaaacga	cgaggatcct	ttgaaccacg	aagctgcagc	120
tgctctccgt	ggcaacccaa	agatgtttga	ggcaaatgtg	aaaagagcca	tgaccggagc	180
tacgtaggcc	aacactattt	ccaaagatgc	ttggcttgat	gtgatggctt	caagccagcg	240
ggcccatgta	tcagcaccag	cgcgccacgg	tttgaggat	ttttgtgat	ttaggggcgt	300
cttgaagca	aaggtcaaat	cggtcgttgt	tgataatgtg	atgtactccc	tcagttcttt	360
ttatt						

(2) INFORMATION FOR SEQ ID NO:2492:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..61

(D) OTHER INFORMATION: / Ceres Seq. ID 1503595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2492:

Leu	Asn	Ile	Leu	Arg	Glu	Asp	Trp	Lys	Pro	Val	Leu	Asn	Ile	Asn	Thr
1			5						10					15	
Val	Ile	Tyr	Gly	Leu	Asn	Leu	Leu	Phe	Thr	Gln	Pro	Asn	Asp	Glu	Asp
			20						25					30	
Pro	Leu	Asn	His	Glu	Ala	Ala	Ala	Val	Leu	Arg	Gly	Asn	Pro	Lys	Met
			35					40						45	
Phe	Glu	Ala	Asn	Val	Lys	Arg	Ala	Met	Thr	Gly	Ala	Thr			
			50					55						60	

(2) INFORMATION FOR SEQ ID NO:2493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1503596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2493:

Met	Ala	Ser	Ser	Gln	Arg	Ala	His	Val	Ser	Ala	Pro	Ala	Arg	Pro	Gly
1				5					10					15	
Leu	Glu	Asp	Phe	Cys	Gly	Phe	Arg	Ala	Leu	Leu	Glu	Ala	Lys	Val	Lys
			20						25					30	
Ser	Val	Val	Val	Asp	Asn	Val	Met	Tyr	Ser	Leu	Ser	Ser	Phe	Tyr	
			35					40						45	

(2) INFORMATION FOR SEQ ID NO:2494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..31

(D) OTHER INFORMATION: / Ceres Seq. ID 1503597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2494:
Met Tyr Gln His Gln Arg Ala Gln Val Trp Arg Ile Phe Val Asp Leu
1 5 10 15
Gly Arg Phe Trp Lys Gln Arg Ser Asn Arg Ser Leu Leu Ile Met
20 25 30

(2) INFORMATION FOR SEQ ID NO:2495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..413
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2495:

atataccgctt	ccaaacccta	gctcttccat	tcttccccct	ccggcgccgc	ctcccccaga	60
cacttcgccc	cgggcaagat	gggcccgtg	attcgcgtc	agssaaaggt	gcggggctcg	120
tggtcaagtc	ccatacccat	caccgcaagg	ccctgcgggt	tccggctcct	cgacttcggc	180
gagcgcaacg	ggtagctgaa	gggctgggtc	accgacgtca	tccacgaccc	gggcccgcgc	240
cgcgcgcttg	ccaaggtcac	cttccgccat	ccattccggt	acaagcacca	gaaggagctg	300
ttcgtggctg	ctgagggcac	gtacactggc	cagttcggtt	actgcggacg	ccgtgtctaca	360
ctctccattg	gcaacgtcct	gccgctcagg	gggatccctg	aggggtgccgt	tgt	

(2) INFORMATION FOR SEQ ID NO:2496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2496:

Ile	Arg	Leu	Gln	Thr	Leu	Ala	Leu	Pro	Phe	Phe	Pro	Leu	Arg	Arg	Arg
1		5							10					15	
Leu	Pro	Gln	Thr	Leu	Arg	Arg	Arg	Gln	Asp	Gly	Pro	Arg	Asp	Ser	Arg
		20						25					30		
Ser	Xaa	Lys	Gly	Ala	Gly	Ser	Val	Phe	Lys	Ser	His	Thr	His	His	Arg
		35					40				45				
Lys	Ala	Leu	Pro	Val	Pro	Val	Pro	Arg	Leu	Arg	Arg	Ala	Gln	Arg	Val
		50				55					60				
Pro	Glu	Gly	Arg	Gly	His	Arg	Arg	His	Pro	Arg	Pro	Gly	Pro	Arg	Arg
		65			70			75						80	
Ala	Ala	Gly	Gln	Gly	His	Leu	Pro	Pro	Ser	Ile	Pro	Val	Gln	Ala	Pro
				85				90						95	
Glu	Gly	Ala	Val	Arg	Gly	Cys									
						100									

(2) INFORMATION FOR SEQ ID NO:2497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2497:
Met Gly Arg Val Ile Arg Ala Gln Xaa Arg Val Arg Gly Pro Cys Ser
1 5 10 15
Ser Pro Ile Pro Ile Thr Ala Arg Pro Cys Arg Phe Arg Ser Leu Asp
20 25 30
Phe Gly Glu Arg Asn Gly Tyr Leu Lys Gly Val Val Thr Asp Val Ile
35 40 45
His Asp Pro Gly Arg Gly Ala Pro Leu Ala Lys Val Thr Phe Arg His
50 55 60
Pro Phe Arg Tyr Lys His Gln Lys Glu Leu Phe Val Ala Ala Glu Gly
65 70 75 80
Met Tyr Thr Gly Gln Phe Val Tyr Cys Gly Arg Arg Ala Thr Leu Ser
85 90 95
Ile Gly Asn Val Leu Pro Leu Arg Gly Ile Pro Glu Gly Ala Val
100 105 110

(2) INFORMATION FOR SEQ ID NO:2498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..466
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2498:

attccattcc	atcgatttgg	attgcattcc	catccattcc	cccgtctctac	tcattcagat	60
ctcgtcaactc	gtctctcaca	agcagagcac	cgcagcagaa	cgaggatgct	ggccattcttc	120
cagaagcagg	tggcgcaagc	gtcagcagga	gcntcaacag	cccccgccgc	ggcgcgtcgc	180
ccagcaagcc	ccggaacccc	gacgagatcc	tgcgcgactt	ccacgcgcgc	cccccgccgc	240
ccgccttctc	cgctctcttc	ggcgcgctgc	gntgctcgcc	ttgcgttcgg	ccccctctcc	300
gccaccgccca	cctaccagcg	ggatgtttct	gcggccttgg	accacatcta	ctgcgtcttc	360
ctcgccgcgc	tcgacaacct	cagcggcctc	atccgccagt	wacggcctgt	gcggccgcctc	420
ccaccaacga	ggcgatgctg	gtcatcgagg	cctaccgcac	gctgctg		

(2) INFORMATION FOR SEQ ID NO:2499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2499:

Ile Pro Phe His Arg Ile Gly Leu His Ser His Pro Ile Pro Arg Ser	
1 5 10 15	
Thr His Ser Asp Leu Val Thr Arg Ser Pro Gln Ala Glu His Arg Ser	
20 25 30	
Arg Thr Arg Met Leu Ala Ile Phe Gln Lys Val Ala His Ala Xaa	
35 40 45	
Ala Gly Xaa Ser Thr Ala Pro Ala Pro Ala Arg Arg Pro Ala Ser Pro	
50 55 60	
Gly Thr Pro Thr Arg Ser Cys Ala Thr Ser Thr Pro Arg Thr Arg Pro	
65 70 75 80	
Pro Pro Ser Pro Pro Ser Ala Ala Cys Xaa Ala Arg Leu Ala Phe	
85 90 95	
Gly Pro Ser Ser Ala Thr Tyr Gln Arg Asp Val Ser Ala Ala	
100 105 110	

Leu Asp His Ile Tyr Cys Val Phe Leu Gly Arg Leu Asp Asn Leu Ser
115 120 125
Gly Leu Ile Arg Gln Xaa Arg Pro Val Arg Pro Leu Pro Pro Thr Arg
130 135 140
Arg Cys Trp Ser Ser Arg Pro Thr Ala Arg Cys
145 150 155

(2) INFORMATION FOR SEQ ID NO:2500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2500:

Phe His Ser Ile Ala Leu Asp Cys Ile Pro Ile Pro Phe Pro Ala Leu
1 5 10 15
Leu Ile Gln Ile Ser Ser Leu Ala Leu His Lys Gln Ser Thr Ala Ala
20 25 30
Glu Arg Gly Cys Trp Pro Ser Ser Arg Ser Arg Trp Arg Thr Arg Xaa
35 40 45
Gln Glu Xaa Gln Gln Pro Pro Arg Arg Arg Val Ala Gln Gln Ala Pro
50 55 60
Glu Pro Arg Arg Asp Pro Ala Arg Leu Pro Arg Arg Ala Pro Gly Arg
65 70 75 80
Arg Leu Leu Arg Leu Leu Arg Arg Arg Ala Xaa Leu Ala Leu Arg Ser
85 90 95
Ala Pro Pro Pro Pro Pro Pro Pro Thr Ser Gly Met Phe Leu Arg Pro
100 105 110
Trp Thr Thr Ser Thr Ala Ser Ser Ser Ala Ala Ser Thr Thr Ser Ala
115 120 125
Ala Ser Ser Ala Ser Xaa Gly Leu Cys Gly Arg Ser His Gln Arg Gly
130 135 140
Asp Ala Gly His Arg Gly Leu Pro His Ala Ala
145 150 155

(2) INFORMATION FOR SEQ ID NO:2501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2501:

Ser Ile Pro Ser His Trp Ile Ala Phe Pro Ser His Ser Pro Leu Tyr
1 5 10 15
Ser Phe Arg Ser Arg His Ser Leu Ser Thr Ser Arg Ala Pro Gln Gln
20 25 30
Asn Glu Asp Ala Gly His Leu Pro Glu Ala Gly Gly Ala Arg Val Xaa
35 40 45
Arg Ser Xaa Asn Ser Pro Arg Ala Gly Ala Ser Pro Ser Lys Pro Arg
50 55 60
Asn Pro Asp Glu Ile Leu Arg Asp Phe His Ala Ala His Pro Ala Ala
65 70 75 80
Ala Phe Ser Ala Ser Phe Gly Gly Val Xaa Cys Ser Pro Cys Val Arg

85 90 95
Pro Leu Leu Arg His Arg His Leu Pro Ala Gly Cys Phe Cys Gly Leu
100 105 110
Gly Pro His Leu Leu Arg Leu Pro Arg Pro Pro Arg Gln Pro Gln Arg
115 120 125
Pro His Pro Pro Xaa Thr Ala Cys Ala Ala Ala Pro Thr Asn Glu Ala
130 135 140
Met Leu Val Ile Glu Ala Tyr Arg Thr Leu
145 150

(2) INFORMATION FOR SEQ ID NO:2502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..403
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2502:

agtgtcggtg tcggcggttg cgagtggcga ctggcgactt ctctgcctcg tccctccccg 60
ttttcccttc cggctccagc cckgcgcgac gccaccacgc acctagccgc ggantccgag 120
cgcgagatcc aatccagcga tggcgctccac ggcggcgagg cggttgccgg asstgcaggc 180
ccagacgggg aacaagacct gcgtggactg cgcgcrssta acccgagtg ggcgagcgtc 240
tcctacggcg tgttcattgt cctcgagtgc tcyggcaacg accggggcct cggcgctcac 300
atcagtttgc tgcgctcggt caccatggac tcttgaccg agcgcasst ccgcaagatg 360
gaggccggcg gcaacgaccg cctcaacgcc ttctcaccg cgc

(2) INFORMATION FOR SEQ ID NO:2503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2503:

Ser Val Gly Val Gly Val Gly Glu Trp Arg Leu Ala Thr Ser Leu Pro
1 5 10 15
Arg Pro Ser Pro Phe Ser Pro Pro Arg Pro Ala Xaa Arg Asp Ala Thr
20 25 30
Thr His Leu Ala Ala Xaa Ser Glu Ala Gln Ile Gln Ser Ser Asp Gly
35 40 45
Val His Gly Gly Glu Ala Val Ala Gly Xaa Ala Gly Pro Asp Gly Glu
50 55 60
Gln Asp Leu Arg Gly Leu Arg Xaa Xaa Asn Pro Gln Trp Ala Ser Val
65 70 75 80
Ser Tyr Gly Val Phe Met Cys Leu Glu Cys Xaa Gly Lys His Arg Gly
85 90 95
Leu Gly Val His Ile Ser Phe Val Arg Ser Val Thr Met Asp Ser Trp
100 105 110
Thr Glu Ala Xaa Xaa Arg Lys Met Glu Ala Gly Gly Asn Asp Arg Leu
115 120 125
Asn Ala Phe Leu Thr Ala
130

(2) INFORMATION FOR SEQ ID NO:2504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..72
(D) OTHER INFORMATION: / Ceres Seq. ID 1503623
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2504:
Cys Arg Cys Arg Arg Trp Arg Val Ala Thr Gly Asp Phe Ser Ala Ser
1 5 10 15
Ser Leu Pro Val Phe Pro Ser Ala Ser Ser Xaa Ala Arg Arg His His
20 25 30
Ala Pro Ser Arg Gly Xaa Arg Gly Ala Asp Pro Ile Gln Arg Trp Arg
35 40 45
Pro Arg Arg Arg Gly Gly Cys Gly Xaa Cys Arg Pro Arg Arg Gly Thr
50 55 60
Arg Pro Ala Trp Thr Ala Arg Xaa
65 70

(2) INFORMATION FOR SEQ ID NO:2505:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..88
(D) OTHER INFORMATION: / Ceres Seq. ID 1503624
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2505:
Met Ala Ser Thr Ala Ala Arg Arg Leu Arg Xaa Xaa Gln Ala Gln Thr
1 5 10 15
Gly Asn Lys Thr Cys Val Asp Cys Ala Xaa Xaa Thr Arg Ser Gly Arg
20 25 30
Ala Ser Pro Thr Ala Cys Ser Cys Ala Ser Ser Ala Xaa Ala Ser Thr
35 40 45
Gly Ala Ser Ala Cys Thr Ser Val Ser Cys Ala Arg Ser Pro Trp Thr
50 55 60
Pro Gly Pro Arg Arg Xaa Ser Ala Arg Trp Arg Pro Ala Ala Thr Thr
65 70 75 80
Ala Ser Thr Pro Ser Ser Gln Arg
85

(2) INFORMATION FOR SEQ ID NO:2506:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..389
(D) OTHER INFORMATION: / Ceres Seq. ID 1503662
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2506:
actcgcgac agsstccaat ttctccacc tccgaacc taccggcggc gcmagcattc 60
acaaccacca cccgaagatg gtgaagtttc tgaagcccg ccaaggccgta atctctctcc 120
agggcgagatt cgccgggccc aagsssgtga tcgtgcgcgt gttcgaggag ggcacccgcg 180
accgtcccta tgggcaactgc ctctgcgcgc gcttgcccaa gtaccccaa aaggtgatcc 240
gcaagactcc gccaaaga cggccaagaa gtcccgctc aagtgtctca tcaagctcat 300
caatttcaat cacctcatgc ccacccgcta caccctcgac gtgacttca aggaagtcg 360

ctcggggggg cccgacgcgc tctccaccc

(2) INFORMATION FOR SEQ ID NO:2507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1503663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2507:

Leu Ala His Xaa Xaa Gln Phe Pro Pro Pro Glu Pro Tyr Arg Arg
1 5 10 15
Arg Xaa His Ser Gln Pro Pro Pro Glu Asp Gly Glu Val Ser Glu Ala
20 25 30
Arg Gln Gly Arg Asn Pro Pro Pro Gly Gln Ile Arg Arg Pro Glu Xaa
35 40 45
Gly Asp Arg Ala Arg Val Arg Gly Gly His Pro Arg Pro Ser Leu Trp
50 55 60
Ala Leu Pro Arg Arg Arg Pro Gly Gln Val Pro Gln Glu Gly Asp Pro
65 70 75 80
Gln Asp Ser Ala Lys Lys Thr Ala Lys Lys Ser Arg Val Lys Cys Phe
85 90 95
Ile Lys Leu Ile Asn Phe Thr His Leu Met Pro Thr Arg Tyr Thr Leu
100 105 110
Asp Val Asp Phe Lys Asp Val Ala Ser Gly Gly Pro Asp Ala Leu Ser
115 120 125
Thr

(2) INFORMATION FOR SEQ ID NO:2508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1503664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2508:

Ser Arg Thr Xaa Ser Asn Phe Leu His Leu Pro Asn Pro Thr Gly Gly
1 5 10 15
Xaa Ser Ile His Asn His His Pro Lys Met Val Lys Phe Leu Lys Pro
20 25 30
Gly Lys Ala Val Ile Leu Leu Gln Gly Arg Phe Ala Gly Arg Lys Xaa
35 40 45
Val Ile Val Arg Val Phe Glu Glu Gly Thr Arg Asp Arg Pro Tyr Gly
50 55 60
His Cys Leu Val Ala Gly Leu Ala Lys Tyr Pro Lys Lys Val Ile Arg
65 70 75 80
Lys Thr Pro Pro Arg Arg Arg Pro Arg Ser Pro Ala Ser Ser Ala Ser
85 90 95
Ser Ser Ser Ser Ile Ser Leu Thr Ser Cys Pro Pro Ala Thr Pro Ser
100 105 110
Thr Ser Thr Ser Arg Thr Ser Pro Arg Gly Gly Pro Thr Arg Ser Pro
115 120 125
Pro

(2) INFORMATION FOR SEQ ID NO:2509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2509:

Met	Val	Lys	Phe	Leu	Lys	Pro	Gly	Lys	Ala	Val	Ile	Leu	Leu	Gln	Gly	
1			5					10					15			
Arg	Phe	Ala	Gly	Arg	Lys	Xaa	Val	Ile	Val	Arg	Val	Phe	Glu	Glu	Gly	
			20					25					30			
Thr	Arg	Asp	Arg	Pro	Tyr	Gly	His	Cys	Leu	Val	Ala	Gly	Leu	Ala	Lys	
			35				40					45				
Tyr	Pro	Lys	Lys	Val	Ile	Arg	Lys	Thr	Pro	Pro	Arg	Arg	Arg	Pro	Arg	
			50				55				60					
Ser	Pro	Ala	Ser	Ser	Ala	Ser	Ser	Ser	Ser	Ser	Ile	Ser	Leu	Thr	Ser	
			65			70				75				80		
Cys	Pro	Pro	Ala	Thr	Pro	Ser	Thr	Ser	Thr	Ser	Arg	Thr	Ser	Pro	Arg	
				85					90					95		
Gly	Gly	Pro	Thr	Arg	Ser	Pro	Pro									
							100									

(2) INFORMATION FOR SEQ ID NO:2510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..420
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2510:

atttgtgcgt	gcacacccac	tcttgagaat	gctaattgtac	gtgaccttga	actcncatt	60
gcangtgccc	ttctgaatac	catatgatta	agtaaccttc	ggcatgttaa	tttcatctcc	120
aaaagtctct	atacgaagcc	gcagcaactt	ggattatata	tccttagtcg	tcgtccacag	180
cgggtgcggt	cgccgaagcc	gacgccgacg	cgccacacct	ctccggcgcg	gcgcgggtgg	240
tgctccttgc	cggggcgcta	cgctccccct	cggagcttcc	cttgtttttc	cggcggttgg	300
acttcttggg	aacggcgggg	aggtccttgc	atgtgccga	ggcgtcgtcg	cggnccgact	360
tgctcgtctt	cttgcggttc	tttcgggttt	gcaacaagag	gaggatgaag	atcgaagacc	420

(2) INFORMATION FOR SEQ ID NO:2511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2511:

Met	Leu	Ile	Ser	Ser	Pro	Lys	Val	Leu	Ile	Arg	Gly	Arg	Ser	Asn	Leu	
1			5					10					15			
Asp	Tyr	Ile	Ser	Leu	Val	Val	Val	His	Gly	Cys	Gly	Arg	Arg	Arg		

[illegible]

(2) INFORMATION FOR SEQ ID NO:2514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..495
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2514:

aaagcagagt	ctgcccctcc	cgcgcgcgtt	ctttttggtt	ccccagtc	ccgcgcgcgc	60
gaaaccgcga	gatggaggtc	gtcgtgcgcg	cgamssaagaa	ggcgaagaaa	cacatacacc	120
tcttctactg	ctcagaatgc	gaggagctcg	ccctcaagat	cgccgccagc	tccgacgcga	180
tcgagctcca	atccatcaac	tgccggasst	tcgacgacgg	gttcccgaac	ctattcatcg	240
ccctattcac	gtctgtgctg	ccattcttcc	ccacggggctc	attcgagcgc	gttgaggagg	300
agggcgatgt	cgccaccgcg	ttcaccctcg	cgcgcattct	ctcgatgatc	cccaagtcgc	360
gcggcgggcc	taccagcgctc	gtcatctacg	acatccacgc	gctccaggag	aggttttact	420
tcggggacga	tgctgtccat	gcttcgagac	agggatcccg	ctcctgtctc	agcgctcccg	480
ccagctcccg	gacgc					

(2) INFORMATION FOR SEQ ID NO:2515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2515:

Lys	Ala	Glu	Ser	Ala	Pro	Pro	Arg	Ala	Val	Leu	Phe	Gly	Ser	Pro	Val
1					5					10				15	
Pro	Ala	Ala	Ala	Glu	Thr	Arg	Arg	Trp	Arg	Ser	Ser	Ser	Pro	Arg	Xaa
				20				25						30	
Arg	Arg	Arg	Arg	Asn	Thr	Tyr	Thr	Ser	Ser	Thr	Ala	Gln	Asn	Ala	Arg
				35				40				45			
Ser	Ser	Pro	Ser	Arg	Ser	Pro	Pro	Ala	Pro	Thr	Pro	Ser	Ser	Ser	Asn
				50				55				60			
Pro	Ser	Thr	Gly	Gly	Xaa	Ser	Thr	Thr	Gly	Ser	Arg	Thr	Tyr	Ser	Ser
65					70					75				80	
Pro	His	Ser	Arg	Ser	Cys	Cys	His	Ser	Ser	Pro	Arg	Ala	His	Ser	Ser
				85				90						95	
Ala	Leu	Arg	Arg	Arg	Ala	Met	Ser	Pro	Pro	Arg	Ser	Pro	Ser	Arg	Ala
				100				105						110	
Phe	Ser	Arg													

(2) INFORMATION FOR SEQ ID NO:2516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2516:


```

Ser Arg Val Cys Pro Ser Pro Arg Arg Ser Phe Trp Phe Pro Ser Pro
1          5          10          15
Arg Arg Arg Arg Asn Pro Gln Met Glu Val Val Ala Ala Xaa Xaa
20          25          30
Lys Ala Lys Lys His Ile His Leu Phe Tyr Cys Ser Glu Cys Glu Glu
35          40          45
Leu Ala Leu Lys Ile Ala Ala Ser Ser Asp Ala Ile Glu Leu Gln Ser
50          55          60
Ile Asn Trp Arg Xaa Phe Asp Asp Gly Phe Pro Asn Leu Phe Ile Ala
65          70          75          80
Ser Phe Thr Leu Val Leu Pro Phe Phe Pro Thr Gly Ser Phe Glu Arg
85          90          95
Val Glu Glu Glu Gly Asp Val Ala Thr Ala Phe Thr Leu Ala Arg Ile
100         105         110
Leu Ser Met Ile Pro Lys Ser Arg Gly Gly Pro Thr Ser Val Val Ile
115         120         125
Tyr Asp Ile His Ala Leu Gln Glu Arg Phe Tyr Phe Gly Asp Asp Val
130         135         140
Cys His Ala Ser Arg Gln Gly Ser Arg Ser Cys Ser Ala Ser Ala
145         150         155         160
Ser Ser Arg Thr

```

(2) INFORMATION FOR SEQ ID NO:2517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2517:

```

Met Glu Val Val Val Ala Ala Xaa Xaa Lys Ala Lys Lys His Ile His
1          5          10          15
Leu Phe Tyr Cys Ser Glu Cys Glu Glu Leu Ala Leu Lys Ile Ala Ala
20          25          30
Ser Ser Asp Ala Ile Glu Leu Gln Ser Ile Asn Trp Arg Xaa Phe Asp
35          40          45
Asp Gly Phe Pro Asn Leu Phe Ile Ala Ser Phe Thr Leu Val Leu Pro
50          55          60
Phe Phe Pro Thr Gly Ser Phe Glu Arg Val Glu Glu Glu Gly Asp Val
65          70          75          80
Ala Thr Ala Phe Thr Leu Ala Arg Ile Leu Ser Met Ile Pro Lys Ser
85          90          95
Arg Gly Gly Pro Thr Ser Val Val Ile Tyr Asp Ile His Ala Leu Gln
100         105         110
Glu Arg Phe Tyr Phe Gly Asp Asp Val Cys His Ala Ser Arg Gln Gly
115         120         125
Ser Arg Ser Cys Cys Ser Ala Ser Ala Ser Ser Arg Thr
130         135         140

```

(2) INFORMATION FOR SEQ ID NO:2518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(D) OTHER INFORMATION: / Ceres Seq. ID 1503714

aacttcaaccg	gcctctctcct	ctctcccgctc	catcgccgctc	cgcgggcgcc	cctacaacctt	60
caaaatggcgc	gctacccgcgc	tctgcatacgt	tatagcaacct	atytctccgc	cgctctcgcat	120
cccatccgcg	ccctctcccat	ccctcccccct	cgggctccgc	ctccgcctctc	aagccctctct	180
tttctgtgct	tcctccgcgc	gcctctctc	atgtttcccaa	agccgcctcc	tgggcagcaat	240
ctctcccgcc	aggatgggtgc	agatcgccgag	gaatcctgtg	cgctcgggga	cgacgaggacc	300
gaggacagaga	acgcgcggcg	cgacgcggctc	tctctcctcg	agttccagtt	cgcgccggcca	360
ccgcagggtg	acgtcagagc	cgcgccaktt	tgacagagcta	ccgcggcgat	cccacaaga	420
cctgagcgctc	gcgtacgaat	ctctctcctt	cgccgccttc	acgcggcgaga	catt	

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1503715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2519:

Asn	Phe	Thr	Gly	Leu	Leu	Leu	Leu	Pro	Val	His	Arg	Arg	Arg	Arg	Gly
1				5				10						15	
Ala	Leu	Gln	Leu	Gln	Asn	Gly	Gly	Tyr	Arg	Thr	Arg	His	Gly	Tyr	Ser
		20						25					30		
Asn	Tyr	Xaa	Pro	Arg	Arg	Ser	Asp	Pro	Ile	Arg	Ala	Leu	Pro	Ile	Pro
		35					40					45			
Pro	Pro	Arg	Pro	Pro	Pro	Pro	Pro	Ser	Thr	Pro	Pro	Phe	Arg	Cys	Phe
		50					55				60				
Pro	Pro	Pro	Pro	Ser	Ser	Met	Phe	Pro	Lys	Pro	Pro	Pro	Gly	Thr	Asn
65				70					75						80
Pro	Ser	Pro	Glu	Asp	Gly	Gly	Asp	Ala	Glu	Glu	Ser	Val	Ala	Ala	Gly
			85					90					95		
Asp	Asp	Glu	Asp	Glu	Asp	Glu	Lys	Pro	Arg	Pro	Glu	Pro	Val	Ser	Ser
			100					105					110		
Ser	Glu	Phe	Gln	Phe	Ala	Ala	Pro	Pro	Glu	Gly	Tyr	Val	Glu	Pro	Ala
		115					120					125			

Xaa Xaa
130

(2) INFORMATION FOR SEQ ID NO:2520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1503716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2520:

Thr	Ser	Pro	Ala	Ser	Ser	Ser	Phe	Pro	Ser	Ile	Ala	Val	Ala	Gly	Ala
1			5						10					15	
Pro	Tyr	Asn	Phe	Lys	Met	Ala	Ala	Thr	Ala	Leu	Ala	Met	Ala	Ile	Ala
			20					25					30		
Thr	Xaa	Ser	Pro	Ala	Ala	Pro	Ile	Pro	Ser	Ala	Pro	Phe	Pro	Ser	Leu
		35					40					45			
Pro	Leu	Gly	Leu	Arg	Leu	Arg	Pro	Gln	Pro	Leu	Leu	Phe	Ala	Ala	Ser
	50					55				60					

Arg Arg Arg Leu Pro Pro Cys Ser Gln Ser Arg Leu Leu Gly Arg Ile
65 70 75 80
Arg Pro Pro Arg Met Val Glu Met Arg Arg Asn Pro Leu Pro Leu Gly
85 90 95
Thr Thr Arg Thr Arg Thr Arg Ser Arg Gly Pro Ser Arg Cys Pro Pro
100 105 110
Pro Ser Ser Ser Ser Arg Arg His Pro Arg Ala Thr Ser Ser Pro Arg
115 120 125
Xaa Phe Asp Glu Leu Pro Pro Glu Ser Pro Xaa Asp Val Ala Ala Ala
130 135 140
Tyr Glu Ser Leu Tyr Gly Pro Ala Phe Ser Gly Glu Thr
145 150 155

(2) INFORMATION FOR SEQ ID NO:2521:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..136
(D) OTHER INFORMATION: / Ceres Seq. ID 1503717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2521:

Met Ala Ala Thr Ala Leu Ala Met Ala Ile Ala Thr Xaa Ser Pro Ala
1 5 10 15
Ala Pro Ile Pro Ser Ala Pro Phe Pro Ser Leu Pro Leu Gly Leu Arg
20 25 30
Leu Arg Pro Gln Pro Leu Leu Phe Ala Ala Ser Arg Arg Arg Leu Pro
35 40 45
Pro Cys Ser Gln Ser Arg Leu Leu Gly Arg Ile Arg Pro Pro Arg Met
50 55 60
Val Glu Met Arg Arg Asn Pro Leu Pro Leu Gly Thr Thr Arg Thr Arg
65 70 75 80
Thr Arg Ser Arg Gly Pro Ser Arg Cys Pro Pro Pro Ser Ser Ser Ser
85 90 95
Arg Arg His Pro Arg Ala Thr Ser Ser Pro Arg Xaa Phe Asp Glu Leu
100 105 110
Pro Pro Glu Ser Pro Xaa Asp Val Ala Ala Tyr Glu Ser Leu Tyr
115 120 125
Gly Pro Ala Phe Ser Gly Glu Thr
130 135

(2) INFORMATION FOR SEQ ID NO:2522:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..412
(D) OTHER INFORMATION: / Ceres Seq. ID 1503718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2522:

agagcagcca	agcgccacac	acacgccgac	gcgaaccaac	caaccagctg	gtagtaggtt	60
cgccgcggcg	ccgcctgac	gatgatgct	cgccgcgcc	ttctcttcg	cgcggtgctc	120
ctcgcgccct	ccgcccgcgc	gtctccgggt	ttcacctcgg	cggggacgag	agcggtctcg	180
tgaggggtgt	gctcgccgcg	ctccgcagcg	kgtcogaggc	cgtggacgcc	gctcgcttcg	240
ccgtgcacca	ctacaacaa	aaccaggcg	ccgctttgga	gtttactagg	gtgctcaaat	300
ccaagcgcca	ggtggtgacc	gggacctgc	atgacctgat	actggaggca	gctgatgctg	360
gaaaaaagag	tgtgtacaga	gcaagggttt	gggtgaagcg	tgggaagatt	tc	

(2) INFORMATION FOR SEQ ID NO:2523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2523:

Ser	Ser	Gln	Ala	Pro	His	Thr	Arg	Arg	Arg	Glu	Pro	Thr	Asn	Gln	Leu
1			5						10					15	
Val	Val	Gly	Ser	Pro	Arg	Arg	Arg	Ala	Asp	Asp	Asp	Ala	Ser	Pro	Arg
			20					25				30			
Pro	Ser	Leu	Arg	Arg	Gly	Ala	Pro	Arg	Gly	Leu	Arg	Arg	Ala	Val	Ser
			35				40				45				
Gly	Phe	His	Leu	Gly	Gly	Asp	Glu	Ser	Gly	Leu	Val	Arg	Gly	Val	Leu
			50			55				60					
Ala	Ala	Leu	Arg	Ser	Xaa	Ser	Glu	Ala	Val	Asp	Ala	Ala	Arg	Phe	Ala
			70					75						80	
Val	Ala	His	Tyr	Asn	Lys	Asn	Gln	Gly	Ala	Ala	Leu	Glu	Phe	Thr	Arg
			85					90					95		
Val	Leu	Lys	Ser	Lys	Arg	Gln	Val	Val	Thr	Gly	Thr	Leu	His	Asp	Leu
			100					105					110		
Ile	Leu	Glu	Ala	Ala	Asp	Ala	Gly	Lys	Lys	Ser	Val	Tyr	Arg	Ala	Lys
			115			120						125			
Val	Trp	Val	Lys	Arg	Gly	Lys	Ile								
			130			135									

(2) INFORMATION FOR SEQ ID NO:2524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..482
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2524:

ccccacacac	tgcacgccnc	cgccgggtcc	tcctagggtt	tcgccgcgat	gtccgtcccg	60
ccgagcgagc	gggagcagat	gcgggaaggg	aactacaagc	agacgggtga	cgcgaggag	120
agcccgccgc	gccgcgaggg	ccagatgatg	gacatgcgca	aggccaaagc	cgaggaaagt	180
ctccagaaga	agcgcgtgca	tgggtttccc	gcctccgccg	ccggtgtgcc	gccgatgggc	240
caetccaccg	cgtccacgca	gaagtccccc	aatcgaagag	gtgatcagca	caggagtgtg	300
gtcgcgattc	attgagtttc	ttacacgtga	ggaccatccc	caactccagt	ttgaggctgc	360
atgggcactc	accaacattg	catcaggcac	atcagagaac	actaagggtg	tcggtgagag	420
tgggtgctgtg	cgccgtgtcc	catctttgtc	aagctactca	actccctcaa	gcgaggatgt	480

(2) INFORMATION FOR SEQ ID NO:2525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1503721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2525:

Pro His Thr Ala Arg Xaa Arg Arg Val Leu Leu Gly Phe Arg Arg Asp
1 5 10 15
Val Ala Pro Ala Glu Arg Ala Gly Ala Asp Ala Glu Gly Gln Leu Gln
20 25 30
Ala Asp Gly Gly Arg Gly Gly Glu Pro Pro Pro Arg Gly Pro Asp
35 40 45
Asp Gly His Ala Gln Gly Gln Ala Arg Gly Lys Ser Pro Glu Glu Ala
50 55 60
Leu Arg Trp Val Ser Arg Leu Arg Arg Arg Cys Ala Ala Asp Gly Pro
65 70 75 80
Leu His Arg Ala Pro Ala Glu Val Pro Gln Ser Lys Arg
85 90

(2) INFORMATION FOR SEQ ID NO:2526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1503722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2526:

Met Ser Leu Arg Pro Ser Glu Arg Glu Gln Met Arg Lys Gly Asn Tyr
1 5 10 15
Lys Gln Thr Val Asp Ala Glu Glu Ser Arg Arg Arg Arg Glu Gly Gln
20 25 30
Met Met Asp Met Arg Lys Ala Lys Arg Glu Glu Ser Leu Gln Lys Lys
35 40 45
Arg Cys Asp Gly Phe Pro Ala Ser Ala Ala Gly Val Pro Pro Met Gly
50 55 60
His Ser Thr Ala Leu Gln Gln Lys Ser Pro Asn Arg Arg Gly Asp Gln
65 70 75 80
His Arg Ser Gly Val Ala Ile His
85

(2) INFORMATION FOR SEQ ID NO:2527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1503723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2527:

Met Gly Phe Pro Pro Pro Pro Val Cys Arg Arg Trp Ala Thr Pro
1 5 10 15
Pro Arg Ser Ser Arg Ser Pro Pro Ile Glu Glu Val Ile Ser Thr Gly
20 25 30
Val Val Ser Arg Phe Ile Glu Phe Leu Thr Arg Glu Asp His Pro Gln
35 40 45
Leu Gln Phe Glu Ala Ala Trp Ala Leu Thr Asn Ile Ala Ser Gly Thr
50 55 60
Ser Glu Asn Thr Lys Val Val Val Glu Ser Gly Ala Val Arg Leu Cys
65 70 75 80
Pro Ser Leu Ser Ser Tyr Ser Thr Pro Ser Ser Glu Asp Val

85 90

(2) INFORMATION FOR SEQ ID NO:2528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..471
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2528:

agataacagg aaaggctctg caacacggct tgagttcaaa caaaggctct caatagctat	60
tggggcagct aaagggttga atcatctgca cagttctgat cctcctttga tacacaagga	120
cttcaagaca aacaatgtgc tggttgatga aaatttcatt gcaaagggtg ctgatgctgg	180
acttgtagg ttaattagag gatctgacga tgccggccca tcgcgtgggt tcagtaacag	240
tgttaccaaa gatccagagg tacagtcgat gactcagttc tctgaaagca gtgatgttta	300
cagcttgtag tttttctttt ggagctaatt actggcaggg aagcagcttc ctgtatacct	360
acagagtcca gagaatattt ggcacactgg atggaagcgc atttcagttc aaatgaactg	420
attgacccaa gattagccgg caacttcact gcagaaggta tgaaggagct t	

(2) INFORMATION FOR SEQ ID NO:2529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2529:

Asp Asn Arg Lys Gly Ser Ala Thr Arg Leu Glu Phe Lys Gln Arg Leu	
1 5 10 15	
Ser Ile Ala Ile Gly Ala Ala Lys Gly Leu Asn His Leu His Ser Leu	
20 25 30	
Asp Pro Pro Leu Ile His Lys Asp Phe Lys Thr Asn Asn Val Leu Val	
35 40 45	
Asp Glu Asn Phe Ile Ala Lys Val Ala Asp Ala Gly Leu Val Arg Leu	
50 55 60	
Ile Arg Gly Ser Asp Asp Ala Gly Pro Ser Arg Gly Phe Ser Asn Ser	
65 70 75 80	
Val Tyr Gln Asp Pro Glu Val Gln Ser Met Thr Gln Phe Ser Glu Ser	
85 90 95	
Ser Asp Val Tyr Ser Leu Glu Phe Phe Phe Trp Ser	
100 105	

(2) INFORMATION FOR SEQ ID NO:2530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..469
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2530:

atcctttggc aaccgaactg gtttggtgtg cccacctctc tctctccat ggggatatggc	60
agggacggaa tcagatgatg gatgaactcg tggcaggagc gcgtcacggg caccaactgc	120

cccatccctc	ccggatggaa	ctggacctac	gagttccagc	tcaaggacca	gatcggcagc	180
ttcttctact	tcccgctcgt	cgccctccag	cgagctgccg	gcgggttcgg	ccccatcacc	240
gtcaacaacc	gcgcaccgt	gcnntcccc	ttcgaccagc	ctcatggcga	catcaccctg	300
ttcatcgggg	actggtacac	caaggggcoac	gttgtaagag	ctttgttttt	ctgtttctgt	360
caatgcgaat	ctagctagat	ggttcgtcct	ttgttttcag	atcgagatat	atagccaggg	420
aaaaatatcg	cgcttttccc	ttgatctcag	tgaactggat	ttcactgag		

(2) INFORMATION FOR SEQ ID NO:2531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1503735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2531:

Ile	Leu	Trp	Gln	Pro	Asn	Trp	Phe	Gly	Val	Pro	Thr	Ser	Leu	Ser	Ser
1			5						10					15	
Met	Gly	Tyr	Gly	Arg	Asp	Gly	Ile	Gln	Met	Arg	Met	Asn	Ser	Trp	Gln
			20					25					30		
Asp	Gly	Val	Thr	Gly	Thr	Asn	Cys	Pro	Ile	Pro	Pro	Gly	Trp	Asn	Trp
			35				40					45			
Thr	Tyr	Glu	Phe	Gln	Leu	Lys	Asp	Gln	Ile	Gly	Ser	Phe	Phe	Tyr	Phe
			50				55				60				
Pro	Ser	Leu	Gly	Leu	Gln	Arg	Ala	Ala	Gly	Gly	Phe	Gly	Pro	Ile	Thr
65					70					75				80	
Val	Asn	Asn	Arg	Ala	Thr	Val	Xaa	Xaa	Pro	Phe	Asp	Gln	Pro	His	Gly
			85						90				95		
Asp	Ile	Thr	Leu	Phe	Ile	Gly	Asp	Trp	Tyr	Thr	Lys	Gly	His	Val	Val
			100				105						110		
Arg	Ala	Leu	Phe	Phe	Cys	Phe	Cys	Gln	Cys	Lys	Ser	Ser			
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:2532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1503736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2532:

Pro	Leu	Ala	Thr	Glu	Leu	Val	Trp	Cys	Ala	His	Leu	Ser	Leu	Phe	His
1				5					10					15	
Gly	Ile	Trp	Gln	Gly	Arg	Asn	Pro	Asp	Glu	Asp	Glu	Leu	Val	Ala	Gly
			20					25					30		
Arg	Arg	His	Gly	His	Gln	Leu	Pro	His	Pro	Ser	Arg	Met	Glu	Leu	Asp
			35				40					45			
Leu	Arg	Val	Pro	Ala	Gln	Gly	Pro	Asp	Arg	Gln	Leu	Leu	Leu	Leu	Pro
			50				55				60				
Val	Ala	Arg	Pro	Pro	Ala	Ser	Cys	Arg	Arg	Val	Arg	Pro	His	His	Arg
65					70					75				80	
Gln	Gln	Pro	Arg	His	Arg	Ala	Xaa	Pro	Leu	Arg	Pro	Ala	Ser	Trp	Arg
			85					90					95		
His	His	Pro	Val	His	Arg	Gly	Leu	Val	His	Gln	Gly	Pro	Arg	Cys	Lys
			100				105					110			
Ser	Phe	Val	Phe	Leu	Phe	Leu	Ser	Met	Gln	Ile					

115 120
(2) INFORMATION FOR SEQ ID NO:2533:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..109
(D) OTHER INFORMATION: / Ceres Seq. ID 1503737
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2533:
Met Gly Tyr Gly Arg Asp Gly Ile Gln Met Arg Met Asn Ser Trp Gln
1 5 10 15
Asp Gly Val Thr Gly Thr Asn Cys Pro Ile Pro Pro Gly Trp Asn Trp
20 25 30
Thr Tyr Glu Phe Gln Leu Lys Asp Gln Ile Gly Ser Phe Phe Tyr Phe
35 40 45
Pro Ser Leu Gly Leu Gln Arg Ala Ala Gly Gly Phe Gly Pro Ile Thr
50 55 60
Val Asn Asn Arg Ala Thr Val Xaa Xaa Pro Phe Asp Gln Pro His Gly
65 70 75 80
Asp Ile Thr Leu Phe Ile Gly Asp Trp Tyr Thr Lys Gly His Val Val
85 90 95
Arg Ala Leu Phe Phe Cys Phe Cys Gln Cys Lys Ser Ser
100 105

(2) INFORMATION FOR SEQ ID NO:2534:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..129
(D) OTHER INFORMATION: / Ceres Seq. ID 1503743
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2534:
aattctttca ctcaactctcc agatccgggtg cttgtgggag cctaacacgc cccccgcctc 60
cctctccgcc gtccgcgagtg ccctgcgccg cttaccctcg cgctggcgaa ggcaactcgg 120
cgtggcagcg

(2) INFORMATION FOR SEQ ID NO:2535:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..42
(D) OTHER INFORMATION: / Ceres Seq. ID 1503744
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2535:
Ile Leu Ser Leu Thr Leu Gln Ile Arg Cys Leu Trp Glu Pro Asn Thr
1 5 10 15
Pro Pro Ala Ser Leu Ser Ala Val Ala Glu Ser Leu Ala Gly Leu Pro
20 25 30
Arg Arg Trp Arg Arg His Ser Gly Val Asp
35 40

(2) INFORMATION FOR SEQ ID NO:2536:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..42
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503745
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2536:
Phe Phe His Ser Leu Ser Arg Ser Gly Ala Cys Gly Ser Leu Thr Arg
1 5 10 15
Pro Pro Pro Pro Ser Pro Ser Pro Ser Pro Ser Pro Ala Tyr Pro
 20 25 30
Val Ala Gly Glu Gly Thr Pro Ala Trp Thr
 35 40

(2) INFORMATION FOR SEQ ID NO:2537:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 409 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..409
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503746
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2537:
ctagccgccc ccagaccatt cgttctcgc gagccatcct tctgtaattc tcaggcatcc 60
ggaagaaatg gccaaagtca agaaccacac ggcgcacaac cagtcgttca aggcgcacaaa 120
gaacggcatt aagaaaccca agcgccaccg ccagacctcc accaagggga tggaccccaa 180
gttctctagg aacctgaggt attctaggaa gggcaacaaa aagagtgggt aggcggaagc 240
tgaggagtat gaaggaaagc atggctttgt ggtaatgtgc tgctgtgggg gtcattagt 300
atgaagagga agacgctgct ggcgcggagt cttttctct tattagtat ttgttttaa 360
actatgtatg accgaatggt ggtatttatt tgtgtcatcc ttgactctc

(2) INFORMATION FOR SEQ ID NO:2538:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..43
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503747
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2538:
Leu Ala Ala Ala Arg Pro Phe Val Ser Arg Glu Pro Ser Phe Cys Asn
1 5 10 15
Ser Gln Ala Ser Gly Arg Asn Gly Gln Val Glu Glu Pro His Gly Ala
 20 25 30
Gln Pro Val Val Gln Gly Ala Gln Glu Arg His
 35 40

(2) INFORMATION FOR SEQ ID NO:2539:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2539:

Met Ala Lys Ser Lys Asn His Thr Ala His Asn Gln Ser Phe Lys Ala
1 5 10 15
His Lys Asn Gly Ile Lys Lys Pro Lys Arg His Arg Gln Thr Ser Thr
20 25 30
Lys Gly Met Asp Pro Lys Phe Leu Arg Asn Leu Arg Tyr Ser Arg Lys
35 40 45
Gly Asn Lys Lys Ser Gly Glu Ala Glu Ala Glu Glu
50 55 60

(2) INFORMATION FOR SEQ ID NO:2540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2540:

Met Lys Arg Lys Thr Leu Leu Ala Arg Ser Leu Phe Leu Phe Ile Ser
1 5 10 15
Ile Leu Phe Lys Thr Met Tyr Asp Arg Met Val Val Phe Ile Cys Val
20 25 30
Ile Leu Asp Ser
35

(2) INFORMATION FOR SEQ ID NO:2541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..450
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2541:

aaaatgatgc agtgggctcc catgtgattt tgtcatccta gtgacagaaa ttttctccct	60
ttttttttct caagctcaca acactcctct gctgtgattc gagattgtga accgattcga	120
tgcacatcaag cccgacggcg tcacaagagg cctgatttct gagattgtga accgattcga	180
gagaaaaaggc tacaagcttg ttgccatcaa gctgattgtc ccatccaaag gattcgctga	240
gaagcactac catgatctca aggaaaaggcc tttcttcaac gggttgtgtg acttcctcag	300
ctctggccct gtacttgcaa tggtttggga agggaggggt gtcacaaat atgggagaaa	360
actaattggg gccacagacc cacagaaatc tgaaccagga accatcaggg gcgatcttgg	420
cgttgttgtg ggaagaaaca tcatctatgg	

(2) INFORMATION FOR SEQ ID NO:2542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1503770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2542:

Met Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg Gly
1 5 10 15
Leu Ile Ser Glu Ile Val Asn Arg Phe Glu Arg Lys Gly Tyr Lys Leu
20 25 30
Val Ala Ile Lys Leu Ile Val Pro Ser Lys Gly Phe Ala Glu Lys His
35 40 45
Tyr His Asp Leu Lys Glu Arg Pro Phe Phe Asn Gly Leu Cys Asp Phe
50 55 60
Leu Ser Ser Gly Pro Val Leu Ala Met Val Trp Glu Gly Glu Gly Val
65 70 75 80
Ile Lys Tyr Gly Arg Lys Leu Ile Gly Ala Thr Asp Pro Gln Lys Ser
85 90 95
Glu Pro Gly Thr Ile Arg Gly Asp Leu Gly Val Val Val Gly Arg Asn
100 105 110
Ile Ile His
115

(2) INFORMATION FOR SEQ ID NO:2543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..499

(D) OTHER INFORMATION: / Ceres Seq. ID 1503775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2543:

tgattatttg cacaaaaagc aatctggcgg tcaaggtcag tatggacgag tttgtgggta 60
cattgagcct ctaccttcag gttctgatgg taaattcgaa ttgtataaca tgattattgg 120
acaagcaatt ccttcaaaact ttataccagc aatagagaag ggttttaagg aagcttgcaa 180
ttcagctcog ttgattggtc atcctgttga aaatttaaga attgtattga ctgatggggc 240
ttcacatcag gtggattcca gtgaacttgc ttttaagcta gctgctatct atgcttttcg 300
acagtgctac acttctgcc aacctgtaat attagaacct gtgatgaagg tggaaactcaa 360
ttttccaaact gagtttcagg gcacagtaac tgggtgatatg aacaagagaa aagggatcat 420
tgtttggaat gacgaggaag gtgacgacac cattgtagtt tgccatgtcc gctaaacaat 480
atgtttggat atgcacagc

(2) INFORMATION FOR SEQ ID NO:2544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1503776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2544:

Asp Tyr Leu His Lys Lys Gln Ser Gly Gly Gln Gly Gln Tyr Gly Arg
1 5 10 15
Val Cys Gly Tyr Ile Glu Pro Leu Pro Ser Gly Ser Asp Gly Lys Phe
20 25 30
Glu Phe Asp Asn Met Ile Ile Gly Gln Ala Ile Pro Ser Asn Phe Ile
35 40 45
Pro Ala Ile Glu Lys Gly Phe Lys Glu Ala Cys Asn Ser Gly Ser Leu
50 55 60
Ile Gly His Pro Val Glu Asn Leu Arg Ile Val Leu Thr Asp Gly Ala
65 70 75 80

Ser His Gln Val Asp Ser Ser Glu Leu Ala Phe Lys Leu Ala Ala Ile
85 90 95
Tyr Ala Phe Arg Gln Cys Tyr Thr Ser Ala Lys Pro Val Ile Leu Glu
100 105 110
Pro Val Met Lys Val Glu Leu Lys Phe Pro Thr Glu Phe Gln Gly Thr
115 120 125
Val Thr Gly Asp Met Asn Lys Arg Lys Gly Ile Ile Val Gly Asn Glu
130 135 140
Gln Glu Gly Asp Asp Thr Ile Val Val Cys His Val Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:2545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1503777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2545:

Met Ile Ile Gly Gln Ala Ile Pro Ser Asn Phe Ile Pro Ala Ile Glu
1 5 10 15
Lys Gly Phe Lys Glu Ala Cys Asn Ser Gly Ser Leu Ile Gly His Pro
20 25 30
Val Glu Asn Leu Arg Ile Val Leu Thr Asp Gly Ala Ser His Gln Val
35 40 45
Asp Ser Ser Glu Leu Ala Phe Lys Leu Ala Ala Ile Tyr Ala Phe Arg
50 55 60
Gln Cys Tyr Thr Ser Ala Lys Pro Val Ile Leu Glu Pro Val Met Lys
65 70 75 80
Val Glu Leu Lys Phe Pro Thr Glu Phe Gln Gly Thr Val Thr Gly Asp
85 90 95
Met Asn Lys Arg Lys Gly Ile Ile Val Gly Asn Glu Gln Glu Gly Asp
100 105 110
Asp Thr Ile Val Val Cys His Val Arg
115 120

(2) INFORMATION FOR SEQ ID NO:2546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1503778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2546:

ttgattacat tattcatgga gatgatccct gtcttctacc tgatggcact gatgcataatg 60
cgctacgaag aaggtcgggc gttacaagca aatcaagcga acagaagggt tctcgagcac 120
tgacatagtt gggaggatat tgctaacatt caggcagaaa gatgctggca ctgatttaag 180
tgttgtcgtt gctgagaagt ctggagagaa atcaaatgat gaagtgaaaa gtcagctatc 240
tcatttcctt ccaactcttc gccggatcat gcagttttca aatgggcagg ctccctgcgc 300
agggtcctgt gttgtctatg tagatggcac atttgatcct ttccacgctg gccatgttga 360
gttcctcagg agtgcacagc aacttggtga ctttctctt gtcggtatct atgacgacga 420
gtctatcagg gatagaagg gctgccgtcc tataatgcac ctccatgagc g

(2) INFORMATION FOR SEQ ID NO:2547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..41
(D) OTHER INFORMATION: / Ceres Seq. ID 1503779
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2547:
Asp Tyr Ile Ile His Gly Asp Asp Pro Cys Leu Leu Pro Asp Gly Thr
1 5 10 15
Asp Ala Tyr Ala Leu Arg Arg Arg Ser Gly Val Thr Ser Lys Ser Ser
20 25 30
Glu Gln Lys Val Ser Arg Ala Leu Thr
35 40
(2) INFORMATION FOR SEQ ID NO:2548:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..67
(D) OTHER INFORMATION: / Ceres Seq. ID 1503780
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2548:
Met Gln Phe Ser Asn Gly Gln Ala Pro Ser Pro Gly Ala Arg Val Val
1 5 10 15
Tyr Val Asp Gly Thr Phe Asp Leu Phe His Ala Gly His Val Glu Phe
20 25 30
Leu Arg Ser Ala Arg Gln Leu Gly Asp Phe Leu Leu Val Gly Ile Tyr
35 40 45
Asp Asp Glu Ser Ile Arg Asp Arg Arg Gly Cys Arg Pro Ile Met His
50 55 60
Leu His Glu
65
(2) INFORMATION FOR SEQ ID NO:2549:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..43
(D) OTHER INFORMATION: / Ceres Seq. ID 1503781
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2549:
Met Ala His Leu Ile Phe Ser Thr Leu Ala Met Leu Ser Ser Ser Gly
1 5 10 15
Val Pro Asp Asn Leu Val Thr Phe Phe Leu Ser Val Ser Met Thr Thr
20 25 30
Ser Leu Ser Gly Ile Glu Glu Ala Ala Val Leu
35 40
(2) INFORMATION FOR SEQ ID NO:2550:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..395

(D) OTHER INFORMATION: / Ceres Seq. ID 1503796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2550:

caacattaatt	aaacattttt	tgtgttttctt	tttataacctt	aatttttttc	tttccctttt	60
tctctataag	tatctgactc	tacttctgct	gttgacagaat	cattcgagat	atcattcaga	120
atcatttact	gcaggttttc	tgtttggttg	caatggaaaa	gcctgtctcc	cttaagcctg	180
agcacatcag	agatkagaaa	gtcaaagttc	tgcaatctgt	gaaccttatt	aagcctgaag	240
aggtagtctc	tgggcaatac	gatggtctac	aaggatgacc	ctacagtgcc	agatgacttg	300
aatactccaa	cttttgcata	tgttgttctt	cgggtacaca	atgaaagatg	ggaaggtggt	360
cccttcattc	ttaaagctgg	taaagcattg	agtttc			

(2) INFORMATION FOR SEQ ID NO:2551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1503797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2551:

Thr	Leu	Ile	Lys	His	Phe	Leu	Cys	Phe	Phe	Leu	Tyr	Leu	Asn	Phe	Phe	
1			5						10					15		
Leu	Ser	Leu	Phe	Leu	Tyr	Lys	Tyr	Leu	Thr	Leu	Leu	Leu	Leu	Gln		
			20					25					30			
Asn	His	Ser	Arg	Tyr	His	Ser	Glu	Ser	Phe	Thr	Ala	Gly	Phe	Leu	Phe	
			35				40					45				
Gly	Cys	Asn	Gly	Lys	Ala	Cys	Leu	Pro								
50						55										

(2) INFORMATION FOR SEQ ID NO:2552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..41

(D) OTHER INFORMATION: / Ceres Seq. ID 1503798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2552:

Met	Glu	Lys	Pro	Val	Ser	Leu	Lys	Pro	Glu	His	Ile	Arg	Asp	Xaa	Lys	
1				5					10					15		
Val	Lys	Val	Leu	Gln	Ser	Val	Asn	Pro	Ile	Lys	Pro	Glu	Glu	Val	Val	
			20				25					30				
Leu	Gly	Gln	Tyr	Asp	Gly	Leu	Gln	Gly								
			35				40									

(2) INFORMATION FOR SEQ ID NO:2553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..44

(D) OTHER INFORMATION: / Ceres Seq. ID 1503799
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2553:
Met Val Tyr Lys Asp Asp Pro Thr Val Pro Asp Asp Leu Asn Thr Pro
1 5 10 15
Thr Phe Ala Ser Val Val Leu Arg Val His Asn Glu Arg Trp Glu Gly
20 25 30
Val Pro Phe Ile Leu Lys Ala Gly Lys Ala Leu Ser
35 40

(2) INFORMATION FOR SEQ ID NO:2554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..505

(D) OTHER INFORMATION: / Ceres Seq. ID 1503810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2554:

gaagttttcgg	cgccggcgta	ggtagcggcg	gtgtgcttgt	gatctcaatc	tcaaccccgag	60
gcgagctcgg	ctccggctac	ccgtcgatcc	acgcaaccat	gtcgaggagg	aagaccaggg	120
agcccaagga	ggagaacggt	acccttggac	ccactgtccg	tgaaggagag	ttgtctttg	180
gtgtgtgtcga	catctttgca	tcttccaatg	acaccttcat	tgtgagtgtc	atatgtttt	240
ccctgtggat	ggcccttttc	attatctttc	ccattgtaac	tgtgatgggt	taatagcag	300
catgtcaactg	atttctctgg	gagggaacct	ttgtttcgga	tcaactgttg	catgaagggt	360
aaggctgac	gtgatgagtc	gtctccttat	gctgctatgc	ttgctgcccc	agatgttgca	420
cagcgttgca	agagagctgg	tatcacagcg	ctgcacatta	agcttctgtc	cactggaggc	480
aacaagacca	atgacctcgt	gacct				

(2) INFORMATION FOR SEQ ID NO:2555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1503811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2555:

Ser Phe Gly Gly Gly Val Gly Ser Gly Gly Val Leu Val Ile Ser Ile	
1 5 10 15	
Ser Thr Pro Gly Glu Leu Gly Ser Gly His Pro Ser Ile His Ala Thr	
20 25 30	
Met Ser Arg Arg Lys Thr Arg Glu Pro Lys Glu Asn Val Thr Leu	
35 40 45	
Gly Pro Thr Val Arg Glu Gly Glu Phe Val Phe Gly Val Ala His Ile	
50 55 60	
Phe Ala Ser Phe Asn Asp Thr Phe Ile Val Ser Ala Ile Cys Phe Ser	
65 70 75 80	
Leu Trp Met Gly Leu Phe Ile Ile Phe Pro Ile Val Thr Val Met Val	
85 90 95	

(2) INFORMATION FOR SEQ ID NO:2556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..64
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503812
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2556:
Met Ser Arg Arg Lys Thr Arg Glu Pro Lys Glu Glu Asn Val Thr Leu
1 5 10 15
Gly Pro Thr Val Arg Glu Gly Glu Phe Val Phe Gly Val Ala His Ile
 20 25 30
Phe Ala Ser Phe Asn Asp Thr Phe Ile Val Ser Ala Ile Cys Phe Ser
 35 40 45
Leu Trp Met Gly Leu Phe Ile Ile Phe Pro Ile Val Thr Val Met Val
50 55 60

(2) INFORMATION FOR SEQ ID NO:2557:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..70
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503813
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2557:
Met Gln His Val Thr Asp Leu Ser Gly Arg Glu Thr Leu Val Arg Ile
1 5 10 15
Thr Gly Gly Met Lys Val Lys Ala Asp Arg Asp Glu Ser Ser Pro Tyr
 20 25 30
Ala Ala Met Leu Ala Ala Gln Asp Val Ala Gln Arg Cys Lys Glu Leu
 35 40 45
Gly Ile Thr Ala Leu His Ile Lys Leu Arg Ala Thr Gly Gly Asn Lys
50 55 60
Thr Asn Asp Pro Trp Thr
65 70

(2) INFORMATION FOR SEQ ID NO:2558:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 456 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..456
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503822
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2558:
gnkccgcgcg cctacaacag gtgccccagg tcttcgctgc gccattcgcc agcgacgagc 60
accaacacag atggtcaacc gcaatgacct catgtactgg attgtogcgg cactctgatg 120
tggttgccck ckckgkqcac cagaagtgtg tgggtgtctt gaacaacaac gaggkactca 180
tggttggggt ggttggtgca ckgttcaacg aggtcgtgac aaatttgtaa ctacagggtg 240
ccctggaaac ttctgagcga tactctgtta aagcagaaaa tataacagtt gttagtgttc 300
ctggaagctt tgaagttcct ataacgkcaac aaaagcttgg gaaatctgga aaatttgatg 360
caattctgtg cattggagct gtgattagag gtgacacaaac ccactatgat gccgttgcaa 420
actcagctgc atcagggtga ctcaatgctg gattat

(2) INFORMATION FOR SEQ ID NO:2559:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..151
(D) OTHER INFORMATION: / Ceres Seq. ID 1503823
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2559:
Xaa Arg Arg Leu Gln Gln Val Pro Gln Val Phe Ala Ala Pro Phe Ala
1 5 10 15
Ser Asp Glu His Pro Thr Ala Trp Ser Thr Ala Met Thr Ser Cys Thr
20 25 30
Gly Leu Ser Arg His Ser Asp Val Val Ala Xaa Xaa Xaa His Gln Lys
35 40 45
Leu Met Gly Ser Leu Asn Asn Asn Glu Xaa Leu Met Phe Gly Val Val
50 55 60
Val Ala Xaa Phe Asn Glu Val Val Thr Asn Leu Leu Gln Gly Ala
65 70 75 80
Leu Glu Thr Phe Glu Arg Tyr Ser Val Lys Ala Glu Asn Ile Thr Val
85 90 95
Val Ser Val Pro Gly Ser Phe Glu Val Pro Ile Thr Xaa Gln Lys Leu
100 105 110
Gly Lys Ser Gly Lys Phe Asp Ala Ile Leu Cys Ile Gly Ala Val Ile
115 120 125
Arg Gly Asp Thr Thr His Tyr Asp Ala Val Ala Asn Ser Ala Ala Ser
130 135 140
Gly Val Leu Asn Ala Gly Leu
145 150

(2) INFORMATION FOR SEQ ID NO:2560:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..124
(D) OTHER INFORMATION: / Ceres Seq. ID 1503824
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2560:
Met Thr Ser Cys Thr Gly Leu Ser Arg His Ser Asp Val Val Ala Xaa
1 5 10 15
Xaa Xaa His Gln Lys Leu Met Gly Ser Leu Asn Asn Asn Glu Xaa Leu
20 25 30
Met Phe Gly Val Val Val Ala Xaa Phe Asn Glu Val Val Thr Asn Leu
35 40 45
Leu Leu Gln Gly Ala Leu Glu Thr Phe Glu Arg Tyr Ser Val Lys Ala
50 55 60
Glu Asn Ile Thr Val Val Ser Val Pro Gly Ser Phe Glu Val Pro Ile
65 70 75 80
Thr Xaa Gln Lys Leu Gly Lys Ser Gly Lys Phe Asp Ala Ile Leu Cys
85 90 95
Ile Gly Ala Val Ile Arg Gly Asp Thr Thr His Tyr Asp Ala Val Ala
100 105 110
Asn Ser Ala Ala Ser Gly Val Leu Asn Ala Gly Leu
115 120
(2) INFORMATION FOR SEQ ID NO:2561:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..102
(D) OTHER INFORMATION: / Ceres Seq. ID 1503825
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2561:
Met Gly Ser Leu Asn Asn Glu Xaa Leu Met Phe Gly Val Val Val
1 5 10 15
Ala Xaa Phe Asn Glu Val Val Thr Asn Leu Leu Gln Gly Ala Leu
20 25 30
Glu Thr Phe Glu Arg Tyr Ser Val Lys Ala Glu Asn Ile Thr Val Val
35 40 45
Ser Val Pro Gly Ser Phe Glu Val Pro Ile Thr Xaa Gln Lys Leu Gly
50 55 60
Lys Ser Gly Lys Phe Asp Ala Ile Leu Cys Ile Gly Ala Val Ile Arg
65 70 75 80
Gly Asp Thr Thr His Tyr Asp Ala Val Ala Asn Ser Ala Ala Ser Gly
85 90 95
Val Leu Asn Ala Gly Leu
100

(2) INFORMATION FOR SEQ ID NO:2562:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..392
(D) OTHER INFORMATION: / Ceres Seq. ID 1503826
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2562:
gaagtgcgag tcaatgctat catgatcacc agcacagtta ttgttgttct attcagcacaca 60
atgggttttcg gcctctctgac gaagccgctg ctcagttotc tcattcccacc aaggactgga 120
ctgaacacgt cgtctctgct ctcaagccag tctatgctgg acccactect tactagcatg 180
atgggggtctg actttgatgt agggcagatc aactccccc aatacaacct ccagtttcatt 240
ctcaccgcgc cassctgctc cgtccatcgc ctttgkycaa gtttgacgat cggtttcattg 300
cgccccgggt tcgggggggg aggttttcgt ccccttggtgc ctggttcgcc kktkkagagk 360
agtgtccctg aatctcacct gggcaactgtg ac

(2) INFORMATION FOR SEQ ID NO:2563:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..130
(D) OTHER INFORMATION: / Ceres Seq. ID 1503827
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2563:
Glu Val Arg Val Asn Ala Ile Met Ile Thr Ser Thr Val Ile Val Val
1 5 10 15
Leu Phe Ser Thr Met Val Phe Gly Xaa Leu Thr Lys Pro Leu Leu Ser
20 25 30
Leu Leu Ile Pro Pro Arg Thr Gly Leu Asn Thr Ser Ser Leu Leu Ser
35 40 45
Ser Gln Ser Met Leu Asp Pro Leu Leu Thr Ser Met Met Gly Ser Asp
50 55 60

Phe Asp Val Gly Gln Ile Asn Ser Pro Gln Tyr Asn Leu Gln Phe Ile
65 70 75 80
Leu Thr Ala Pro Xaa Arg Ser Val His Arg Leu Xaa Xaa Ser Leu Thr
85 90 95
Ile Gly Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Phe
100 105 110
Val Pro Gly Ser Xaa Xaa Xaa Xaa Ser Val Pro Glu Ser His Leu Gly
115 120 125
Thr Val
130

(2) INFORMATION FOR SEQ ID NO:2564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1503828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2564:

Met Ile Thr Ser Thr Val Ile Val Val Leu Phe Ser Thr Met Val Phe
1 5 10 15
Gly Xaa Leu Thr Lys Pro Leu Leu Ser Leu Leu Ile Pro Pro Arg Thr
20 25 30
Gly Leu Asn Thr Ser Ser Leu Leu Ser Ser Gln Ser Met Leu Asp Pro
35 40 45
Leu Leu Thr Ser Met Met Gly Ser Asp Phe Asp Val Gly Gln Ile Asn
50 55 60
Ser Pro Gln Tyr Asn Leu Gln Phe Ile Leu Thr Ala Pro Xaa Arg Ser
65 70 75 80
Val His Arg Leu Xaa Xaa Ser Leu Thr Ile Gly Phe Met Arg Pro Val
85 90 95
Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Xaa Xaa Xaa
100 105 110
Xaa Ser Val Pro Glu Ser His Leu Gly Thr Val
115 120

(2) INFORMATION FOR SEQ ID NO:2565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1503829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2565:

Met Val Phe Gly Xaa Leu Thr Lys Pro Leu Leu Ser Leu Leu Ile Pro
1 5 10 15
Pro Arg Thr Gly Leu Asn Thr Ser Ser Leu Leu Ser Ser Gln Ser Met
20 25 30
Leu Asp Pro Leu Leu Thr Ser Met Met Gly Ser Asp Phe Asp Val Gly
35 40 45
Gln Ile Asn Ser Pro Gln Tyr Asn Leu Gln Phe Ile Leu Thr Ala Pro
50 55 60
Xaa Arg Ser Val His Arg Leu Xaa Xaa Ser Leu Thr Ile Gly Phe Met
65 70 75 80
Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser

85 90 95
Xaa Xaa Xaa Xaa Ser Val Pro Glu Ser His Leu Gly Thr Val
100 105 110

(2) INFORMATION FOR SEQ ID NO:2566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..464

(D) OTHER INFORMATION: / Ceres Seq. ID 1503869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2566:

```
gtagtgggaa ggggtacgtt agcktttgck ggcggtmrac tccccacgca aagccgccgc 60
cgttccctct cgtcttcccc agttccocta cgcggtaaat cccacgtcct atcagccgnc 120
gatccagocct tgcttccatc catccatcca tccatccatc catctcgtcg cttctctctg 180
ttccgcgtgc gatcgagtag atcaaaaagga ggaggaggat ggcgaggagt tcgttcaagt 240
tggagcacc cttcgaaaag aggcaagctg aggcctaaccg catcaggggag aaataccctg 300
acagaaatccc tgtcattggt gagaaggccg agaggagtga catcccagac attgacaaga 360
aaaagtacct tgttcctgcc gacctcacag tcggacagtt tgtgtatgtg gtacggaagc 420
ggatcaagct aagcgctgag aaggcaatct tcattctcgt aaag
```

(2) INFORMATION FOR SEQ ID NO:2567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1503870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2567:

```
Ser Gly Lys Gly Tyr Val Ser Xaa Cys Xaa Ala Xaa Thr Pro His Ala
1 5 10 15
Lys Pro Pro Pro Phe Pro Leu Val Phe Pro Ser Ser Pro Thr Pro Val
20 25 30
Ile Pro Arg Pro Ile Ser Xaa Arg Ser Ser Leu Ala Ser Ile His Pro
35 40 45
Ser Ile His Pro Ser Ile Ser Ser Leu Leu Ser Val Pro Arg Ala Ile
50 55 60
```

Glu

65

(2) INFORMATION FOR SEQ ID NO:2568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1503871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2568:

```
Met Ala Arg Ser Ser Phe Lys Leu Glu His Pro Phe Glu Arg Arg Gln
1 5 10 15
Ala Glu Ala Asn Arg Ile Arg Glu Lys Tyr Pro Asp Arg Ile Pro Val
20 25 30
```

Ile Val Glu Lys Ala Glu Arg Ser Asp Ile Pro Asp Ile Asp Lys Lys
35 40 45
Lys Tyr Leu Val Pro Ala Asp Leu Thr Val Gly Gln Phe Val Tyr Val
50 55 60
Val Arg Lys Arg Ile Lys Leu Ser Ala Glu Lys Ala Ile Phe Ile Phe
65 70 75 80
Val Lys

(2) INFORMATION FOR SEQ ID NO:2569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..479
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2569:

ccagtcacg atgcaccga tccatgagat cgtcgagaca aggttcagat ccaacagatg 60
ctttcggaag ctacagccaca acgatggcgg cgcgagagtg ataggcttgc acgcwagcggc 120
tgtcctcgtg gtggcggtcc tcaactgtgt gggtctcttc atccccttct ttgggtcctt 180
catctcgttc gtccggagca ccatgtggcg cttctctctt ttgtgtctgc ggctctcttc 240
catctcagca ttgttaggct gtcaataccc ttgtggagcg gggtgtctgc actacggcat 300
ccttctcttt ggtctggcct tcgtgtgata tggctctgtc actgtctctc cctcgcattg 360
aacaatggcc caaacagctc aaaaagtgc gagatcagga tatctgtga tgacacagat 420
caaattggat ctaggagcac catatatcag atagcacggc tcggattagt gcgtgattg

(2) INFORMATION FOR SEQ ID NO:2570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2570:

Pro Val Met Met His Pro Ile His Glu Ile Val Glu Thr Arg Phe Arg
1 5 10 15
Ser Asn Arg Cys Phe Arg Lys Leu Ser His Asn Asp Gly Gly Ala Glu
20 25 30
Trp Ile Gly Leu His Xaa Xaa Ala Val Leu Val Val Ala Val Leu Thr
35 40 45
Val Val Ala Ser Phe Ile Pro Phe Phe Gly Ser Phe Ile Ser Phe Val
50 55 60
Gly Ser Thr Met Trp Arg Phe Ser Pro Leu Cys Cys Arg Leu Ser Ser
65 70 75 80
Ile Ser Ala Leu

(2) INFORMATION FOR SEQ ID NO:2571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1503875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2571:

Met	Met	His	Pro	Ile	His	Glu	Ile	Val	Glu	Thr	Arg	Phe	Arg	Ser	Asn	
1															15	
Arg	Cys	Phe	Arg	Lys	Leu	Ser	His	Asn	Asp	Gly	Gly	Ala	Glu	Trp	Ile	
			20					25						30		
Gly	Leu	His	Xaa	Xaa	Ala	Val	Leu	Val	Val	Ala	Val	Leu	Thr	Val	Val	
		35					40						45			
Ala	Ser	Phe	Ile	Pro	Phe	Phe	Gly	Ser	Phe	Ile	Ser	Phe	Val	Gly	Ser	
	50					55				60						
Thr	Met	Trp	Arg	Phe	Ser	Pro	Leu	Cys	Cys	Arg	Leu	Ser	Ser	Ile	Ser	
	65			70						75					80	
Ala	Leu															

(2) INFORMATION FOR SEQ ID NO:2572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1503876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2572:

Met	Leu	Ser	Glu	Ala	Gln	Pro	Gln	Arg	Trp	Arg	Arg	Gly	Val	Asp	Arg	
1															15	
Leu	Ala	Arg	Xaa	Xaa	Cys	Pro	Arg	Gly	Gly	Gly	Pro	His	Cys	Gly	Gly	
			20					25					30			
Val	Leu	His	Pro	Leu	Leu	Trp	Val	Leu	His	Leu	Val	Arg	Arg	Glu	His	
		35					40						45			
His	Val	Ala	Leu	Leu	Ser	Phe	Val	Leu	Pro	Ala	Leu	Phe	His	Leu	Ser	
	50					55					60					
Ile	Val	Gly	Ser	Ser	Ile	Pro	Leu	Trp	Arg	Arg	Val	Ala	Gly	Leu	Arg	
	65				70				75						80	
His	Pro	Ser	Leu	Trp	Ser	Gly	Phe	Arg	Trp	Ile	Trp	Ser	Cys	His	Cys	
			85						90					95		
Ser	Leu	Leu	Ala	Leu	Asn	Asn	Gly	Pro	Asn	Ser	Gln	Lys	Ser	Ala	Glu	
			100				105						110			
Ile	Arg	Ile	Ser	Cys	Asp	Asp	Xaa	Ser	Gln	Met	Asp	Ala	Arg	Ser	Thr	
	115					120							125			
Ile	Tyr	Gln	Ile	Ala	Arg	Leu	Gly	Leu	Val	Arg	Asp					
	130					135										

(2) INFORMATION FOR SEQ ID NO:2573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1503886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2573:

aaacctcc accacctcct cccctcctc ccaacagtc aacagtcgca ctaccgagcc	60
atgtcctccg ctaccaacct ccgtttattg tcgtgggact gcgcgcgagga cccgctggat	120
ttcgggtcgt tcgccgacac cgcgtttctc ccgctccagc	

(2) INFORMATION FOR SEQ ID NO:2574:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..53
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503887
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2574:
Lys Pro Ser His His Leu Leu Pro Leu Leu Pro Thr Val Thr Thr Ser
1 5 10 15
His Tyr Arg Ala Met Ser Ser Ala Thr Asn Leu Arg Leu Leu Ser Trp
 20 25 30
Asp Cys Ala Glu Asp Pro Leu Asp Phe Gly Ala Phe Ala Asp Thr Ala
 35 40 45
Phe Leu Pro Leu Gln
50
(2) INFORMATION FOR SEQ ID NO:2575:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..53
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503888
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2575:
Asn Leu Pro Thr Thr Ser Ser Pro Ser Ser Gln Gln Ser Pro Arg Arg
1 5 10 15
Thr Thr Glu Pro Cys Pro Pro Leu Pro Thr Ser Val Tyr Cys Arg Gly
 20 25 30
Thr Ala Pro Arg Thr Arg Trp Ile Ser Val Arg Ser Pro Thr Pro Arg
 35 40 45
Phe Ser Arg Ser Ser
50
(2) INFORMATION FOR SEQ ID NO:2576:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..52
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503889
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2576:
Thr Phe Pro Pro Pro Pro Pro Pro Pro Asn Ser His His Val Ala
1 5 10 15
Leu Pro Ser His Val Leu Arg Tyr Gln Pro Pro Phe Ile Val Val Gly
 20 25 30
Leu Arg Arg Gly Pro Ala Gly Phe Arg Cys Val Arg Arg His Arg Val
 35 40 45
Ser Pro Ala Pro
50
(2) INFORMATION FOR SEQ ID NO:2577:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..338
(D) OTHER INFORMATION: / Ceres Seq. ID 1503890
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2577:
agctcgctct gggagaggtt aatggcggca agtctccagc tcgccatttt catgtccgcc 60
gccatcgccg tcgggttcgg cggcgctcag gccggcgagg cgcasstgtg cagcgagtac 120
tacgaccgga cgtgccccgt cgtgcaccgg gtcgtgcggc ggggtcgtga gaagggcacc 180
gagtcgcagc tccgcattta cgccagccct acccgccctc acttccacga ctgcttcgtg 240
caagggtcgg acgggtccat cctgctggac aacagctcca gcattcgtgc ggagaagttc 300
ggcacgcccc acaacaactc ggcgcgcggg taccocgt
(2) INFORMATION FOR SEQ ID NO:2578:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..112
(D) OTHER INFORMATION: / Ceres Seq. ID 1503891
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2578:
Ser Ser Leu Trp Glu Arg Leu Met Ala Ala Ser Leu Gln Leu Ala Ile
1 5 10 15
Phe Met Ser Ala Ala Ile Ala Leu Gly Phe Gly Gly Val Gln Ala Gly
20 25 30
Ala Ala Xaa Xaa Cys Ser Glu Tyr Tyr Asp Arg Thr Cys Pro Val Val
35 40 45
His Arg Val Val Arg Arg Val Leu Lys Lys Ala His Glu Ser Asp Val
50 55 60
Arg Ile Tyr Ala Ser Leu Thr Arg Leu His Phe His Asp Cys Phe Val
65 70 75 80
Gln Gly Cys Asp Gly Ser Ile Leu Leu Asp Asn Ser Ser Ser Ile Val
85 90 95
Ser Glu Lys Phe Ala Thr Pro Asn Asn Asn Ser Ala Arg Gly Tyr Pro
100 105 110
(2) INFORMATION FOR SEQ ID NO:2579:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..112
(D) OTHER INFORMATION: / Ceres Seq. ID 1503892
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2579:
Leu Ala Leu Gly Glu Val Asn Gly Gly Lys Ser Pro Ala Arg His Phe
1 5 10 15
His Val Arg Arg His Arg Ala Arg Val Arg Arg Arg Pro Gly Arg Arg
20 25 30
Gly Ala Xaa Val Gln Arg Val Leu Arg Pro Asp Val Pro Arg Arg Ala

35	40	45
Pro Gly Arg Ala Ala Gly Ala Glu Glu Gly Ala Arg Val Arg Arg Pro		
50	55	60
His Leu Arg Gln Pro His Pro Pro Pro Leu Pro Arg Leu Leu Arg Ala		
65	70	75
Arg Leu Arg Arg Leu His Pro Ala Gly Gln Gln Leu Gln His Arg Val		
85	90	95
Gly Glu Val Arg His Ala Gln Gln Gln Leu Gly Ala Arg Val Pro Arg		
100	105	110

(2) INFORMATION FOR SEQ ID NO:2580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2580:

Met	Ala	Ala	Ser	Leu	Gln	Leu	Ala	Ile	Phe	Met	Ser	Ala	Ala	Ile	Ala
1			5					10						15	
Leu	Gly	Phe	Gly	Gly	Val	Gln	Ala	Gly	Ala	Ala	Xaa	Xaa	Cys	Ser	Glu
			20					25						30	
Tyr	Tyr	Asp	Arg	Thr	Cys	Pro	Val	Val	His	Arg	Val	Val	Arg	Arg	Val
			35					40						45	
Leu	Lys	Lys	Ala	His	Glu	Ser	Asp	Val	Arg	Ile	Tyr	Ala	Ser	Leu	Thr
			50					55						60	
Arg	Glu	His	Phe	His	Asp	Cys	Phe	Val	Gln	Gly	Cys	Asp	Gly	Ser	Ile
65								70						75	
Leu	Leu	Asp	Asn	Ser	Ser	Ser	Ile	Val	Ser	Glu	Lys	Phe	Ala	Thr	Pro
								85						90	
Asn	Asn	Asn	Ser	Ala	Arg	Gly	Tyr	Pro						95	
			100					105							

(2) INFORMATION FOR SEQ ID NO:2581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..510
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2581:

agggtttttt	gccaaagtgc	cgccgtgcgt	ctgcccgcat	tcctctccac	aacaccgaga	60
cgccaggatg	acggcgcgaga	ctcgggagga	gctcgccacc	cagatcgagc	agcagaagct	120
cgaggagcag	aagaccgagg	cagaggaggt	tgtggtggag	gatgaggagg	acgacgacga	180
tgaggacgat	gaggatgatg	atgaacttga	cggacaagaa	ggggatgcc	gcggcaagtc	240
aaagcaaaagc	aggagttaga	agaagagccg	caaaagccatg	ctgaagcttg	gcataagacc	300
catcactggt	gtcagccgtg	tcactgtgaa	gaaaagcaag	aatatactgt	tgttcattct	360
gaagccagat	gtgttcaaga	gcccgaaactc	agacacatac	gtcatattcg	gcgaggccaa	420
gatcgaggagc	ctcagctccc	agctgcagac	ccaggccgca	gaacagttca	aggccccctg	480
acttgagcca	gatcagcagt	ccagagactt				

(2) INFORMATION FOR SEQ ID NO:2582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..159
(D) OTHER INFORMATION: / Ceres Seq. ID 1503895
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2582:
Gly Phe Phe Ala Lys Ser Pro Pro Ser Leu Cys Pro His Ser Leu Pro
1 5 10 15
Gln His Arg Asp Ala Arg Met Thr Ala Gln Thr Ala Glu Glu Leu Ala
20 25 30
Thr Gln Ile Glu Gln Gln Lys Leu Glu Glu Gln Lys Thr Glu Ala Glu
35 40 45
Glu Val Val Val Glu Asp Glu Glu Asp Asp Asp Glu Asp Asp Glu
50 55 60
Asp Asp Asp Glu Leu Asp Gly Gln Glu Gly Asp Ala Ser Gly Lys Ser
65 70 75 80
Lys Gln Ser Arg Ser Glu Lys Lys Ser Arg Lys Ala Met Leu Lys Leu
85 90 95
Gly Met Lys Pro Ile Thr Gly Val Ser Arg Val Thr Val Lys Lys Ser
100 105 110
Lys Asn Ile Leu Phe Val Ile Ser Lys Pro Asp Val Phe Lys Ser Pro
115 120 125
Asn Ser Asp Thr Tyr Val Ile Phe Gly Glu Ala Lys Ile Glu Asp Leu
130 135 140
Ser Ser Gln Leu Gln Thr Gln Ala Ala Glu Gln Phe Lys Ala Pro
145 150 155

(2) INFORMATION FOR SEQ ID NO:2583:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..137
(D) OTHER INFORMATION: / Ceres Seq. ID 1503896
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2583:
Met Thr Ala Gln Thr Ala Glu Glu Leu Ala Thr Gln Ile Glu Gln Gln
1 5 10 15
Lys Leu Glu Glu Gln Lys Thr Glu Ala Glu Glu Val Val Val Glu Asp
20 25 30
Glu Glu Asp Asp Asp Asp Glu Asp Asp Glu Asp Asp Asp Glu Leu Asp
35 40 45
Gly Gln Glu Gly Asp Ala Ser Gly Lys Ser Lys Gln Ser Arg Ser Glu
50 55 60
Lys Lys Ser Arg Lys Ala Met Leu Lys Leu Gly Met Lys Pro Ile Thr
65 70 75 80
Gly Val Ser Arg Val Thr Val Lys Lys Ser Lys Asn Ile Leu Phe Val
85 90 95
Ile Ser Lys Pro Asp Val Phe Lys Ser Pro Asn Ser Asp Thr Tyr Val
100 105 110
Ile Phe Gly Glu Ala Lys Ile Glu Asp Leu Ser Ser Gln Leu Gln Thr
115 120 125
Gln Ala Ala Glu Gln Phe Lys Ala Pro
130 135

(2) INFORMATION FOR SEQ ID NO:2584:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..459
(D) OTHER INFORMATION: / Ceres Seq. ID 1503899
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2584:
acaactttac agctaacatg gagacagagc tagataatgt ctctgctggg tcaactgaat 60
ggaagggtct tctgaaagac tactgggaac gattcagcaa atattgtgca gatgtgagta 120
aactggatgg cagaaaggta gagagaatgc ttgaagaaaa atttggtcct atcctctttt 180
ccgatgttta caaggattgt agaatttgcc ctagtgttic tgaagggaacc ttgagattca 240
aagtttagtag gtacgggtgaa ggctattttg taggttgtag tcgacatcca aaatgcaagt 300
acattgtctg ctcaactgtca cagcaagaag atgaaactga acccatagaa gaaaatgcga 360
aatcttttga acccagggtta cttgggtgca tgctgtattc tgatcaaaa ggtgtttttga 420
aacaagggcc atatggctac tatgttcaag ttggagagg

(2) INFORMATION FOR SEQ ID NO:2585:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..152
(D) OTHER INFORMATION: / Ceres Seq. ID 1503900
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2585:
Asn Phe Thr Ala Asn Met Glu Thr Glu Leu Asp Asn Val Ser Ala Gly
1 5 10 15
Ser Thr Glu Trp Lys Gly Leu Leu Lys Asp Tyr Trp Glu Arg Phe Ser
20 25 30
Lys Tyr Cys Ala Asp Val Ser Lys Leu Asp Gly Arg Lys Val Glu Arg
35 40 45
Met Leu Glu Glu Lys Phe Gly Pro Ile Leu Phe Ser Asp Val Tyr Lys
50 55 60
Asp Cys Arg Ile Cys Pro Ser Cys Ser Glu Gly Thr Leu Arg Phe Lys
65 70 75 80
Val Ser Arg Tyr Gly Glu Gly Tyr Phe Val Gly Cys Asp Arg His Pro
85 90 95
Lys Cys Lys Tyr Ile Ala Arg Ser Leu Ser Gln Gln Glu Asp Glu Thr
100 105 110
Glu Pro Ile Glu Glu Asn Ala Lys Ser Phe Glu Pro Arg Leu Leu Gly
115 120 125
Val Met Pro Asp Ser Asp Gln Lys Val Phe Leu Lys Gln Gly Pro Tyr
130 135 140
Gly Tyr Tyr Val Gln Val Gly Glu
145 150

(2) INFORMATION FOR SEQ ID NO:2586:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..147
(D) OTHER INFORMATION: / Ceres Seq. ID 1503901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2586:
Met Glu Thr Glu Leu Asp Asn Val Ser Ala Gly Ser Thr Glu Trp Lys
1 5 10 15
Gly Leu Leu Lys Asp Tyr Trp Glu Arg Phe Ser Lys Tyr Cys Ala Asp
20 25 30
Val Ser Lys Leu Asp Gly Arg Lys Val Glu Arg Met Leu Glu Glu Lys
35 40 45
Phe Gly Pro Ile Leu Phe Ser Asp Val Tyr Lys Asp Cys Arg Ile Cys
50 55 60
Pro Ser Cys Ser Glu Gly Thr Leu Arg Phe Lys Val Ser Arg Tyr Gly
65 70 75 80
Glu Gly Tyr Phe Val Gly Cys Asp Arg His Pro Lys Cys Lys Tyr Ile
85 90 95
Ala Arg Ser Leu Ser Gln Gln Glu Asp Glu Thr Glu Pro Ile Glu Glu
100 105 110
Asn Ala Lys Ser Phe Glu Pro Arg Leu Leu Gly Val Met Pro Asp Ser
115 120 125
Asp Gln Lys Val Phe Leu Lys Gln Gly Pro Tyr Gly Tyr Tyr Val Gln
130 135 140
Val Gly Glu
145

(2) INFORMATION FOR SEQ ID NO:2587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2587:

Met Leu Glu Glu Lys Phe Gly Pro Ile Leu Phe Ser Asp Val Tyr Lys
1 5 10 15
Asp Cys Arg Ile Cys Pro Ser Cys Ser Glu Gly Thr Leu Arg Phe Lys
20 25 30
Val Ser Arg Tyr Gly Glu Gly Tyr Phe Val Gly Cys Asp Arg His Pro
35 40 45
Lys Cys Lys Tyr Ile Ala Arg Ser Leu Ser Gln Gln Glu Asp Glu Thr
50 55 60
Glu Pro Ile Glu Glu Asn Ala Lys Ser Phe Glu Pro Arg Leu Leu Gly
65 70 75 80
Val Met Pro Asp Ser Asp Gln Lys Val Phe Leu Lys Gln Gly Pro Tyr
85 90 95
Gly Tyr Tyr Val Gln Val Gly Glu
100

(2) INFORMATION FOR SEQ ID NO:2588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..444
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2588:

cggaagaatt ttgatatttg ggggtcagtg ggcaggtctt cactcagcgt cacagcttta 60
tctgttgat ccaactgaag aaaakccgac ctggagaata ttgaatatcc ctggctgctac 120

tccccgtttc	gcctggggcc	acagcacctg	tgttgttga	ggaacaaagg	cgatagtgtc	180
tggtggacaa	actggagaag	agtggatgct	tacagaaata	catgagcttt	ctttgggtcag	240
ccgctcagtt	tgagttctgg	aatggtttgt	agtoatgttc	cttgcaaat	agatgcgctt	300
tcttatgcaa	cctgaagttt	gattgccctc	ttcagaagaa	ctagaagaat	gaatgctggg	360
catactgaat	cttctggcag	ctacctggcg	gacttggga	atgaaatggc	atcgactggt	420
ttgctcgttt	tgtgtagaaa	aggg				

(2) INFORMATION FOR SEQ ID NO:2589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1503925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2589:

Gly	Arg	Ile	Leu	Ile	Phe	Gly	Gly	Ser	Val	Ala	Gly	Leu	His	Ser	Ala
1				5					10					15	
Ser	Gln	Leu	Tyr	Leu	Leu	Asp	Pro	Thr	Glu	Xaa	Pro	Thr	Trp	Arg	
				20				25				30			
Ile	Leu	Asn	Ile	Pro	Gly	Arg	Pro	Pro	Arg	Phe	Ala	Trp	Gly	His	Ser
		35				40					45				
Thr	Cys	Val	Val	Gly	Gly	Thr	Lys	Ala	Ile	Val	Leu	Gly	Gly	Gln	Thr
		50				55					60				
Gly	Glu	Glu	Trp	Met	Leu	Thr	Glu	Ile	His	Glu	Leu	Ser	Leu	Val	Ser
		65			70					75				80	
Arg	Ser	Val													

(2) INFORMATION FOR SEQ ID NO:2590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..510

(D) OTHER INFORMATION: / Ceres Seq. ID 1503926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2590:

tctgtgcac	ttaaatatgg	gggacagtag	agctgtgctt	gcttccatgc	catatgtaga	60
aaatggtgct	ttgaaggcta	ctcaactgac	agagagccac	tcgcttgaaa	atcctttgga	120
gtacccaaaa	cttttagctg	aacatcccaa	tgattcttca	gttgtaagg	gtaacaaaat	180
aaaaggaaa	ctgaaggtta	ctcgtgcttt	tggagtggc	tatctgaagc	agaggaaagt	240
caacgatgca	ctcatgggca	ttctgcgagt	ccgcatttg	agcagccctc	catatgttta	300
cacaaatcca	cacacattga	gccacaaagt	tacagaagat	gattattttg	ttgtgcttgg	360
tagtgcgtgc	tattttgatt	tcttcagcaa	tgatgaagtt	gttcgggttg	tttatcaatt	420
tatgcgatgat	aatccaatgg	gggacctctg	aaaatatctt	attgagcaac	tttatactca	480
aagcagccaa	gggagcagct	ctacacagcg				

(2) INFORMATION FOR SEQ ID NO:2591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1503927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2591:

Leu Cys Ile Leu Asn Met Gly Asp Ser Arg Ala Val Leu Ala Ser Met
1 5 10 15
Pro Tyr Val Glu Asn Gly Ala Leu Lys Ala Thr Gln Leu Thr Glu Thr
20 25 30
His Ser Leu Glu Asn Pro Leu Glu Tyr Gln Lys Leu Leu Ala Glu His
35 40 45
Pro Asn Asp Ser Ser Val Val Arg Gly Asn Lys Ile Lys Gly Lys Leu
50 55 60
Lys Val Thr Arg Ala Phe Gly Val Gly Tyr Leu Lys Gln Arg Lys Phe
65 70 75 80
Asn Asp Ala Leu Met Gly Ile Leu Arg Val Arg Asp Leu Ser Ser Pro
85 90 95
Pro Tyr Val Tyr Thr Asn Pro His Thr Leu Ser His Lys Val Thr Glu
100 105 110
Asp Asp Leu Phe Val Val Leu Gly Ser Asp Gly Leu Phe Asp Phe Phe
115 120 125
Ser Asn Asp Glu Val Val Arg Leu Val Tyr Gln Phe Met His Asp Asn
130 135 140
Pro Met Gly Asp Pro Ala Lys Tyr Leu Ile Glu Gln Leu Tyr Thr Gln
145 150 155 160
Ser Ser Gln Gly Ser Ser Asn Ser
165

(2) INFORMATION FOR SEQ ID NO:2592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1503928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2592:

Met Gly Asp Ser Arg Ala Val Leu Ala Ser Met Pro Tyr Val Glu Asn
1 5 10 15
Gly Ala Leu Lys Ala Thr Gln Leu Thr Glu Thr His Ser Leu Glu Asn
20 25 30
Pro Leu Glu Tyr Gln Lys Leu Leu Ala Glu His Pro Asn Asp Ser Ser
35 40 45
Val Val Arg Gly Asn Lys Ile Lys Gly Lys Leu Lys Val Thr Arg Ala
50 55 60
Phe Gly Val Gly Tyr Leu Lys Gln Arg Lys Phe Asn Asp Ala Leu Met
65 70 75 80
Gly Ile Leu Arg Val Arg Asp Leu Ser Ser Pro Pro Tyr Val Tyr Thr
85 90 95
Asn Pro His Thr Leu Ser His Lys Val Thr Glu Asp Asp Leu Phe Val
100 105 110
Val Leu Gly Ser Asp Gly Leu Phe Asp Phe Phe Ser Asn Asp Glu Val
115 120 125
Val Arg Leu Val Tyr Gln Phe Met His Asp Asn Pro Met Gly Asp Pro
130 135 140
Ala Lys Tyr Leu Ile Glu Gln Leu Tyr Thr Gln Ser Ser Gln Gly Ser
145 150 155 160
Ser Ser Asn Ser

(2) INFORMATION FOR SEQ ID NO:2593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..154
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503929
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2593:
Met Pro Tyr Val Glu Asn Gly Ala Leu Lys Ala Thr Gln Leu Thr Glu
1 5 10 15
Thr His Ser Leu Glu Asn Pro Leu Glu Tyr Gln Lys Leu Leu Ala Glu
 20 25 30
His Pro Asn Asp Ser Ser Val Val Arg Gly Asn Lys Ile Lys Gly Lys
 35 40 45
Leu Lys Val Thr Arg Ala Phe Gly Val Gly Tyr Leu Lys Gln Arg Lys
 50 55 60
Phe Asn Asp Ala Leu Met Gly Ile Leu Arg Val Arg Asp Leu Ser Ser
65 70 75 80
Pro Pro Tyr Val Tyr Thr Asn Pro His Thr Leu Ser His Lys Val Thr
 85 90 95
Glu Asp Asp Leu Phe Val Val Leu Gly Ser Asp Gly Leu Phe Asp Phe
 100 105 110
Phe Ser Asn Asp Glu Val Val Arg Leu Val Tyr Gln Phe Met His Asp
 115 120 125
Asn Pro Met Gly Asp Pro Ala Lys Tyr Leu Ile Glu Gln Leu Tyr Thr
 130 135 140
Gln Ser Ser Gln Gly Ser Ser Ser Asn Ser
145 150
(2) INFORMATION FOR SEQ ID NO:2594:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..161
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503934
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2594:
accgcaccca gagggagcaa ggagcccatc cacatccacc tggtcctgct ctcaccacac 60
cgccggcgca attggggctc gcgcgagcac cgccggcggt tcccgtggt ccgcgtcctg 120
ctctccctcc tggccgcgcc gcgctacggc gcgcctcatct c
(2) INFORMATION FOR SEQ ID NO:2595:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..53
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503935
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2595:
Thr Ala Pro Arg Gly Gly Lys Glu Pro Ile His Ile His Leu Val Leu
1 5 10 15
Leu Ser Pro His Arg Arg Ala Asn Trp Gly Ser Arg Gln His Arg Arg
 20 25 30
Gly Phe Pro Leu Val Pro Leu Leu Ser Leu Leu Ala Ala Ala

35 40 45
Tyr Gly Arg Leu Ile
50
(2) INFORMATION FOR SEQ ID NO:2596:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..53
(D) OTHER INFORMATION: / Ceres Seq. ID 1503936
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2596:
Pro His Pro Glu Ala Arg Ser Pro Ser Thr Ser Thr Ser Cys
1 5 10 15
Ser His His Thr Ala Ala Pro Ile Gly Ala Arg Gly Ser Thr Ala Ala
20 25 30
Ala Ser Arg Trp Ser Arg Ser Cys Ser Pro Ser Trp Pro Pro Arg
35 40 45
Thr Ala Ala Ser Ser
50

(2) INFORMATION FOR SEQ ID NO:2597:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..53
(D) OTHER INFORMATION: / Ceres Seq. ID 1503937
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2597:
Arg Thr Gln Arg Arg Gln Gly Ala His Pro His Pro Pro Gly Pro Ala
1 5 10 15
Leu Thr Thr Pro Pro Arg Gln Leu Gly Leu Ala Ala Ala Pro Pro Arg
20 25 30
Leu Pro Ala Gly Pro Ala Pro Ala Leu Pro Pro Gly Arg Arg Arg Val
35 40 45
Arg Pro Pro His Leu
50

(2) INFORMATION FOR SEQ ID NO:2598:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..435
(D) OTHER INFORMATION: / Ceres Seq. ID 1503942
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2598:
gaaccacttc acagaagaag tgctttacc tcacccgcc cagcgcggt agttcggtcg 60
acacagtcac agtcacagac cagtcgtttc tcccttctct ccccggggcc cggagaggag 120
aggatggccg gccggagcag cctctccatg gtcgcgctcg acggctctt cagcgcggtc 180
aaccagtggt gcggcgccga ccacggcggt ggagctcgac gaggccgacg tcactctggg 240
cggcgggcgc ggatacccg cgtcgtctct accgtctcg tcgctgttc tgtctctcgc 300
ggtcgaccgc tacgcgcggt cgccgcggt ggccgcgccg tccaagcaga agcgcggtgg 360

gggtgggtgcc ggcgctccgg ggccggcgcta cggtgcccgt caacatcccg gactgggtcca 420
agatcctggg cgccg

(2) INFORMATION FOR SEQ ID NO:2599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1503943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2599:

Glu Pro Leu His Arg Arg Ser Ala Leu Pro Ser Pro Ala Pro Arg Ala
1 5 10 15
Val Val Arg Ser Thr Gln Ser Gln Ser Gln Thr Ser Arg Phe Ser Leu
20 25 30
Leu Ser Pro Gly Pro Gly Glu Glu Arg Met Ala Gly Arg Ser Ser Leu
35 40 45
Ser Met Val Ala Ser His Arg Leu Phe Thr Pro Val Asn Pro Val Gly
50 55 60
Gly Ala Asp His Gly Val Gly Ala Arg Arg Gly Arg Arg His Leu Gly
65 70 75 80
Arg Arg Arg Arg Ile Pro Gly Val Val Leu Thr Val Val Val Ala Val
85 90 95
Pro Val Leu Arg Gly Arg Pro Val Arg Ala Val Ala Ala Gly Arg
100 105 110
Ala Val Gln Ala Glu Ala Ala Trp Gly Gly Gly Arg Ser Gly Ala
115 120 125
Gly Val Arg Cys Pro Ser Thr Ser Arg Thr Gly Pro Arg Ser Trp Ala
130 135 140

Pro
145

(2) INFORMATION FOR SEQ ID NO:2600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1503944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2600:

Thr Thr Ser Gln Lys Lys Cys Phe Thr Leu Thr Arg Pro Thr Arg Gly
1 5 10 15
Ser Ser Phe Asp Thr Val Thr Val Thr Asp Gln Ser Phe Leu Pro Ser
20 25 30
Leu Pro Arg Ala Arg Arg Gly Glu Asp Gly Arg Pro Glu Gln Pro Leu
35 40 45
His Gly Arg Val Ala Pro Ala Leu His Ala Gly Gln Pro Ser Gly Arg
50 55 60
Arg Arg Pro Arg Arg Gly Ser Ser Thr Arg Pro Thr Ser Ser Gly Ala
65 70 75 80
Ala Ala Ala Asp Thr Arg Arg Arg Pro His Arg Arg Arg Arg Arg Ser
85 90 95
Cys Pro Pro Arg Ser Thr Arg Thr Arg Gly Arg Arg Arg Trp Pro Arg
100 105 110
Arg Pro Ser Arg Ser Arg Val Gly Trp Trp Pro Ala Leu Arg Gly Arg

(2) INFORMATION FOR SEQ ID NO:2601:

(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..104
(D) OTHER INFORMATION: / Ceres Seq. ID 1503945

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..494
(D) OTHER INFORMATION: / Ceres Seq. ID 1503946

(X1) SEQUENCE DESCRIPTION FILE						
tgtctcaggt	caagaaagtgt	tacggggctgt	tgatgttttc	cttgctgcac	cgctgtgttc	60
tcacgacgaat	gaaaaatctta	tggagctctct	gatcatgatt	gatccctgta	ggagagcattc	120
tgcataaagt	atcacctgcag	tattccctta	ttttgtgtat	cgacagggctg	acaggaagtc	180
ccaggggcag	gaatctatag	ctgcaaaact	tgtagctaatt	atgatatccg	aagctgtctgc	240
caacgtgttc	tgttttgtga	tctctaatc	agtcacagcaa	tggataactt	tgacatccca	300
gtgatgacg	tttatggcca	gcctctgatt	cttgattatc	tcggcagcag	gacaaattgt	360
tcagatgact	tgttagttgt	atctctcgt	gttggcaggt	ttgcagggcc	acctgtcctt	420
gtccaaaagg	tgtcagatgc	acctctagct	attgtagata	aaagaaagcca	aggacataat	480
gctcctgaag	tqat					

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 100 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1503947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2603:

Val Gln Leu Gln Glu Ser Val Arg Gly Cys Asp Val Phe Leu Val Gln
1 5 10 15
Pro Ser Cys Pro Pro Ala Asn Glu Asn Leu Met Glu Leu Ile Met
20 25 30
Ile Asp Ala Cys Arg Arg Ala Ser Ala Lys Asn Ile Thr Ala Val Ile
35 40 45
Pro Tyr Phe Gly Tyr Ala Arg Ala Asp Arg Lys Ser Gln Gly Arg Glu
50 55 60
Ser Ile Ala Ala Lys Leu Val Ala Asn Met Ile Thr Glu Ala Gly Ala
65 70 75 80
Asn Val Ser Leu Phe Val Ile Phe Ile Leu Val Lys Gln Trp Asp Thr
85 90 95
Leu Thr Ser Gln
100

(2) INFORMATION FOR SEQ ID NO:2604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1503948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2604:

Met Gly Leu Leu Ile Met Ile Asp Ala Cys Arg Arg Ala Ser Ala Lys
1 5 10 15
Asn Ile Thr Ala Val Ile Pro Tyr Phe Gly Tyr Ala Arg Ala Asp Arg
20 25 30
Lys Ser Gln Gly Arg Glu Ser Ile Ala Ala Lys Leu Val Ala Asn Met
35 40 45
Ile Thr Glu Ala Gly Ala Asn Val Ser Leu Phe Val Ile Phe Ile Leu
50 55 60
Val Lys Gln Trp Asp Thr Leu Thr Ser Gln
65 70

(2) INFORMATION FOR SEQ ID NO:2605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1503949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2605:

Met Gly Tyr Phe Asp Ile Pro Val Asp His Val Tyr Gly Gln Pro Val
1 5 10 15
Ile Leu Asp Tyr Leu Ala Ser Lys Thr Ile Cys Ser Asp Asp Leu Val
20 25 30
Val Val Ser Pro Asp Val Gly Gly Val Ala Arg Ala Arg Ala Phe Ala
35 40 45
Lys Lys Leu Ser Asp Ala Pro Leu Ala Ile Val Asp Lys Arg Arg Gln
50 55 60
Gly His Asn Val Ala Glu Val
65 70

(2) INFORMATION FOR SEQ ID NO:2606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..435
(D) OTHER INFORMATION: / Ceres Seq. ID 1503969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2606:

gattttgaaa	ggggtttcat	atgcgctgag	gtaatgaagt	ttgaagatct	gaagaactg	60
ggcagtgaa	ctgctgtaaa	ggctgtcgga	aaatacaagc	aggaggggaa	aacctatgtg	120
gtccaggacg	gggacatcat	ctttttcaaa	ttcaacgtgt	ctgggtggcg	gaagaagtga	180
ataatgtatg	aaagtgttag	catcaaacagt	gttttaactg	ttaccctcgaa	tttctcattc	240
aacagtgttt	acaccttgcc	cgtattttcc	acatttttga	ggctgcttcc	cagtactctt	300
aggttccggg	atcgaaaact	tgtacaacaa	ggctccagac	cgttgaagga	ttgtatttaa	360
taacatgcac	aattgtatgg	cttgtgcttg	agctctcgct	gttaccagaa	gcttagaata	420
gtttgagttc	gttgg					

(2) INFORMATION FOR SEQ ID NO:2607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..59
(D) OTHER INFORMATION: / Ceres Seq. ID 1503970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2607:

Asp	Phe	Glu	Arg	Gly	Phe	Ile	Cys	Ala	Glu	Val	Met	Lys	Phe	Glu	Asp	
1			5						10					15		
Leu	Lys	Glu	Leu	Gly	Ser	Glu	Ser	Ala	Val	Lys	Ala	Ala	Gly	Lys	Tyr	
			20						25					30		
Lys	Gln	Glu	Gly	Lys	Thr	Tyr	Val	Val	Gln	Asp	Gly	Asp	Ile	Ile	Phe	
			35						40					45		
Phe	Lys	Phe	Asn	Val	Ser	Gly	Gly	Lys	Lys							
			50						55							

(2) INFORMATION FOR SEQ ID NO:2608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..48
(D) OTHER INFORMATION: / Ceres Seq. ID 1503971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2608:

Met	Lys	Phe	Glu	Asp	Leu	Lys	Glu	Leu	Gly	Ser	Glu	Ser	Ala	Val	Lys	
1				5					10					15		
Ala	Ala	Gly	Lys	Tyr	Lys	Gln	Glu	Gly	Lys	Thr	Tyr	Val	Val	Gln	Asp	
			20						25					30		
Gly	Asp	Ile	Ile	Phe	Phe	Lys	Phe	Asn	Val	Ser	Gly	Gly	Gly	Lys	Lys	
			35						40					45		

(2) INFORMATION FOR SEQ ID NO:2609:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..58
(D) OTHER INFORMATION: / Ceres Seq. ID 1503972
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2609:
Met Tyr Glu Asp Gly Ser Ile Asn Ser Val Leu Arg Leu Thr Pro Asn
1 5 10 15
Phe Ser Phe Asn Ser Val Tyr Thr Leu Pro Arg Ile Ser Thr Phe Leu
20 25 30
Arg Ser Leu Pro Ser Ser Ser Arg Phe Arg Tyr Arg Lys Leu Val Gln
35 40 45
Gln Gly Ser Arg Pro Leu Lys Asp Leu Tyr
50 55

(2) INFORMATION FOR SEQ ID NO:2610:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..506
(D) OTHER INFORMATION: / Ceres Seq. ID 1503989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2610:

acccgccct gatccactct ccgcttcccg ctccgatoga cctgctccct cccaccacc 60
gagcccatgg cggaccagct caccgacgac cagatcgccg agttcaagga ggccctcagc 120
ctcttgaca aggacgggga tggttgcac acgaccaag agctgggacac tgtcatgccc 180
tcgctggggc aaaatcctac agaggctgag ctccaggaca tgatcaacga ggtcgatgct 240
gatggcaacg gcaccatoga ttcccgagag ttctcaacc ttatggctcg caagatgaag 300
gacaccgact ctgaggaaga gctcaaggag gccctccgtg tggttgacaa ggaccagaac 360
ggcttcatct cggccgccga gctccgccat gtcatgacaa atcttggtga gaagctaact 420
gatgaggagg tggacgagat gatccgtgag gctgatgctg atggtgatgg ccagatcaac 480
tacgaggagt ttgtcaaggt catgat

(2) INFORMATION FOR SEQ ID NO:2611:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..146
(D) OTHER INFORMATION: / Ceres Seq. ID 1503990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2611:

Met Ala Asp Gln Leu Thr Asp Asp Gln Ile Ala Glu Phe Lys Glu Ala
1 5 10 15
Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu
20 25 30
Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu
35 40 45
Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile
50 55 60
Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr

65 70 75 80
Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp
85 90 95
Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn
100 105 110
Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu
115 120 125
Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu Phe Val Lys
130 135 140
Val Met
145

(2) INFORMATION FOR SEQ ID NO:2612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1503991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2612:

Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met
1 5 10 15
Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro Glu
20 25 30
Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr Asp Ser Glu Glu
35 40 45
Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp Gln Asn Gly Phe
50 55 60
Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu Gly Glu Lys
65 70 75 80
Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala Asp Val Asp
85 90 95
Cly Asp Gly Gln Ile Asn Tyr Glu Glu Phe Val Lys Val Met
100 105 110

(2) INFORMATION FOR SEQ ID NO:2613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1503992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2613:

Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro
1 5 10 15
Glu Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr Asp Ser Glu
20 25 30
Glu Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp Gln Asn Gly
35 40 45
Phe Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu Gly Glu
50 55 60
Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala Asp Val
65 70 75 80
Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu Phe Val Lys Val Met
85 90 95

(2) INFORMATION FOR SEQ ID NO:2614:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..479
(D) OTHER INFORMATION: / Ceres Seq. ID 1504001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2614:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2615:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..77
(D) OTHER INFORMATION: / Ceres Seq. ID 1504002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2615:

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524
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(2) INFORMATION FOR SEQ ID NO:2616:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..79
(D) OTHER INFORMATION: / Ceres Seq. ID 1504003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2616:

Gln	Arg	Thr	Ser	Pro	Pro	Ser	Ser	Ala	Ala	Ala	Glu	Asp	Gly	Arg	Arg
1			5					10					15		
Arg	Gly	Tyr	Gly	Arg	Leu	Leu	Ala	Pro	Met	Ala	His	Glu	Lys	Lys	Leu
			20					25					30		
Ser	Asn	Pro	Met	Arg	Glu	Ile	Lys	Val	Gln	Lys	Leu	Val	Leu	Asn	Ile
			35					40					45		
Ser	Val	Gly	Glu	Ser	Gly	Asp	Arg	Leu	Thr	Arg	Ala	Ala	Lys	Val	Leu

50 55 60
Glu Gln Leu Ser Gly Gln Thr Pro Val Phe Ser Lys Gly Glu Tyr
65 70 75

(2) INFORMATION FOR SEQ ID NO:2617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: linear
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1504004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2617:

Asn Ala His Leu His Arg Arg Pro Pro Pro Lys Thr Glu Gly Glu
1 5 10 15
Glu Gly Thr Ala Val Ser Ser Pro Pro Trp Pro Thr Arg Arg Ser Cys
20 25 30
Pro Thr Arg Cys Gly Arg Ser Arg Cys Arg Ser Ser Ser Ile Ser
35 40 45
Pro Ser Gly Arg Ala Ala Thr Val Ser Pro Ala Pro Gln Arg Cys Ser
50 55 60
Ser Ser Ser Ala Ala Arg Pro Pro Ser Ser Pro Arg Val Ser Thr Glu
65 70 75 80
Phe Ser Arg Leu Arg Phe Met Pro Ser Ala Asp Gly Val Leu Pro Ser
85 90 95
Ala Cys Trp Arg Cys Trp Phe Val Leu Gln Arg Gly Thr Arg Cys Gly
100 105 110
Arg Ser Ala Ser Gly Val Thr Arg Arg Ser Pro Ala Thr Ser Arg
115 120 125

(2) INFORMATION FOR SEQ ID NO:2618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2618:

atcgagacac acacagaact tctctgtctg cctactaat acagctagct agctgccctc 60
ttagggtatac tgtgatggcc acaaccttgt cctccacagt agtagttgca cttggtgacc 120
tctctctcttg ctccttggtaa cgtgtggctc gtgcgcgagg ccggtgagct ttaacgcctc 180
cgacctcacc gcgatcccc gctgggatgc tggcaggggc acctgttacg gtgcgccacc 240
cggcgccgcc ctgatgacga cgtgtgtgcc tgtggattca agaactgtgaa tctgcgccgc 300
ttctcgggcaa tgacgtctgt cggaacagag cccctgttca aggcacggcaa gggctgcggc 360
tctgtctacc agatacagatg ccaaaaccac ccggcctgtg ccggcaaccc agagacggtg 420
atcatactg acatgaacta ctaccccggtg gccaaagtacc acctcgacct yagcggc

(2) INFORMATION FOR SEQ ID NO:2619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: linear
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45

(D) OTHER INFORMATION: / Ceres Seq. ID 1504017
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2619:
Arg Asp Thr His Arg Thr Ser Pro Val Gly Leu Leu Ile Gln Leu Ala
1 5 10 15
Ser Cys Pro Leu Arg Tyr Thr Val Met Ala Thr Thr Leu Ser Ser Thr
20 25 30
Val Val Val Ala Leu Gly Asp Leu Ser Ser Cys Ser Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:2620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1504018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2620:

Met Thr Ser Cys Gly Asn Glu Pro Leu Phe Lys Asp Gly Lys Gly Cys
1 5 10 15
Gly Ser Cys Tyr Gln Ile Arg Cys Gln Asn His Pro Ala Cys Ser Gly
20 25 30
Asn Pro Glu Thr Val Ile Ile Thr Asp Met Asn Tyr Tyr Pro Val Ala
35 40 45
Lys Tyr His Phe Asp Xaa Ser Gly
50 55

(2) INFORMATION FOR SEQ ID NO:2621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..430

(D) OTHER INFORMATION: / Ceres Seq. ID 1504025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2621:

catgtggttg tgggcaactgt gaaagctctt tggcactca cagaagccct agaataagaa 60
tattgtctaatt gatgagaagt aactaaaaca atatcataca attgcagtgct tctctccaat 120
agtttgagagg gtatgctcct tggaagattt ttggtaggaa cagggatggg attgggtcca 180
ccagtagctt caactttatat aacggaggtt tctccttcta cagtgagggg tacatatggt 240
agctttgttc agattgcaac ctgccttggga attatagtat cactactcat tggtaacact 300
gtcaaagata ttgatagatg gtggagagtg tgtttctggg ttgccgttat cccagcaact 360
ttacaagctc tcggatggga gttttgtgct gagagccctc agtggcttta taagtgtgga 420
aaaaaagtg

(2) INFORMATION FOR SEQ ID NO:2622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1504026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2622:

Met Leu Leu Gly Arg Phe Leu Val Gly Thr Gly Met Gly Leu Gly Pro

1 5 10 15
Pro Val Ala Ser Leu Tyr Ile Thr Glu Val Ser Pro Ser Thr Val Arg
20 25 30
Gly Thr Tyr Gly Ser Phe Val Gln Ile Ala Thr Cys Leu Gly Ile Ile
35 40 45
Val Ser Leu Leu Ile Gly Thr Pro Val Lys Asp Ile Asp Arg Trp Trp
50 55 60
Arg Val Cys Phe Trp Val Ala Val Ile Pro Ala Thr Leu Gln Ala Leu
65 70 75 80
Gly Met Glu Phe Cys Ala Glu Ser Pro Gln Trp Leu Tyr Lys Cys Gly
85 90 95
Lys Ile Ser

(2) INFORMATION FOR SEQ ID NO:2623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2623:

Met Gly Leu Gly Pro Pro Val Ala Ser Leu Tyr Ile Thr Glu Val Ser
1 5 10 15
Pro Ser Thr Val Arg Gly Thr Tyr Gly Ser Phe Val Gln Ile Ala Thr
20 25 30
Cys Leu Gly Ile Ile Val Ser Leu Leu Ile Gly Thr Pro Val Lys Asp
35 40 45
Ile Asp Arg Trp Trp Arg Val Cys Phe Trp Val Ala Val Ile Pro Ala
50 55 60
Thr Leu Gln Ala Leu Gly Met Glu Phe Cys Ala Glu Ser Pro Gln Trp
65 70 75 80
Leu Tyr Lys Cys Gly Lys Ile Ser
85

(2) INFORMATION FOR SEQ ID NO:2624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..462
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2624:

tattatcaga gaacaagag ctgtgcttct ctgttgctc attgctctgg cagaagctca 60
tagcttctcc tgaatgcag atgtctgcag aaagtacatc agctcaccaa ggatgggagga 120
aggttgttga tgcactttgt gatgtcgttt cagcctcacc aaccaaggca tcagctgcta 180
tcgttctcca ggcagagaag gacttgcagc ctgtgattgc tagagatgac gaacaaggctc 240
agaagatgtg gagagtcacac cagcgtatag tgaagcttat agctgagctt atgaggaacc 300
atgacagccc tgaagcgttg gtgatactcg ctagtgcctc cgaccttcta cttcgtgcta 360
ccgatggaa tgcctgcgat ggtgaagctt gtactttgcc acagcttgag cttctggaag 420
tgaccgcctg gctgtccat cttatcatcg aatggggaga tc

(2) INFORMATION FOR SEQ ID NO:2625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..153
(D) OTHER INFORMATION: / Ceres Seq. ID 1504037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2625:

Leu	Ser	Glu	Lys	Gln	Glu	Leu	Cys	Phe	Ser	Val	Val	Ser	Leu	Leu	Trp	
1			5					10					15			
Gln	Lys	Leu	Ile	Ala	Ser	Pro	Glu	Met	Gln	Met	Ser	Ala	Glu	Ser	Thr	
			20					25					30			
Ser	Ala	His	Gln	Gly	Trp	Arg	Lys	Val	Val	Asp	Ala	Leu	Cys	Asp	Val	
			35					40				45				
Val	Ser	Ala	Ser	Pro	Thr	Lys	Ala	Ser	Ala	Ala	Ile	Val	Leu	Gln	Ala	
			50				55				60					
Glu	Lys	Asp	Leu	Gln	Pro	Trp	Ile	Ala	Arg	Asp	Asp	Glu	Gln	Gly	Gln	
			65			70				75				80		
Lys	Met	Trp	Arg	Val	Asn	Gln	Arg	Ile	Val	Lys	Leu	Ile	Ala	Glu	Leu	
				85				90					95			
Met	Arg	Asn	His	Asp	Ser	Pro	Glu	Ala	Leu	Val	Ile	Leu	Ala	Ser	Ala	
				100				105					110			
Ser	Asp	Leu	Leu	Leu	Arg	Ala	Thr	Asp	Gly	Met	Leu	Val	Asp	Gly	Glu	
				115				120					125			
Ala	Cys	Thr	Leu	Pro	Gln	Leu	Glu	Leu	Leu	Glu	Val	Thr	Ala	Arg	Ala	
				130			135					140				
Val	His	Leu	Ile	Ile	Glu	Trp	Gly	Asp								
					145		150									

(2) INFORMATION FOR SEQ ID NO:2626:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..129
(D) OTHER INFORMATION: / Ceres Seq. ID 1504038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2626:

Met	Gln	Met	Ser	Ala	Glu	Ser	Thr	Ser	Ala	His	Gln	Gly	Trp	Arg	Lys	
1				5					10					15		
Val	Val	Asp	Ala	Leu	Cys	Asp	Val	Val	Ser	Ala	Ser	Pro	Thr	Lys	Ala	
				20				25					30			
Ser	Ala	Ala	Ile	Val	Leu	Gln	Ala	Glu	Lys	Asp	Leu	Gln	Pro	Trp	Ile	
				35				40				45				
Ala	Arg	Asp	Asp	Glu	Gln	Gly	Gln	Lys	Met	Trp	Arg	Val	Asn	Gln	Arg	
				50			55				60					
Ile	Val	Lys	Leu	Ile	Ala	Glu	Leu	Met	Arg	Asn	His	Asp	Ser	Pro	Glu	
				65		70			75					80		
Ala	Leu	Val	Ile	Leu	Ala	Ser	Ala	Ser	Asp	Leu	Leu	Leu	Arg	Ala	Thr	
				85				90					95			
Asp	Gly	Met	Leu	Val	Asp	Gly	Glu	Ala	Cys	Thr	Leu	Pro	Gln	Leu	Glu	
				100				105					110			
Leu	Leu	Glu	Val	Thr	Ala	Arg	Ala	Val	His	Leu	Ile	Ile	Glu	Trp	Gly	
				115			120						125			

Asp

(2) INFORMATION FOR SEQ ID NO:2627:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..127
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504039
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2627:
Met Ser Ala Glu Ser Thr Ser Ala His Gln Gly Trp Arg Lys Val Val
1 5 10 15
Asp Ala Leu Cys Asp Val Val Ser Ala Ser Pro Thr Lys Ala Ser Ala
 20 25 30
Ala Ile Val Leu Gln Ala Glu Lys Asp Leu Gln Pro Trp Ile Ala Arg
 35 40 45
Asp Asp Glu Gln Gly Gln Lys Met Trp Arg Val Asn Gln Arg Ile Val
 50 55 60
Lys Leu Ile Ala Glu Leu Met Arg Asn His Asp Ser Pro Glu Ala Leu
65 70 75 80
Val Ile Leu Ala Ser Ala Ser Asp Leu Leu Leu Arg Ala Thr Asp Gly
 85 90 95
Met Leu Val Asp Gly Glu Ala Cys Thr Leu Pro Gln Leu Glu Leu Leu
 100 105 110
Glu Val Thr Ala Arg Ala Val His Leu Ile Ile Glu Trp Gly Asp
 115 120 125

(2) INFORMATION FOR SEQ ID NO:2628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..463

(D) OTHER INFORMATION: / Ceres Seq. ID 1504044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2628:

aaatctctct ctctctctcg cctcgcccttg gtgttcacgc cgtcgctagc gcctgckcct 60
gccasggcka asttctgcc ctcccggcg ccgggctcg gtctgctcg gccaggaaga 120
tggctggcgg cttcagggta ctgcactcgg tcaggccttt tctggctttc ttgccatakk 180
ttgcagagcg cggatagkaa gataccgttc agagaaaaag ttatctacac tgttatttcc 240
ctcttcattt tcttggtctg cagccagctc ccaactatg gcatttcatt aacaactgga 300
gctgacccct tctaactgat cgtgtttatc ctgcacatca accgtggcac tgtgatggag 360
ttgggtatta ctccaattgt gacatctggg atggtaatgc aacttcttgt tggatcgaag 420
atcattttaa gttgacaaca gtgtgagaka ggaatgtgct ctg

(2) INFORMATION FOR SEQ ID NO:2629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1504045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2629:

Lys Ser Leu Ser Ser Pro Arg Leu Ala Leu Val Phe Thr Pro Ser Leu
1 5 10 15
Ala Pro Xaa Pro Ala Xaa Xaa Xaa Phe Leu Pro Ser Pro Ala Pro Gly
 20 25 30

Ser Gly Arg Arg Arg Pro Gly Arg Trp Leu Ala Ala Ser Gly Tyr Cys
35 40 45
Ile Trp Ser Gly Leu Phe Trp Leu Ser Cys His Xaa Leu Gln Ser Ala
50 55 60
Asp Xaa Lys Ile Pro Phe Arg Glu Lys Val Ile Tyr Thr Val Ile Ser
65 70 75 80
Leu Phe Ile Phe Leu Val Cys Ser Gln Leu Pro Leu Tyr Gly Ile His
85 90 95
Ser Thr Thr Gly Ala Asp Pro Phe Tyr Trp Met Arg Val Ile Leu Ala
100 105 110
Ser Asn Arg Gly Thr Val Met Glu Leu Gly Ile Thr Pro Ile Val Thr
115 120 125
Ser Gly Met Val Met Gln Leu Leu Val Gly Ser Lys Ile Ile
130 135 140

(2) INFORMATION FOR SEQ ID NO:2630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..502
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2630:

atctgaagga	tatggcttat	catggagtat	ttttaaagag	ggacatttgt	taagtgggtc	60
tgacgatgct	caaatttgct	tgtgggacat	taaaagcaaat	agtagaaaca	aaagtcttga	120
cgccctgcag	atttttaagc	atcatgatgg	tgtcgttgaa	gatgttgctt	ggcacttgag	180
gcacgagtac	ttatttgggt	cagttgggtga	cgattatcat	cttttgattt	gggacctgcg	240
gtctcccgcc	cctactaac	ctgttcagtc	agtgtggcgc	caccagggtg	agggtgaactg	300
cctgtgctttt	aaccgcgttca	acgaatgggt	tgttgcaact	ggttctactg	acaagactgt	360
caaattattt	gatcttagga	agattgatac	ttctctgcac	acctttgact	gtcacaaaga	420
ggaagttttt	caagttggat	ggagtccaaa	gaatgaaact	gtacttgcat	cctgtgtgtc	480
gggcagaagg	ctcatggtct	gg				

(2) INFORMATION FOR SEQ ID NO:2631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2631:

Ser	Glu	Gly	Tyr	Gly	Leu	Ser	Trp	Ser	Ile	Phe	Lys	Glu	Gly	His	Leu
1				5					10					15	
Leu	Ser	Gly	Ser	Asp	Ala	Gln	Ile	Cys	Leu	Trp	Asp	Ile	Lys	Ala	
			20				25					30			
Asn	Ser	Arg	Asn	Lys	Ser	Leu	Asp	Ala	Leu	Gln	Ile	Phe	Lys	His	His
			35				40					45			
Asp	Gly	Val	Val	Glu	Asp	Val	Ala	Trp	His	Leu	Arg	His	Glu	Tyr	Leu
			50				55				60				
Phe	Gly	Ser	Val	Gly	Asp	Asp	Tyr	His	Leu	Leu	Ile	Trp	Asp	Leu	Arg
			65				70				75			80	
Ser	Pro	Ala	Pro	Thr	Lys	Pro	Val	Gln	Ser	Val	Val	Ala	His	Gln	Gly
				85					90					95	
Glu	Val	Asn	Cys	Leu	Ala	Phe	Asn	Pro	Phe	Asn	Glu	Trp	Val	Val	Ala
			100					105					110		

Thr Gly Ser Thr Asp Lys Thr Val Lys Leu Phe Asp Leu Arg Lys Ile
115 120 125
Asp Thr Ser Leu His Thr Phe Asp Cys His Lys Glu Glu Val Phe Gln
130 135 140
Val Gly Trp Ser Pro Lys Asn Glu Thr Val Leu Ala Ser Cys Cys Leu
145 150 155 160
Gly Arg Arg Leu Met Val Trp
165

(2) INFORMATION FOR SEQ ID NO:2632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..514
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2632:

attccgttcc	gagagccaaa	aactccactg	ctttcatcaa	ctccggcgac	ttggagaaga	60
cgaaktccag	aatccgatcg	gaagtttggt	gctcgcgccct	tgacggattg	atttcggtgc	120
gcccgatggg	caggcgttcc	gcaagctgtt	cgattccttc	ttcggcacca	gcgagatgag	180
ggttgtgatg	cttggctctg	atgctgccgg	taaaaccacc	atattgtaca	agctgcataa	240
cgggggaggtt	ttgtctgactg	ttcccacgat	tggtttcaac	gtcgagaaaag	ttcaatacat	300
gaatgtgatg	tttactgtgt	gggatgttgg	tgcccaagaa	aagttgaggg	tgactacgtc	360
cgcaaaaggag	atagttttgg	gtatttctcc	tttgaggagg	gtacagtgat	atgcgtcttc	420
gagaaggacg	ccatccaatt	tgacgctgat	ctcgtggcaa	acagcgaaaag	gtcactggag	480
accaagtccc	ggatctgcag	aaagtttcgc	tcgg			

(2) INFORMATION FOR SEQ ID NO:2633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2633:

Met	Gly	Gln	Ala	Phe	Arg	Lys	Leu	Phe	Asp	Ser	Phe	Phe	Gly	Thr	Ser	
1		5					10						15			
Glu	Met	Arg	Val	Val	Met	Leu	Gly	Leu	Asp	Ala	Ala	Gly	Lys	Thr	Thr	
		20					25						30			
Ile	Leu	Tyr	Lys	Leu	His	Ile	Gly	Glu	Val	Leu	Ser	Thr	Val	Pro	Thr	
		35					40						45			
Ile	Gly	Phe	Asn	Val	Glu	Lys	Val	Gln	Tyr	Lys	Asn	Val	Met	Phe	Thr	
		50					55					60				
Val	Trp	Asp	Val	Gly	Gly	Gln	Glu	Lys	Leu	Arg	Val	Thr	Thr	Ser	Ala	
		65					70			75				80		
Lys	Glu	Met	Ser	Leu	Gly	Ile	Ser	Pro	Leu	Glu	Gly	Val	Gln			
		85					90									

(2) INFORMATION FOR SEQ ID NO:2634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..77
(D) OTHER INFORMATION: / Ceres Seq. ID 1504100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2634:

Met	Arg	Val	Val	Met	Leu	Gly	Leu	Asp	Ala	Ala	Gly	Lys	Thr	Ile
1				5				10					15	
Leu	Tyr	Lys	Leu	His	Ile	Gly	Glu	Val	Leu	Ser	Thr	Val	Pro	Thr
			20					25					30	
Gly	Phe	Asn	Val	Glu	Lys	Val	Gln	Tyr	Lys	Asn	Val	Met	Phe	Thr
			35					40					45	
Trp	Asp	Val	Gly	Gly	Gln	Glu	Lys	Leu	Arg	Val	Thr	Ser	Ala	Lys
			50					55					60	
Glu	Met	Ser	Leu	Gly	Ile	Ser	Pro	Leu	Glu	Gly	Val	Gln		
65					70								75	

(2) INFORMATION FOR SEQ ID NO:2635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..73
(D) OTHER INFORMATION: / Ceres Seq. ID 1504101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2635:

Met	Leu	Gly	Leu	Asp	Ala	Ala	Gly	Lys	Thr	Thr	Ile	Leu	Tyr	Lys	Leu
1				5				10					15		
His	Ile	Gly	Glu	Val	Leu	Ser	Thr	Val	Pro	Thr	Ile	Gly	Phe	Asn	Val
			20					25					30		
Glu	Lys	Val	Gln	Tyr	Lys	Asn	Val	Met	Phe	Thr	Val	Trp	Asp	Val	Gly
			35					40					45		
Gly	Gln	Glu	Lys	Leu	Arg	Val	Thr	Thr	Ser	Ala	Lys	Glu	Met	Ser	Leu
			50					55					60		
Gly	Ile	Ser	Pro	Leu	Glu	Gly	Val	Gln							
65					70										

(2) INFORMATION FOR SEQ ID NO:2636:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..460
(D) OTHER INFORMATION: / Ceres Seq. ID 1504102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2636:

atatatactc	ctgttgcgta	gaatcggcac	aagggtgcac	gttcaggagg	agctctcggtg	60
gcgtcctagt	ctgtggaagg	tccaaagaag	aagatggacg	gcgagatgga	cgaggacggtt	120
ctcacggaga	tcttcgcgag	gtgcgcgtgc	aggtcgctgtg	cgcggttcca	gtcgcgtgtcc	180
acgtcgtgtg	gcgcatacat	tccagcgact	acctccgcgc	ccggtgtccg	ctcatcacgt	240
cgggcggtgt	ctaccacgat	ggtggcaggga	ggcagcagtc	gtacacgtac	gcgtgcgcgt	300
caggcggtgc	cgcgcgcggc	ggcgcatgtg	cggaggccgc	ggacatgcgc	ttcttcccg	360
gccacagagc	gtccaccatc	atcgacggtc	gcaacggcct	gctgctctac	tacgcgtccc	420
gcccgcgcg	ttccacgtcg	tgagcccgac	cacgcggcgg			

(2) INFORMATION FOR SEQ ID NO:2637:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..153
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2637:
Tyr Ile Leu Leu Leu Arg Arg Ile Gly Thr Arg Val His Val Gln Glu
1 5 10 15
Glu Leu Ser Trp Arg Pro Ser Leu Trp Lys Val Gln Arg Arg Arg Trp
20 25 30
Thr Ala Arg Trp Thr Arg Thr Phe Ser Arg Arg Ser Ser Arg Gly Cys
35 40 45
Arg Ala Gly Arg Trp Arg Gly Ser Ser Ala Cys Pro Arg Arg Ala Ala
50 55 60
His His Leu Gln Arg Leu Pro Pro Pro Pro Ala Ala His His Val
65 70 75 80
Gly Arg Ala Leu Pro Arg Trp Trp Gln Glu Ala Ala Val Val His Val
85 90 95
Arg Val Arg Val Arg Arg Arg Arg Arg Arg Ile Gly Gly Gly
100 105 110
Arg Gly His Ala Leu Leu Pro Ala Pro Arg Asp Val His His Arg
115 120 125
Arg Leu Gln Arg Pro Ala Ala Leu Leu Arg Val Pro Pro Gly Ala Phe
130 135 140
His Val Val Ser Pro Thr Thr Arg Arg
145 150

(2) INFORMATION FOR SEQ ID NO:2638:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 146 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..146
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2638:
Ile Tyr Ser Cys Cys Val Glu Ser Ala Gln Gly Cys Thr Phe Arg Arg
1 5 10 15
Ser Ser Arg Gly Val Leu Val Cys Gly Arg Ser Lys Glu Glu Asp Gly
20 25 30
Arg Arg Asp Gly Arg Gly Arg Ser His Gly Asp Pro Arg Glu Ala Ala
35 40 45
Val Gln Val Ala Gly Ala Val Pro Val Arg Val His Val Val Arg Arg
50 55 60
Ile Ile Ser Ser Asp Tyr Leu Arg Arg Arg Leu Pro Leu Ile Thr Ser
65 70 75 80
Gly Val Leu Tyr His Asp Gly Gly Arg Arg Gln Gln Ser Tyr Thr Tyr
85 90 95
Ala Cys Ala Ser Gly Gly Gly Gly Gly Gly Ala Leu Ala Glu Ala
100 105 110
Ala Asp Met Arg Phe Phe Pro Arg His Glu Thr Ser Thr Ile Ile Asp
115 120 125
Gly Cys Asn Gly Leu Leu Leu Tyr Tyr Ala Ser Arg Pro Ala Arg Ser
130 135 140
Thr Ser
145

(2) INFORMATION FOR SEQ ID NO:2639:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..122
(D) OTHER INFORMATION: / Ceres Seq. ID 1504105
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2639:
Met Asp Gly Glu Met Asp Glu Asp Val Leu Thr Glu Ile Leu Ala Arg
1 5 10 15
Leu Pro Cys Arg Ser Leu Ala Arg Phe Gln Cys Val Ser Thr Ser Cys
20 25 30
Gly Ala Ser Ser Pro Ala Thr Thr Ser Ala Ala Gly Cys Arg Ser Ser
35 40 45
Arg Arg Ala Cys Ser Thr Thr Met Val Ala Gly Gly Ser Ser Arg Thr
50 55 60
Arg Thr Arg Ala Arg Gln Ala Ala Ala Ala Ala Ala His Trp Arg
65 70 75 80
Arg Pro Arg Thr Cys Ala Ser Ser Arg Ala Thr Arg Arg Pro Pro Ser
85 90 95
Ser Thr Ala Ala Thr Ala Cys Cys Ser Thr Thr Arg Pro Ala Arg Arg
100 105 110
Val Pro Arg Arg Glu Pro Asp His Ala Ala
115 120

(2) INFORMATION FOR SEQ ID NO:2640:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..469
(D) OTHER INFORMATION: / Ceres Seq. ID 1504107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2640:

aactgaggct gtgcgcttcg ttcagttcag ttcattccgt ttcttggttg cgaggtgcgag 60
agagactgag agaggatgtc gtgctgcgga ggcaactgcg ggtgcggcto cggtcgcaag 120
tgcggcaacg gctgcggagg gtgcagcaag atgtaccgcg agaatgggta tcgacctcgt 180
cgccggtggg aggaataaga agaccaagcg cactgcgccc aagtctgacg atgtctacct 240
caagctctct gtcaagctct accgtttctt ggtcaggagg accaagagca atttcaacgc 300
tgtcattctc aagaggcttt tcatgagtaa aaccaaccga ccaccaatct ccatgcgcgcg 360
ccttgccaag tttatggaag gaaaggagaa gaacattgct gtcattgttg gcacagtcac 420
agatgacaaa aggatccagg aggttccagc aatgaaggtt actgcacctg

(2) INFORMATION FOR SEQ ID NO:2641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..156
(D) OTHER INFORMATION: / Ceres Seq. ID 1504108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2641:

Thr Ala Ala Val Arg Phe Val Gln Phe Ser Ser Ser Val Phe Leu Phe
1 5 10 15
Ala Arg Ser Arg Glu Thr Glu Arg Gly Cys Arg Ala Ala Glu Ala Thr

20 25 30
Ala Gly Ala Ala Pro Ala Ala Ser Ala Ala Thr Ala Ala Glu Gly Ala
35 40 45
Ala Arg Cys Thr Arg Arg Met Gly Ile Asp Leu Val Ala Gly Gly Arg
50 55 60
Asn Lys Lys Thr Lys Arg Thr Ala Pro Lys Ser Asp Asp Val Tyr Leu
65 70 75 80
Lys Leu Leu Val Lys Leu Tyr Arg Phe Leu Val Arg Arg Thr Lys Ser
85 90 95
Asn Phe Asn Ala Val Ile Leu Lys Arg Leu Phe Met Ser Lys Thr Asn
100 105 110
Arg Pro Pro Ile Ser Met Arg Arg Leu Val Lys Phe Met Glu Gly Lys
115 120 125
Glu Lys Asn Ile Ala Val Ile Val Gly Thr Val Thr Asp Asp Lys Arg
130 135 140
Ile Gln Glu Val Pro Ala Met Lys Val Thr Ala Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO:2642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2642:

Leu Arg Leu Cys Ala Ser Phe Ser Ser Val His Pro Cys Ser Cys Leu
1 5 10 15
Arg Gly Arg Glu Arg Leu Arg Glu Asp Val Val Leu Arg Arg Gln Leu
20 25 30
Arg Val Arg Leu Arg Leu Gln Val Arg Gln Arg Leu Arg Arg Val Gln
35 40 45
Gln Asp Val Pro Ala Glu Trp Val Ser Thr Ser Ser Pro Val Gly Gly
50 55 60
Ile Arg Arg Pro Ser Ala Leu Arg Pro Ser Leu Thr Met Ser Thr Ser
65 70 75 80
Ser Ser Ser Ser Ser Ser Thr Val Ser Trp Ser Gly Gly Pro Arg Ala
85 90 95
Ile Ser Thr Leu Ser Phe Ser Arg Gly Phe Ser
100 105

(2) INFORMATION FOR SEQ ID NO:2643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2643:

Met Gly Ile Asp Leu Val Ala Gly Gly Arg Asn Lys Lys Thr Lys Arg
1 5 10 15
Thr Ala Pro Lys Ser Asp Asp Val Tyr Leu Lys Leu Val Lys Leu
20 25 30
Tyr Arg Phe Leu Val Arg Arg Thr Lys Ser Asn Phe Asn Ala Val Ile
35 40 45

Leu Lys Arg Leu Phe Met Ser Lys Thr Asn Arg Pro Pro Ile Ser Met
50 55 60
Arg Arg Leu Val Lys Phe Met Glu Gly Lys Glu Lys Asn Ile Ala Val
65 70 75 80
Ile Val Gly Thr Val Thr Asp Asp Lys Arg Ile Gln Glu Val Pro Ala
85 90 95
Met Lys Val Thr Ala Leu
100

(2) INFORMATION FOR SEQ ID NO:2644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..437
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2644:

acataccacg cgcacagctt tccatcaga ggcgcgagtc ctgctctgat ggccgaccgac	60
gtggctgaga ctcccgcgcc gttggtggat ggcgcgccctg aggcgcgccgc ggacacccccc	120
gcggcgctgc tggtagcgcg amscggccaa ggccaagaag gccacagcgc cgaagaagcgc	180
cgccassccg acccatccgc cgtacgcgca gatggtctcg gaggcgatcg cgtcgctcaa	240
ggagaggacg gggctccagca gcttgctat tgccaagtgc ttggaggaca agcacaagga	300
caagctcccg cccaacttcc gcaagcttct gaacgttcag ctaagaagc tcgtcgccgcg	360
cgccaagctg accaaggtga agaactcgta caagctgtcg tccgccacca agccaaaagg	420
cgcccccga gaagacc	

(2) INFORMATION FOR SEQ ID NO:2645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2645:

Thr Ser Pro Ala His Ser Phe Pro His Arg Gly Pro Ser Pro Ala Leu	
1 5 10 15	
Met Ala Thr Asp Val Ala Glu Thr Pro Ala Pro Leu Val Asp Ala Ala	
20 25 30	
Pro Glu Ala Pro Ala Asp Thr Pro Ala Ala Leu Leu Leu Thr Arg Xaa	
35 40 45	
Gly Gln Gly Gln Glu Gly His Ser Ala Glu Glu Ala Arg Xaa Xaa Asp	
50 55 60	
Pro Ser Ala Val Arg Arg Asp Gly Leu Gly Gly Asp Arg Val Ala Gln	
65 70 75 80	
Gly Glu Asp Gly Val Gln Gln Leu Cys Tyr Cys Gln Val Leu Gly Gly	
85 90 95	
Gln Ala Gln Gly Gln Ala Pro Ala Gln Leu Pro Gln Ala Ser Glu Arg	
100 105 110	
Ser Ala Gln Glu Ala Arg Arg Arg Gln Ala Asp Gln Gly Glu Glu	
115 120 125	
Leu Val Gln Ala Val Val Arg His Gln Ala Lys Arg Pro Pro Arg Arg	
130 135 140	

Arg
145

(2) INFORMATION FOR SEQ ID NO:2646:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..129
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504113
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2646:
Met Ala Thr Asp Val Ala Glu Thr Pro Ala Pro Leu Val Asp Ala Ala
1 5 10 15
Pro Glu Ala Pro Ala Asp Thr Pro Ala Ala Leu Leu Leu Thr Arg Xaa
 20 25 30
Gly Gln Gly Gln Glu Gly His Ser Ala Glu Glu Ala Arg Xaa Xaa Asp
 35 40 45
Pro Ser Ala Val Arg Arg Asp Gly Leu Gly Gly Asp Arg Val Ala Gln
 50 55 60
Gly Glu Asp Gly Val Gln Gln Leu Cys Tyr Cys Gln Val Leu Gly Gly
65 70 75 80
Gln Ala Gln Gly Gln Ala Pro Ala Gln Leu Pro Gln Ala Ser Glu Arg
 85 90 95
Ser Ala Gln Glu Ala Arg Arg Arg Arg Gln Ala Asp Gln Gly Glu Glu
 100 105 110
Leu Val Gln Ala Val Val Arg His Gln Ala Lys Arg Pro Pro Arg Arg
 115 120 125
Arg

(2) INFORMATION FOR SEQ ID NO:2647:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..75
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504114
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2647:
Met Val Ser Glu Ala Ile Ala Ser Leu Lys Glu Arg Thr Gly Ser Ser
1 5 10 15
Ser Phe Ala Ile Ala Lys Phe Leu Glu Asp Lys His Lys Asp Lys Leu
 20 25 30
Pro Pro Asn Phe Arg Lys Leu Leu Asn Val Gln Leu Lys Lys Leu Val
 35 40 45
Ala Gly Gly Lys Leu Thr Lys Val Lys Asn Ser Tyr Lys Leu Ser Ser
 50 55 60
Ala Thr Lys Pro Lys Gly Arg Pro Glu Glu Asp
65 70 75

(2) INFORMATION FOR SEQ ID NO:2648:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..257

(D) OTHER INFORMATION: / Ceres Seq. ID 1504119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2648:

cacccaaaag cgagagscgn gggctggtgg ctgctgacca aaacgaatcc ctcgcccgcg	60
cttccccgaaa tcccccaaat ccggagccaa tgccgcccgc cctccccacc ccggcggcac	120
ncaaaactat cgcgcacttc ttcgcgcgcc ccgccaagcg cctgtgcgtg ccccgccgcg	180
ctccctctcc tcaactctct ctccctctct gctgtgcggc gagcagcgcc gtcgcgscga	240
caccaaactg gcgctcg	

(2) INFORMATION FOR SEQ ID NO:2649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1504120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2649:

His Pro Lys Ala Arg Xaa Xaa Gly Trp Trp Leu Leu Thr Lys Thr Asn	
1 5 10 15	
Pro Ser Pro Pro Leu Pro Glu Ile Pro Gln Ile Arg Ser Gln Cys Arg	
20 25 30	
Arg Pro Leu Pro Pro Arg Arg His Xaa Lys Leu Ser Pro Thr Ser Ser	
35 40 45	
Arg Ala Pro Pro Ser Ala Cys Ala Cys Pro Gly Arg Leu Pro Leu Leu	
50 55 60	
Gln Leu Leu Ser Leu Leu Ala Val Ala Gly Ala Ala Pro Ser Xaa Arg	
65 70 75 80	
His Gln Pro Gly Ala	
85	

(2) INFORMATION FOR SEQ ID NO:2650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1504121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2650:

Pro Lys Ser Glu Xaa Xaa Gly Leu Val Ala Ala Asp Gln Asn Glu Ser	
1 5 10 15	
Leu Ala Ala Ala Ser Arg Asn Pro Pro Asn Pro Glu Pro Met Pro Pro	
20 25 30	
Ser Pro Pro Thr Pro Ala Ala Xaa Lys Thr Ile Ala Asp Phe Phe Ala	
35 40 45	
Arg Pro Ala Lys Arg Leu Cys Val Pro Arg Pro Pro Pro Ser Pro Pro	
50 55 60	
Thr Pro Leu Pro Pro Arg Cys Arg Arg Ser Ser Ala Val Ala Xaa Thr	
65 70 75 80	
Pro Thr Trp Arg Ser	
85	

(2) INFORMATION FOR SEQ ID NO:2651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..56
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504122
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2651:
Met Pro Pro Ser Pro Pro Thr Pro Ala Ala Xaa Lys Thr Ile Ala Asp
1 5 10 15
Phe Phe Ala Arg Pro Ala Lys Arg Leu Cys Val Pro Arg Pro Pro Pro
 20 25 30
Ser Pro Pro Thr Pro Leu Pro Pro Arg Cys Arg Arg Ser Ser Ala Val
 35 40 45
Ala Xaa Thr Pro Thr Trp Arg Ser
50 55
(2) INFORMATION FOR SEQ ID NO:2652:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 426 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..426
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504161
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2652:
acgcgcctcc tctcgccctc gctcgcgcgc cgccgcgcgc gccgcacaw gccccgcgcc 60
cgccgctgcg tgaggtagac accaatccgc cgccatgdgg sstatgcaca gccgcgggaa 120
ctggaggaaac tgagcggtgg ggcconcgcg gccaaagtat cctgttcgct accgtgttgt 180
ttacctagt ccagagtgtt tatcttcggt cgctcgtgt ttgtgtgttc caatctgtgt 240
ttttgattga aggtcgctct gtgtcagttg ttagtctgt gttcacctc gggtccagca 300
gacccatgca tcaccagca tggactgcgg atcgatgggt gctgttacc ccgtcagtt 360
tattctaagt taaatccaa ggaataaaat ggtgctctt ggtgctgcaa aatggttgtg 420
ctcatg
(2) INFORMATION FOR SEQ ID NO:2653:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..121
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504162
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2653:
Ala Pro Pro Leu Ala Leu Ala Pro Pro Pro Pro Pro His Xaa
1 5 10 15
Ala Pro Ala Pro Pro Ser Pro Glu Val Asp Thr Asn Pro Pro Pro Xaa
 20 25 30
Xaa Xaa Cys Thr Ala Ala Gly Thr Gly Gly Thr Glu Arg Trp Gly Xaa
 35 40 45
Arg Gly Gln Val Ile Leu Phe Ala Thr Val Leu Phe Thr Leu Val Gln
50 55 60
Ser Val Tyr Leu Arg Ser Ser Arg Val Cys Cys Cys Pro Ser Val Phe
65 70 75 80
Leu Ile Glu Gly Arg Ser Val Ser Val Val Ser Ala Val Phe Ile Leu
 85 90 95
Gly Ser Ser Arg Pro Met His Gln Pro Ala Trp Thr Ala Asp Arg Trp
100 105 110
Val Leu Leu Pro Pro Ser Ala Leu Phe

115 120

(2) INFORMATION FOR SEQ ID NO:2654:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1504170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2654:

accacacc	cccaaggccc	tcccaaagtc	ccaaaggccg	ccgccgccg	ccagcccacc	60
atggccgcg	agtccttct	cctgcgcgc	actgcgcgc	ccagtcctcc	gggtcttcg	120
ccgtcccta	ttctccgca	cgccctttcc	actcgttcca	cttcgtcgcc	ggcccgtagg	180
ggcgccgcg	cgcc					

(2) INFORMATION FOR SEQ ID NO:2655:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1504171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2655:

Thr	His	Pro	Ile	Gln	Gly	Pro	Pro	Lys	Ala	Ala	Ala	Ala
1				5				10			15	
Arg	Gln	Pro	Thr	Met	Ala	Ala	Gln	Ser	Phe	Leu	Leu	Ala
				20				25			30	Thr
Ala	Ala	Ser	Pro	Pro	Arg	Ser	Ser	Pro	Leu	Pro	Ile	Pro
				35			40			45		His
Leu	Ser	Thr	Arg	Ser	Thr	Ser	Ser	Pro	Ala	Arg	Gly	Ala
				50			55				60	Pro

(2) INFORMATION FOR SEQ ID NO:2656:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1504172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2656:

Pro	Thr	Pro	Ser	Lys	Ala	Leu	Pro	Lys	Ser	Gln	Arg	Pro
1				5				10			15	
Ala	Ser	Pro	Pro	Trp	Pro	Arg	Ser	Pro	Ser	Ser	Pro	Pro
				20				25			30	Leu
Pro	Pro	Val	Pro	Arg	Gly	Leu	Arg	Ser	Leu	Phe	Leu	Arg
				35			40			45		Thr
Phe	Pro	Leu	Gly	Pro	Leu	Arg	Arg	Pro	Val	Gly	Arg	Arg
				50			55				60	

(2) INFORMATION FOR SEQ ID NO:2657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2657:

Pro	Pro	His	Pro	Arg	Pro	Ser	Gln	Ser	Pro	Lys	Gly	Arg	Arg	Arg	Pro	
1				5				10					15			
Pro	Ala	His	His	Gly	Arg	Ala	Val	Leu	Pro	Pro	Arg	Arg	His	Cys	Arg	
			20					25					30			
Arg	Gln	Ser	Pro	Ala	Val	Phe	Ala	Ala	Pro	Tyr	Ser	Ser	Ala	Arg	Pro	
			35					40					45			
Phe	His	Ser	Val	His	Phe	Val	Ala	Gly	Pro	Trp	Gly	Ala	Ala	Ala	Ala	
	50						55					60				

(2) INFORMATION FOR SEQ ID NO:2658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..185
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2658:

tagcaaaata	tggtttaagt	gatgatacag	tggtattcat	tgacatgca	cttgctcttc	60
atagagatga	tcgtatctt	gatgaaccgg	cacttgatac	agtgaaaagg	atgaaactat	120
attcagagtc	tcttgcgcg	tttcaaggag	gctcgccata	tatctatcca	wgtatggct	180
yggt						

(2) INFORMATION FOR SEQ ID NO:2659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2659:

Ala	Lys	Tyr	Gly	Leu	Ser	Asp	Asp	Thr	Val	Asp	Phe	Ile	Gly	His	Ala	
1				5				10					15			
Leu	Ala	Leu	His	Arg	Asp	Asp	Arg	Tyr	Leu	Asp	Glu	Pro	Ala	Leu	Asp	
			20					25					30			
Thr	Val	Lys	Arg	Met	Lys	Leu	Tyr	Ser	Glu	Ser	Leu	Ala	Arg	Phe	Gln	
			35					40					45			
Gly	Gly	Ser	Pro	Tyr	Ile	Tyr	Pro	Xaa	Tyr	Gly	Xaa	Gly				
	50						55					60				

(2) INFORMATION FOR SEQ ID NO:2660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..509
(D) OTHER INFORMATION: / Ceres Seq. ID 1504180
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2660:
caattccaat cccaatccca ccagtgtcca gtgctcgagg aacgacacag ctccctcagca 60
gagaagccag cactgacaagc ccgatcatgca gacagcaggg atggcgctcg cggaggccga 120
cgacggcgcg cgtgtcttcg gcgaggagca ggaggcgctg gtgctcaagt cgtgggccgt 180
catgaagaag gacgccgcca acctgggcct ccgtcttctc ctcaaggctct tcgagatcgc 240
gccgtcggaa gcagatgttc tcgttctctg gcgactccga cgtgccgctg gagaagaacc 300
ccaagctcaa gacgcaagcc atgtccgtct tcgtatgac ctgcgaggcg gcgcgcgast 360
tccgcaaggg cggaagggtc accgtgagga gaccacgctc aagagggtgg gcgccacgca 420
cttgaggtac ggcgtcgag atggacactt gcaggtgacg ggggtcgcg tgcttgagac 480
gatcaaggag gcgctccccg ctgacatgt
(2) INFORMATION FOR SEQ ID NO:2661:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..112
(D) OTHER INFORMATION: / Ceres Seq. ID 1504181
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2661:
Gln Phe Gln Ser Gln Ser His Gln Cys Pro Val Leu Gly Glu Arg His
1 5 10 15
Ser Ser Ser Ala Glu Lys Pro Ala Arg Gln Ala Arg Ser Ala Asp Ser
20 25 30
Arg His Gly Ala Arg Gly Gly Arg Arg Arg Gly Gly Leu Arg Arg
35 40 45
Gly Ala Gly Gly Ala Gly Ala Gln Val Val Gly Arg His Glu Glu Gly
50 55 60
Arg Arg Gln Pro Gly Pro Pro Leu Leu Pro Gln Gly Leu Arg Asp Arg
65 70 75 80
Ala Val Gly Ser Arg Cys Ser Arg Ser Cys Ala Thr Pro Thr Cys Arg
85 90 95
Trp Arg Arg Thr Pro Ser Ser Arg Arg Thr Pro Cys Pro Ser Ser Ser
100 105 110

(2) INFORMATION FOR SEQ ID NO:2662:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..169
(D) OTHER INFORMATION: / Ceres Seq. ID 1504182
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2662:
Asn Ser Asn Pro Asn Pro Thr Ser Val Gln Cys Ser Gly Asn Asp Thr
1 5 10 15
Ala Pro Gln Gln Arg Ser Gln His Asp Lys Pro Asp Gln Gln Thr Ala

20 25 30
Gly Met Ala Leu Ala Glu Ala Asp Asp Gly Ala Val Val Phe Gly Glu
35 40 45
Glu Gln Glu Ala Leu Val Leu Lys Ser Trp Ala Val Met Lys Lys Asp
50 55 60
Ala Ala Asn Leu Gly Leu Arg Phe Phe Leu Lys Val Phe Glu Ile Ala
65 70 75 80
Pro Ser Glu Ala Asp Val Leu Val Pro Ala Arg Leu Arg Arg Ala Ala
85 90 95
Gly Glu Glu Pro Gln Ala Gln Asp Ala Arg His Val Arg Leu Arg His
100 105 110
Asp Leu Arg Gly Gly Ala Xaa Pro Gln Gly Arg Glu Gly His Arg
115 120 125
Glu Glu Thr Thr Leu Lys Arg Leu Gly Ala Thr His Leu Arg Tyr Gly
130 135 140
Val Ala Asp Gly His Phe Glu Val Thr Gly Phe Ala Leu Leu Glu Thr
145 150 155 160
Ile Lys Glu Ala Leu Pro Ala Asp Met
165

(2) INFORMATION FOR SEQ ID NO:2663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2663:

Met Ala Leu Ala Glu Ala Asp Asp Gly Ala Val Val Phe Gly Glu Glu
1 5 10 15
Gln Glu Ala Leu Val Leu Lys Ser Trp Ala Val Met Lys Lys Asp Ala
20 25 30
Ala Asn Leu Gly Leu Arg Phe Phe Leu Lys Val Phe Glu Ile Ala Pro
35 40 45
Ser Glu Ala Asp Val Leu Val Pro Ala Arg Leu Arg Arg Ala Ala Gly
50 55 60
Glu Glu Pro Gln Ala Gln Asp Ala Arg His Val Arg Leu Arg His Asp
65 70 75 80
Leu Arg Gly Gly Gly Ala Xaa Pro Gln Gly Arg Glu Gly His Arg Glu
85 90 95
Glu Thr Thr Leu Lys Arg Leu Gly Ala Thr His Leu Arg Tyr Gly Val
100 105 110
Ala Asp Gly His Phe Glu Val Thr Gly Phe Ala Leu Leu Glu Thr Ile
115 120 125
Lys Glu Ala Leu Pro Ala Asp Met
130 135

(2) INFORMATION FOR SEQ ID NO:2664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..491
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2664:

ttagcatgcc	tacaattggt	catcgagatc	tgaatatctc	aaacttgctg	gttgacaata	60
attggaatgt	taaggtttgt	gactttggac	tttcgcggtt	gaagcacagt	acatttttgt	120
catccaaatc	tacagctggw	acacctgagt	ggatggcacc	tgaggttctg	cggaatgaac	180
aatcgaatga	aaagtgtgat	gtttatagct	ttggtgtcat	cttatgggaa	ctggcaaacac	240
ttagaatgcc	atggagtggg	atgaatccaa	tgcaagtgtg	gggggcagtt	ggtttccagg	300
atagacggct	tgatattccc	aaggaagtgt	atcctctggt	cgcaaggata	atatttgaat	360
gctggcagaa	ggatccaaat	ttgcgccctg	catttgacac	gttaacaaagt	gccctgaaga	420
ctgttcaaa	actagtgcac	ctttgtccac	aggagaacca	gagccccatg	ttcaacaaga	480
aatctcagtg	c					

(2) INFORMATION FOR SEQ ID NO:2665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2665:

Ser	Met	Pro	Thr	Ile	Val	His	Arg	Asp	Leu	Lys	Ser	Pro	Asn	Leu	Leu
1				5				10					15		
Val	Asp	Asn	Asn	Trp	Asn	Val	Lys	Val	Cys	Asp	Phe	Gly	Leu	Ser	Arg
				20				25					30		
Leu	Lys	His	Ser	Thr	Phe	Leu	Ser	Ser	Lys	Ser	Thr	Ala	Xaa	Thr	Pro
				35				40				45			
Glu	Trp	Met	Ala	Pro	Glu	Val	Leu	Arg	Asn	Glu	Gln	Ser	Asn	Glu	Lys
								55				60			
Cys	Asp	Val	Tyr	Ser	Phe	Gly	Val	Ile	Leu	Trp	Glu	Leu	Ala	Thr	Leu
								70				75			80
Arg	Met	Pro	Trp	Ser	Gly	Met	Asn	Pro	Met	Gln	Val	Val	Gly	Ala	Val
								90					95		
Gly	Phe	Gln	Asp	Arg	Arg	Leu	Asp	Ile	Pro	Lys	Glu	Val	Asp	Pro	Leu
								105					110		
Val	Ala	Arg	Ile	Ile	Phe	Glu	Cys	Trp	Gln	Lys	Asp	Pro	Asn	Leu	Arg
								120					125		
Pro	Ser	Phe	Ala	Gln	Leu	Thr	Ser	Ala	Leu	Lys	Thr	Val	Gln	Arg	Leu
								135					140		
Val	Thr	Leu	Cys	His	Gln	Glu	Asn	Gln	Ser	Pro	Met	Phe	Asn	Lys	Lys
								150					155		160
Ser	Gln	Cys													

(2) INFORMATION FOR SEQ ID NO:2666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2666:

Met	Pro	Thr	Ile	Val	His	Arg	Asp	Leu	Lys	Ser	Pro	Asn	Leu	Leu	Val
1				5				10					15		
Asp	Asn	Asn	Trp	Asn	Val	Lys	Val	Cys	Asp	Phe	Gly	Leu	Ser	Arg	Leu
								25					30		
Lys	His	Ser	Thr	Phe	Leu	Ser	Ser	Lys	Ser	Thr	Ala	Xaa	Thr	Pro	Glu
								40					45		

Trp	Met	Ala	Pro	Glu	Val	Leu	Arg	Asn	Glu	Gln	Ser	Asn	Glu	Lys	Cys
50						55				60					
Asp	Val	Tyr	Ser	Phe	Gly	Val	Ile	Leu	Trp	Glu	Leu	Ala	Thr	Leu	Arg
65					70					75				80	
Met	Pro	Trp	Ser	Gly	Met	Asn	Pro	Met	Gln	Val	Val	Gly	Ala	Val	Gly
				85					90					95	
Phe	Gln	Asp	Arg	Arg	Leu	Asp	Ile	Pro	Lys	Glu	Val	Asp	Pro	Leu	Val
			100					105					110		
Ala	Arg	Ile	Ile	Phe	Glu	Cys	Trp	Gln	Lys	Asp	Pro	Asn	Leu	Arg	Pro
			115				120					125			
Ser	Phe	Ala	Gln	Leu	Thr	Ser	Ala	Leu	Lys	Thr	Val	Gln	Arg	Leu	Val
			130				135				140				
Thr	Leu	Cys	His	Gln	Glu	Asn	Gln	Ser	Pro	Met	Phe	Asn	Lys	Lys	Ser
					150					155					160
Gln	Cys														

(2) INFORMATION FOR SEQ ID NO:2667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2667:

Met	Ala	Pro	Glu	Val	Leu	Arg	Asn	Glu	Gln	Ser	Asn	Glu	Lys	Cys	Asp
1			5					10					15		
Val	Tyr	Ser	Phe	Gly	Val	Ile	Leu	Trp	Glu	Leu	Ala	Thr	Leu	Arg	Met
			20				25						30		
Pro	Trp	Ser	Gly	Met	Asn	Pro	Met	Gln	Val	Val	Gly	Ala	Val	Gly	Phe
			35				40				45				
Gln	Asp	Arg	Arg	Leu	Asp	Ile	Pro	Lys	Glu	Val	Asp	Pro	Leu	Val	Ala
			50				55				60				
Arg	Ile	Ile	Phe	Glu	Cys	Trp	Gln	Lys	Asp	Pro	Asn	Leu	Arg	Pro	Ser
			65				70				75			80	
Phe	Ala	Gln	Leu	Thr	Ser	Ala	Leu	Lys	Thr	Val	Gln	Arg	Leu	Val	Thr
				85					90				95		
Leu	Cys	His	Gln	Glu	Asn	Gln	Ser	Pro	Met	Phe	Asn	Lys	Lys	Ser	Gln
			100					105					110		
Cys															

(2) INFORMATION FOR SEQ ID NO:2668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..482
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2668:

aaagctggag	tgaatccagc	aggctgcttc	tgaaaaaaaa	agtagcagat	gcaacgagtg	60
cactccaatg	ctgcagttac	aatgcaatga	ccgggtttgt	tagtgagcta	gcacgcgttg	120
sggtctcctg	agggacaata	atcatcgtga	catggtgcca	taggaacctg	gatacatccg	180
aaacctcgct	aaagcccgat	gaactgagcc	tcctgaggag	gatatgcgac	gcgtactacc	240
tcccgagctg	gtgctcacct	tcagactatg	tgaacattgc	caagtcactg	tctctcgagg	300

atatcaagac agctgactgg tcggagaacg tggcccggt ttggccgcc gtgataaaat	360
cagcgctaac atggaaggcg ttacactctc tgctgacgac cggatggaag acgatcagag	420
gcgcgatggt gatgcgcgta atgatccagg gctacaagaa ggggctcatc aaattcacca	480
tc	

(2) INFORMATION FOR SEQ ID NO:2669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2669:

Ser	Trp	Ser	Glu	Ser	Ser	Arg	Leu	Leu	Leu	Lys	Lys	Lys	Val	Ala	Asp	
1			5						10				15			
Ala	Thr	Ser	Ala	Leu	Gln	Cys	Cys	Ser	Tyr	Asn	Ala	Met	Thr	Gly	Phe	
			20					25				30				
Val	Ser	Glu	Leu	Ala	Arg	Val	Xaa	Ala	Pro	Gly	Gly	Thr	Ile	Ile	Ile	
			35			40					45					
Val	Thr	Trp	Cys	His	Arg	Asn	Leu	Asp	Pro	Ser	Glu	Thr	Ser	Leu	Lys	
			50			55					60					
Pro	Asp	Glu	Leu	Ser	Leu	Leu	Arg	Arg	Ile	Cys	Asp	Ala	Tyr	Tyr	Leu	
65					70				75						80	
Pro	Asp	Trp	Cys	Ser	Pro	Ser	Asp	Tyr	Val	Asn	Ile	Ala	Lys	Ser	Leu	
			85					90						95		
Ser	Leu	Glu	Asp	Ile	Lys	Thr	Ala	Asp	Trp	Ser	Glu	Asn	Val	Ala	Pro	
			100					105					110			
Phe	Trp	Pro	Ala	Val	Ile	Lys	Ser	Ala	Leu	Thr	Trp	Lys	Gly	Phe	Thr	
			115			120						125				
Ser	Leu	Leu	Thr	Thr	Gly	Trp	Lys	Thr	Ile	Arg	Gly	Ala	Met	Val	Met	
			130			135					140					
Pro	Leu	Met	Ile	Gln	Gly	Tyr	Lys	Lys	Gly	Leu	Ile	Lys	Phe	Thr	Ile	
145				150					155						160	

(2) INFORMATION FOR SEQ ID NO:2670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2670:

Met	Thr	Gly	Phe	Val	Ser	Glu	Leu	Ala	Arg	Val	Xaa	Ala	Pro	Gly	Gly	
1			5						10				15			
Thr	Ile	Ile	Ile	Val	Thr	Trp	Cys	His	Arg	Asn	Leu	Asp	Pro	Ser	Glu	
			20				25					30				
Thr	Ser	Leu	Lys	Pro	Asp	Glu	Leu	Ser	Leu	Leu	Arg	Arg	Ile	Cys	Asp	
			35			40					45					
Ala	Tyr	Tyr	Leu	Pro	Asp	Trp	Cys	Ser	Pro	Ser	Asp	Tyr	Val	Asn	Ile	
			50			55					60					
Ala	Lys	Ser	Leu	Ser	Leu	Glu	Asp	Ile	Lys	Thr	Ala	Asp	Trp	Ser	Glu	
65					70				75						80	
Asn	Val	Ala	Pro	Phe	Trp	Pro	Ala	Val	Ile	Lys	Ser	Ala	Leu	Thr	Trp	

	85						90								95
Lys	Gly	Phe	Thr	Ser	Leu	Leu	Thr	Thr	Gly	Trp	Lys	Thr	Ile	Arg	Gly
		100						105						110	
Ala	Met	Val	Met	Pro	Leu	Met	Ile	Gln	Gly	Tyr	Lys	Lys	Gly	Leu	Ile
		115					120						125		
Lys	Phe	Thr	Ile												
			130												

(2) INFORMATION FOR SEQ ID NO:2671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..511
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2671:

agcg	tttaga	gagagagaag	acagggagaa	ggaggaagag	ccgccgcgnt	ggaccgggtg	60
attt	gtcag	gttgcagg	gagtcgtcag	gacacgggca	agctttgtac	gctaccaatt	120
cagc	gaataa	ccgacggggg	tgcttggaat	tgctcaccgc	agcaaacctt	ccgccgcgca	180
accac	cattcc	ttctgagcag	cgcacgctag	cgcccggttc	ctggacgcac	gccgtgaact	240
cgaag	tccac	cgctctgtga	gcatacaagc	ccggcatcgc	tagggtttca	cgcccccatc	300
cccc	cagggc	gccgtcgatc	ccggtcggcc	atctcccggg	gcctggtaac	tgatcgttaa	360
tttc	atcgat	gggtgccatg	gaggaccgca	gtcccaagca	ggcaggcgcg	ggcttgggtg	420
cccc	actcca	cgacgacctc	cttgtggaga	tcctctcccg	cgtecccgcc	aagtcgctct	480
gc	cggttcaa	gtcgtgtccc	aaggcctggc	t			

(2) INFORMATION FOR SEQ ID NO:2672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2672:

Arg	Leu	Glu	Arg	Glu	Lys	Thr	Gly	Arg	Arg	Arg	Lys	Ser	Arg	Arg	Xaa
1				5				10					15		
Gly	Pro	Gly	Asp	Leu	Ser	Gly	Leu	Ser	Gly	Glu	Ser	Ser	Gly	His	Gly
			20					25					30		
Gln	Ala	Leu	Tyr	Ala	Thr	Asn	Ser	Ala	Asn	Asn	Arg	Arg	Gly	Cys	Val
			35					40					45		
Glu	Leu	Leu	Thr	Gly	Ala	Asn	Pro	Pro	Pro	Pro	Asn	His	His	Pro	Ser
			50				55					60			
Glu	Gln	Arg	Thr	Leu	Ala	Ser	Gly	Ser	Trp	Thr	His	Ala	Val	Asn	Ser
			65				70			75				80	
Lys	Ser	Thr	Ala	Leu											
				85											

(2) INFORMATION FOR SEQ ID NO:2673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1504203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2673:

Met Gly Ala Met Glu Asp Arg Ser Ser Lys Gln Ala Gly Ala Gly Leu
1 5 10 15
Val Ala His Leu His Asp Asp Leu Leu Val Glu Ile Leu Ser Arg Val
20 25 30
Pro Ala Lys Ser Val Cys Arg Phe Lys Cys Val Ser Lys Ala Trp
35 40 45

(2) INFORMATION FOR SEQ ID NO:2674:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..44

(D) OTHER INFORMATION: / Ceres Seq. ID 1504204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2674:

Met Glu Asp Arg Ser Ser Lys Gln Ala Gly Ala Gly Leu Val Ala His
1 5 10 15
Leu His Asp Asp Leu Leu Val Glu Ile Leu Ser Arg Val Pro Ala Lys
20 25 30
Ser Val Cys Arg Phe Lys Cys Val Ser Lys Ala Trp
35 40

(2) INFORMATION FOR SEQ ID NO:2675:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..436

(D) OTHER INFORMATION: / Ceres Seq. ID 1504231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2675:

cattgtcaat	ttctcccagg	ataaatcatg	gcgtgttcgt	tatatggctg	ccaatcagtt	60
atatgagctc	tgtgagcgctg	ttggccctga	gccacaaga	gctgatttgg	tgccctgcata	120
tgttcgctct	cttcgcgata	atgaggctga	agtgcgcaata	gcggctgctg	gaaaagtaac	180
taagttctgc	cgcatattga	atccacagct	ttcaatccaa	catattcttc	cgtgcgttaa	240
ggaattgtca	tcattatcat	cccacgatgt	tcgttcagct	ttagcctcag	tcattatggg	300
aatggctcct	gtactgggaa	aggatgctac	catggaaacag	cttcttccaa	tttttctctc	360
tttgctgaag	gatgaatttc	cagatgttgc	gcttaacata	atcagcaagc	ttgatcaggt	420
taatcaggtt	attggc					

(2) INFORMATION FOR SEQ ID NO:2676:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1504232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2676:

Ile Val Asn Phe Ser Gln Asp Lys Ser Trp Arg Val Arg Tyr Met Val
1 5 10 15

Ala Asn Gln Leu Tyr Glu Leu Cys Glu Ala Val Gly Pro Glu Pro Thr
20 25 30
Arg Ala Asp Leu Val Pro Ala Tyr Val Arg Leu Leu Arg Asp Asn Glu
35 40 45
Ala Glu Val Arg Ile Ala Ala Gly Lys Val Thr Lys Phe Cys Arg
50 55 60
Ile Leu Asn Pro Gln Leu Ser Ile Gln His Ile Leu Pro Cys Val Lys
65 70 75 80
Glu Leu Ser Ser Tyr Ser Ser Gln His Val Arg Ser Ala Leu Ala Ser
85 90 95
Val Ile Met Gly Met Ala Pro Val Leu Gly Lys Asp Ala Thr Met Glu
100 105 110
Gln Leu Leu Pro Ile Phe Leu Ser Leu Leu Lys Asp Glu Phe Pro Asp
115 120 125
Val Arg Leu Asn Ile Ile Ser Lys Leu Asp Gln Val Asn Gln Val Ile
130 135 140

Gly
145

(2) INFORMATION FOR SEQ ID NO:2677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2677:

Met Val Ala Asn Gln Leu Tyr Glu Leu Cys Glu Ala Val Gly Pro Glu
1 5 10 15
Pro Thr Arg Ala Asp Leu Val Pro Ala Tyr Val Arg Leu Leu Arg Asp
20 25 30
Asn Glu Ala Glu Val Arg Ile Ala Ala Ala Gly Lys Val Thr Lys Phe
35 40 45
Cys Arg Ile Leu Asn Pro Gln Leu Ser Ile Gln His Ile Leu Pro Cys
50 55 60
Val Lys Glu Leu Ser Ser Tyr Ser Ser Gln His Val Arg Ser Ala Leu
65 70 75 80
Ala Ser Val Ile Met Gly Met Ala Pro Val Leu Gly Lys Asp Ala Thr
85 90 95
Met Glu Gln Leu Leu Pro Ile Phe Leu Ser Leu Leu Lys Asp Glu Phe
100 105 110
Pro Asp Val Arg Leu Asn Ile Ile Ser Lys Leu Asp Gln Val Asn Gln
115 120 125
Val Ile Gly
130

(2) INFORMATION FOR SEQ ID NO:2678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..446
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2678:

cgatccctttt atccgtaact atattgagga cttattgaag aacatcagaa cccaagtgc

gtctcaagctt attaaacccat atactcgaat caggatacca ttcatattcac aggaactcaa 120
ttttccagaa aaggatgtcg agcagctggt ggtgtcactc attctggaca accgtatcca 180
aggccacata gatcaggtta acaagctgct agaactggga gaaaggtcca aggggatgag 240
gaagtacaat gctatcgaca agtggaaatc tcagctggaag tccatttacc aaacattgtc 300
caacagagtt tgatgaggag gatcgctgct gctgctgctg gcattgcaca cctagaattg 360
ttgatagcct gtttttgga tttagggca actgcaaga actgtctggt gacgcttgcc 420
atagaatcct ggatctgggt aaagtt

(2) INFORMATION FOR SEQ ID NO:2679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2679:

Asp Pro Phe Ile Arg Asn Tyr Ile Glu Asp Leu Leu Lys Asn Ile Arg
1 5 10 15
Thr Gln Val Leu Leu Lys Leu Ile Lys Pro Tyr Thr Arg Ile Arg Ile
20 25 30
Pro Phe Ile Ser Gln Glu Leu Asn Phe Pro Glu Lys Asp Val Glu Gln
35 40 45
Leu Leu Val Ser Leu Ile Leu Asp Asn Arg Ile Gln Gly His Ile Asp
50 55 60
Gln Val Asn Lys Leu Leu Glu Arg Gly Glu Arg Ser Lys Gly Met Arg
65 70 75 80
Lys Tyr Asn Ala Ile Asp Lys Trp Asn Thr Gln Leu Lys Ser Ile Tyr
85 90 95
Gln Thr Leu Ser Asn Arg Val
100

(2) INFORMATION FOR SEQ ID NO:2680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2680:

gtttctctctt gatcgctttg tcacttgaat ccgctgctgc tctaacagag agcggagagc 60
accacgacga cggcgaggcc aggcctctgc atggagcagg agccgcaccg gcccatggag 120
ctgcccccgg gcttccgctt ccacccgacc gacgaggagn tcatcacgca ctacctggcc 180
cgcaaggcgc cgacgccgcg ttgcgccgcg ttgccgtcgc cgagggccgac ctcaacaagt 240
gcgagccctg ggacctgcca tcgctggcga ggatggggga gaaggagtgg tactttctct 300
gcctcaagga ccgcaagtac ccgacg

(2) INFORMATION FOR SEQ ID NO:2681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1504255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2681:

Phe Leu Leu Ile Ala Leu Ser Leu Glu Ser Val Pro Ala Leu Thr Glu
1 5 10 15
Ser Gly Asp Asp His Asp Asp Gly Glu Ala Arg Leu Cys Asp Gly Ala
20 25 30
Gly Ala Ala Pro Ala His Gly Ala Ala Pro Gly Leu Pro Leu Pro Pro
35 40 45
Asp Arg Arg Gly Xaa His His Ala Leu Pro Gly Pro Gln Gly Ala Asp
50 55 60
Ala Arg Phe Ala Ala Leu Ala Val Ala Glu Ala Asp Leu Asn Lys Cys
65 70 75 80
Glu Pro Trp Asp Leu Pro Ser Leu Ala Arg Met Gly Glu Lys Glu Trp
85 90 95
Tyr Phe Phe Cys Leu Lys Asp Arg Lys Tyr Pro Thr
100 105

(2) INFORMATION FOR SEQ ID NO:2682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2682:

Met Glu Gln Glu Pro His Arg Pro Met Glu Leu Pro Pro Gly Phe Arg
1 5 10 15
Phe His Pro Thr Asp Glu Glu Xaa Ile Thr His Tyr Leu Ala Arg Lys
20 25 30
Ala Pro Thr Pro Ala Ser Pro Arg Leu Pro Ser Pro Arg Pro Thr Ser
35 40 45
Thr Ser Ala Ser Pro Gly Thr Cys His Arg Trp Arg Gly Trp Gly Arg
50 55 60
Arg Ser Gly Thr Ser Ser Ala Ser Arg Thr Ala Ser Thr Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:2683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2683:

Met Glu Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Xaa
1 5 10 15
Ile Thr His Tyr Leu Ala Arg Lys Ala Pro Thr Pro Ala Ser Pro Arg
20 25 30
Leu Pro Ser Pro Arg Pro Thr Ser Thr Ser Ala Ser Pro Gly Thr Cys
35 40 45
His Arg Trp Arg Gly Trp Gly Arg Arg Ser Gly Thr Ser Ser Ala Ser
50 55 60
Arg Thr Ala Ser Thr Arg
65 70

(2) INFORMATION FOR SEQ ID NO:2684:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..307
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504258
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2684:
aattccctc cccgtgtgtc gtctccctc accgaagcc ccgdttcgaa accgcgcgcg 60
ttcgatttgg ggatttcggc gtctcgtctc ccggaatttc ttgatctga gtctgtccgc 120
cgtcttcgat ttgcggctgc agtagcctg cgagttttcc ggctctgatt tggwcggggh 180
cttcgatttc ggggatggcg tcgtctccgg tgcctactg gtgctacagc tgcagccgct 240
tcgtgagggt attctcgttc accgtgtct gcccgagtg cgatggcggc ttccctggagc 300
agttttac
(2) INFORMATION FOR SEQ ID NO:2685:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..55
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504259
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2685:
Asn Ser Pro Leu Ser Ser Ser Pro Leu Thr Arg Ser Pro Xaa Ser
1 5 10 15
Lys Pro Ala Ala Phe Asp Leu Gly Ile Ser Ala Ser Arg Ser Pro Glu
20 25 30
Phe Leu Gly Ser Glu Ser Val Arg Arg Leu Arg Phe Ala Ala Val
35 40 45
Ser Leu Arg Val Phe Arg Leu
50 55
(2) INFORMATION FOR SEQ ID NO:2686:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..47
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504260
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2686:
Ile Pro Leu Pro Cys Arg Arg Leu Pro Ser Pro Glu Ala Pro Xaa Arg
1 5 10 15
Asn Arg Arg Arg Ser Ile Trp Gly Phe Arg Arg Leu Ala Pro Arg Asn
20 25 30
Phe Leu Asp Leu Ser Leu Ser Ala Val Phe Asp Leu Arg Leu Gln
35 40 45
(2) INFORMATION FOR SEQ ID NO:2687:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..37
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504261
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2687:
Met Ala Ser Ser Pro Val Ser Tyr Trp Cys Tyr Ser Cys Ser Arg Phe
1 5 10 15
Val Arg Val Ser Pro Ser Thr Xaa Val Cys Pro Glu Cys Asp Gly Gly
 20 25 30
Phe Leu Glu Gln Phe
 35

(2) INFORMATION FOR SEQ ID NO:2688:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..234
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2688:

actcggtcg sacccttcca ctgcaccagc gtcatggcgg tggctctgac ctgcgcgctg 60
tcgcgcaagc ccgcacaggc cccctcgccg cccgctcccg gatccgggct cctcgctctc 120
ggcgcttcgc cgccccccgc cactgcgcgg tggaggaggg tcgcggtgga ggcgatcagg 180
acgcagcggg agaagcagcg ggcggagggt cccgtcgagg agtccgcccc cgcc

(2) INFORMATION FOR SEQ ID NO:2689:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..78
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2689:

Thr Arg Val Xaa Pro Leu His Cys Thr Ser Val Met Ala Val Ala Ser
1 5 10 15
Thr Ser Pro Leu Ser Ala Lys Pro Ala Thr Ala Pro Ser Pro Pro Ala
 20 25 30
Pro Gly Ser Gly Leu Leu Ala Leu Gly Val Arg Xaa Ala Pro Ala Thr
 35 40 45
Ala Ala Trp Arg Arg Leu Arg Val Glu Ala Ile Arg Thr Gln Arg Glu
 50 55 60
Lys Gln Arg Ala Glu Val Pro Val Glu Glu Ser Ala Pro Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:2690:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..77
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2690:

```

Leu Ala Ser Xaa Pro Ser Thr Ala Pro Ala Ser Trp Arg Trp Pro Arg
1          5          10          15
Pro Arg Arg Cys Pro Pro Ser Pro Pro Arg Pro Pro Arg Arg Pro Leu
20          25          30
Pro Asp Pro Gly Ser Ser Leu Ser Ala Phe Xaa Arg Pro Pro Pro Leu
35          40          45
Pro Arg Gly Gly Gly Ser Ala Trp Arg Arg Ser Gly Arg Ser Gly Arg
50          55          60
Ser Ser Gly Arg Arg Cys Pro Ser Arg Ser Pro Pro Pro
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:2691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2691:

```

Ser Arg Xaa Xaa Pro Pro Leu His Gln Arg His Gly Gly Gly Leu Asp
1          5          10          15
Leu Ala Ala Val Arg Gln Ala Arg His Gly Pro Leu Ala Ala Arg Ser
20          25          30
Arg Ile Arg Ala Pro Arg Ser Arg Arg Ser Xaa Gly Pro Arg His Cys
35          40          45
Arg Val Glu Glu Ala Pro Arg Gly Gly Asp Gln Asp Ala Ala Gly Glu
50          55          60
Ala Ala Gly Gly Gly Ala Arg Arg Gly Val Arg Pro Arg
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:2692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..429
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2692:

```

agtcggagca gggcaggggt tgcgtctcag ttctctggtt gtgtgtgtga agctcacagg 60
ttctctctct tcgctgtgass tagctagagt gggatcgcga ggaagaagga tgtcgtgtgtg 120
cggaggcaac tgcgggtgcy gcaaggantg caagtgcggc assggctgcy gagggtgcaa 180
gatgtaccgc gacatgggtt agcagggtgac caccaccacc accaccagga ctctcatcat 240
gggtgtgtgc ccatccacgg gccaccgcgt tgcctccctc ggcagccagg atgacagaag 300
taccattctt gccgcgtgag aggcctctca agcagcaaca ttacttccag aacttgacca 360
agcacacctc cctgaagggc gctacgacgt gatcacctcc gtcgcacctc cccttgacct 420
cgctgcctc

```

(2) INFORMATION FOR SEQ ID NO:2693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..105
(D) OTHER INFORMATION: / Ceres Seq. ID 1504275
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2693:
Val Gly Ala Gly Gln Gly Leu Arg Leu Ser Trp Leu Cys Cys Cys
1 5 10 15
Lys Leu Thr Gly Phe Phe Ser Ser Arg Xaa Xaa Ala Arg Val Gly Ser
20 25 30
Arg Gly Arg Arg Met Ser Cys Cys Gly Gly Asn Cys Gly Cys Gly Xaa
35 40 45
Xaa Cys Lys Cys Gly Xaa Gly Cys Gly Gly Cys Lys Met Tyr Pro Asp
50 55 60
Met Val Glu Gln Val Thr Thr Thr Thr Thr Gln Thr Leu Ile Met
65 70 75 80
Gly Val Ala Pro Ser Thr Gly His Arg Val Ala Pro Leu Gly Ser Gln
85 90 95
Asp Asp Arg Ser Thr Ile Ser Ala Ala
100 105

(2) INFORMATION FOR SEQ ID NO:2694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..69
(D) OTHER INFORMATION: / Ceres Seq. ID 1504276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2694:

Met Ser Cys Cys Gly Gly Asn Cys Gly Cys Gly Xaa Xaa Cys Lys Cys
1 5 10 15
Gly Xaa Gly Cys Gly Gly Cys Lys Met Tyr Pro Asp Met Val Glu Gln
20 25 30
Val Thr Thr Thr Thr Thr Thr Gln Thr Leu Ile Met Gly Val Ala Pro
35 40 45
Ser Thr Gly His Arg Val Ala Pro Leu Gly Ser Gln Asp Asp Arg Ser
50 55 60
Thr Ile Ser Ala Ala
65

(2) INFORMATION FOR SEQ ID NO:2695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..244
(D) OTHER INFORMATION: / Ceres Seq. ID 1504277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2695:

agttgatccc atcggtctcc ccttctcttt ccccgatccc cttctctccc cgatcccatc 60
caattccact tccacacccc gggcctcgcc gccgaagccg acgccgaagc cgccggccat 120
gtccaagtag gccaccattc ccacctctc ctccgcgggc ggagggcccg tgccctctcg 180
cggcgctccc cgctgatatt catctcccgc gccaaaggctc ggggcgcctc ggctgtggcg 240
acgc

(2) INFORMATION FOR SEQ ID NO:2696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..81
(D) OTHER INFORMATION: / Ceres Seq. ID 1504278
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2696:
Val Asp Pro Ile Gly Phe Pro Phe Leu Phe Pro Asp Pro Leu Pro Pro
1 5 10 15
Pro Ile Pro Ser Asn Ser Thr Ser Thr Pro Arg Ala Ser Pro Pro Thr
20 25 30
Pro Thr Pro Thr Pro Pro Ala Met Ser Lys Tyr Gly Thr Ile Pro Thr
35 40 45
Ser Ser Ser Ala Gly Gly Gly Pro Val Pro Leu Gly Gly Ala Pro Arg
50 55 60
Ser Ile Ser Ser Pro Ala Pro Arg Leu Gly Ala Pro Arg Xaa Gly Arg
65 70 75 80
Arg

(2) INFORMATION FOR SEQ ID NO:2697:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..80
(D) OTHER INFORMATION: / Ceres Seq. ID 1504279
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2697:
Leu Ile Pro Ser Ala Ser Pro Ser Ser Ser Pro Ile Pro Phe Leu Pro
1 5 10 15
Arg Ser His Pro Ile Pro Leu Pro His Pro Gly Pro Arg Arg Arg Arg
20 25 30
Arg Arg Arg Arg Arg Arg Pro Cys Pro Ser Thr Ala Pro Phe Pro Pro
35 40 45
Pro Pro Pro Arg Ala Glu Gly Pro Cys Pro Ser Ala Ala Leu Pro Ala
50 55 60
Arg Phe His Leu Pro Arg Gln Gly Ser Gly Arg Leu Gly Xaa Gly Asp
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:2698:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..42
(D) OTHER INFORMATION: / Ceres Seq. ID 1504280
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2698:
Met Ser Lys Tyr Gly Thr Ile Pro Thr Ser Ser Ser Ala Gly Gly Gly
1 5 10 15
Pro Val Pro Leu Gly Gly Ala Pro Arg Ser Ile Ser Ser Pro Ala Pro
20 25 30
Arg Leu Gly Ala Pro Arg Xaa Gly Arg Arg

35 40

(2) INFORMATION FOR SEQ ID NO:2699:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1504299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2699:

cctgatttcc	tgaaacacag	atcatcatca	tcatgtgtca	tggtatggc	aaactcggca	60
acgatcctga	cgcgcgttct	ggctctcggg	ctagcgttcc	tccgcgcgc	agctccggcc	120
tccgcgcaga	actcggcgtg	cccgcacagg	tactgtgca	gcaagtccg	ttactcggc	180
accagcttcg	actactgcaa	tgccaacacg	tgccagtcg	gcccgtgcac	g	

(2) INFORMATION FOR SEQ ID NO:2700:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1504300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2700:

Pro Asp Phe Leu Lys His Arg Ser Ser Phe Met Val Met Ala Met	
1 5 10 15	
Ala Asn Ser Ala Thr Ile Leu Thr Val Val Leu Ala Leu Gly Leu Ala	
20 25 30	
Phe Leu Arg Ala Ala Pro Ala Ser Ala Gln Asn Cys Gly Cys Pro	
35 40 45	
Pro Gly Tyr Cys Cys Ser Lys Phe Gly Tyr Cys Gly Thr Ser Phe Asp	
50 55 60	
Tyr Cys Asn Ala Asn Thr Cys Gln Ser Gly Pro Cys Thr	
65 70 75	

(2) INFORMATION FOR SEQ ID NO:2701:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1504301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2701:

Met Val Met Ala Met Ala Asn Ser Ala Thr Ile Leu Thr Val Val Leu	
1 5 10 15	
Ala Leu Gly Leu Ala Phe Leu Arg Ala Ala Pro Ala Ser Ala Gln	
20 25 30	
Asn Cys Gly Cys Pro Pro Gly Tyr Cys Cys Ser Lys Phe Gly Tyr Cys	
35 40 45	
Gly Thr Ser Phe Asp Tyr Cys Asn Ala Asn Thr Cys Gln Ser Gly Pro	
50 55 60	
Cys Thr	
65	

(2) INFORMATION FOR SEQ ID NO:2702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2702:

Met	Ala	Met	Ala	Asn	Ser	Ala	Thr	Ile	Leu	Thr	Val	Val	Leu	Ala	Leu	
1			5						10				15			
Gly	Leu	Ala	Phe	Leu	Arg	Ala	Ala	Ala	Pro	Ala	Ser	Ala	Gln	Asn	Cys	
		20						25					30			
Gly	Cys	Pro	Pro	Gly	Tyr	Cys	Cys	Ser	Lys	Phe	Gly	Tyr	Cys	Gly	Thr	
		35					40				45					
Ser	Phe	Asp	Tyr	Cys	Asn	Ala	Asn	Thr	Cys	Gln	Ser	Gly	Pro	Cys	Thr	
		50				55					60					

(2) INFORMATION FOR SEQ ID NO:2703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..452
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2703:

tacaaggcta	tttatgat	tccagcaata	aaagaggatc	caacaaagt	gataccgatt	60
cttaggaaga	tctgttgga	cttggtgcta	gcacctcatg	atcctatgca	atcaagcctt	120
ctcaatgcta	cactagagga	taaaaacctt	tcagaaatcc	caaatttcag	gttattactg	180
aagcagctgg	tcaccatgga	ggtgatacac	tggaacaagt	tgtgggaatt	cttcaaggag	240
gaatatgaga	aggagaagga	tcttcttggg	ggagctttgg	gtgccaaagc	ttcagaagat	300
ttgaggctga	ggattatcga	acataatatc	ttggttgat	ccaagtacta	tgcaagggtt	360
accctcaaga	ggcttgccga	tcttctttgc	ctgactttgc	aggaggcaga	gaagcatctc	420
tcagacatgg	ttaaactcga	atctctagt	gc			

(2) INFORMATION FOR SEQ ID NO:2704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2704:

Tyr	Lys	Ala	Ile	Tyr	Asp	Ile	Pro	Ala	Ile	Lys	Glu	Asp	Pro	Thr	Lys	
1			5						10					15		
Trp	Ile	Pro	Ile	Leu	Arg	Lys	Ile	Cys	Trp	Tyr	Leu	Val	Leu	Ala	Pro	
		20					25				30					
His	Asp	Pro	Met	Gln	Ser	Ser	Leu	Leu	Asn	Ala	Thr	Leu	Glu	Asp	Lys	
		35					40				45					
Asn	Leu	Ser	Glu	Ile	Pro	Asn	Phe	Arg	Leu	Leu	Leu	Lys	Gln	Leu	Val	

50 55 60
Thr Met Glu Val Ile Gln Trp Thr Ser Leu Trp Glu Phe Phe Lys Glu
65 70 75 80
Glu Tyr Glu Lys Glu Lys Asp Leu Leu Gly Gly Ala Leu Gly Ala Lys
85 90 95
Ala Ser Glu Asp Leu Arg Leu Arg Ile Ile Glu His Asn Ile Leu Val
100 105 110
Val Ser Lys Tyr Tyr Ala Arg Val Thr Leu Lys Arg Leu Ala Asp Leu
115 120 125
Leu Cys Leu Thr Leu Gln Glu Ala Glu Lys His Leu Ser Asp Met Val
130 135 140
Asn Ser Lys Ser Leu Val
145 150

(2) INFORMATION FOR SEQ ID NO:2705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2705:

Met Gln Ser Ser Leu Leu Asn Ala Thr Leu Glu Asp Lys Asn Leu Ser
1 5 10 15
Glu Ile Pro Asn Phe Arg Leu Leu Leu Lys Gln Leu Val Thr Met Glu
20 25 30
Val Ile Gln Trp Thr Ser Leu Trp Glu Phe Phe Lys Glu Glu Tyr Glu
35 40 45
Lys Glu Lys Asp Leu Leu Gly Gly Ala Leu Gly Ala Lys Ala Ser Glu
50 55 60
Asp Leu Arg Leu Arg Ile Ile Glu His Asn Ile Leu Val Val Ser Lys
65 70 75 80
Tyr Tyr Ala Arg Val Thr Leu Lys Arg Leu Ala Asp Leu Cys Leu
85 90 95
Thr Leu Gln Glu Ala Glu Lys His Leu Ser Asp Met Val Asn Ser Lys
100 105 110
Ser Leu Val
115

(2) INFORMATION FOR SEQ ID NO:2706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2706:

Met Glu Val Ile Gln Trp Thr Ser Leu Trp Glu Phe Phe Lys Glu Glu
1 5 10 15
Tyr Glu Lys Glu Lys Asp Leu Leu Gly Gly Ala Leu Gly Ala Lys Ala
20 25 30
Ser Glu Asp Leu Arg Leu Arg Ile Ile Glu His Asn Ile Leu Val Val
35 40 45
Ser Lys Tyr Tyr Ala Arg Val Thr Leu Lys Arg Leu Ala Asp Leu Leu
50 55 60

Cys Leu Thr Leu Gln Glu Ala Glu Lys His Leu Ser Asp Met Val Asn
65 70 75 80
Ser Lys Ser Leu Val
85

(2) INFORMATION FOR SEQ ID NO:2707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..302
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2707:

ctcccggctc	agactttctg	tgcagcgctt	ccgycgccgc	cggcgcctat	aacgcaktcc	60
ctccgccgca	gcccgaaggc	agatggttct	ccagaacgac	attgatctgc	kcaacccgcc	120
ggcagaactc	gagaagctca	agcacaagaa	aaagagactc	gtccagtcgc	ccaactcctt	180
cttcctggtg	gttaagtgcc	aggggtgctt	cagcataacc	actgtkttca	gcaactccca	240
gactgctgnt	gkgtnngtca	gaagctatgc	agcggtacgc	gggtacattta	tcgacagtkk	300
tc						

(2) INFORMATION FOR SEQ ID NO:2708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2708:

Pro Gly Ser Asp Phe Cys Cys Ser Ala Ser Xaa Ala Ala Ala Ala Ser	
1 5 10 15	
Asn Ala Xaa Pro Pro Gln Pro Glu Ala Arg Trp Phe Ser Arg Thr	
20 25 30	
Thr Leu Ile Cys Xaa Thr Arg Arg Gln Asn Ser Arg Ser Ser Thr	
35 40 45	
Arg Lys Arg Asp Ser Ser Ser Arg Pro Thr Pro Ser Ser Trp Met Leu	
50 55 60	
Ser Ala Arg Gly Ala Ser Ala	
65 70	

(2) INFORMATION FOR SEQ ID NO:2709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2709:

Met Val Leu Gln Asn Asp Ile Asp Leu Xaa Asn Pro Pro Ala Glu Leu	
1 5 10 15	
Glu Lys Leu Lys His Lys Lys Lys Arg Leu Val Gln Ser Pro Asn Ser	
20 25 30	
Phe Phe Met Asp Val Lys Cys Gln Gly Cys Phe Ser Ile Thr Thr Xaa	

35 40 45
Phe Ser His Ser Gln Thr Ala Xaa Xaa Xaa Val Arg Ser Tyr Ala Ala
50 55 60
Asp Thr Gly Thr Phe Ile Asp Ser
65 70

(2) INFORMATION FOR SEQ ID NO:2710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2710:

Met Asp Val Lys Cys Gln Gly Cys Phe Ser Ile Thr Thr Xaa Phe Ser
1 5 10 15
His Ser Gln Thr Ala Xaa Xaa Xaa Val Arg Ser Tyr Ala Ala Asp Thr
20 25 30
Gly Thr Phe Ile Asp Ser
35

(2) INFORMATION FOR SEQ ID NO:2711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..249
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2711:

accaaggaaa ttcacaaaga gatactagtc cctaccacaaag catacttcct gaaacactct 60
tgcaatccac tgagtcctgt ttgttgagac ttgagacgca tagagctagc gtcgacaatg 120
tcgctcgtga ggcgcmssaa cgtgttcgac cccttctcga tggacctctg ggacccttc 180
gacaccatgt tccgctccat cgtcccgtcg gcggcctcca ccaactccga gaccgcgcgtc 240
ttcgccagc

(2) INFORMATION FOR SEQ ID NO:2712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2712:

Gln Gly Asn Ser Gln Arg Asp Thr Ser Pro Tyr Gln Ser Ile Leu Pro
1 5 10 15
Glu Thr Leu Leu Gln Ser Thr Glu Ser Cys Leu Leu Arg Leu Glu Thr
20 25 30
His Arg Ala Ser Val Asp Asn Val Ala Arg Glu Ala Xaa Xaa Arg Val
35 40 45
Arg Pro Leu Leu Asp Gly Pro Leu Gly Pro Leu Arg His His Val Pro
50 55 60
Leu His Arg Pro Val Gly Gly Leu His Gln Leu Arg Asp Arg Arg Leu

65

70

75

80

Arg Gln

(2) INFORMATION FOR SEQ ID NO:2713:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..44
(D) OTHER INFORMATION: / Ceres Seq. ID 1504313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2713:

Met	Ser	Leu	Val	Arg	Arg	Xaa	Asn	Val	Phe	Asp	Pro	Phe	Ser	Met	Asp
1			5					10					15		
Leu	Trp	Asp	Pro	Phe	Asp	Thr	Met	Phe	Arg	Ser	Ile	Val	Pro	Ser	Ala
			20				25					30			
Ala	Ser	Thr	Asn	Ser	Glu	Thr	Ala	Val	Phe	Ala	Ser				
			35				40								

(2) INFORMATION FOR SEQ ID NO:2714:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 464 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..464
(D) OTHER INFORMATION: / Ceres Seq. ID 1504333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2714:

cagaataaag	ataaaaaata	tggaactgga	aattaggcgt	agggaatcaa	caggatcagg	60
ctctaacaca	tatgttgaaa	ctgagactct	tgcaaatgtt	gagttgatgg	atgggtgctcc	120
tgtgagaggt	gaatctatct	cagtgaggct	gttcttgaca	ccctatgagt	tgaccccgac	180
ttaccgcaac	ataaacaaca	aattcagcgt	caagtattac	ctgaactctg	tccctgtgga	240
cgaggaagat	cggagggtact	tcaagcagca	agagatcaca	atgtaccgtc	tccaagaatc	300
tccccctgcc	tcctagatcc	caacctgttg	catcatgttc	acttctcagg	ttttgtacaa	360
gtggacgctg	aggttagagc	aatgtctctg	atataaacta	aaatccagaa	gagcgccaca	420
gctgggtact	gctatggcca	tgcacgctgc	actgtcgtgt	tcat		

(2) INFORMATION FOR SEQ ID NO:2715:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..104
(D) OTHER INFORMATION: / Ceres Seq. ID 1504334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2715:

Arg	Ile	Lys	Ile	Asn	Met	Glu	Leu	Glu	Ile	Arg	Arg	Glu	Ser
1			5					10				15	
Thr	Gly	Ser	Gly	Ser	Asn	Thr	Tyr	Val	Glu	Thr	Glu	Thr	Ala
			20				25				30		
Phe	Glu	Leu	Met	Asp	Gly	Ala	Pro	Val	Arg	Gly	Glu	Ser	Ile
			35				40				45		
Arg	Leu	Phe	Leu	Thr	Pro	Tyr	Glu	Leu	Thr	Pro	Thr	Tyr	Arg
			50				55				60		

Asn Asn Lys Phe Ser Val Lys Tyr Tyr Leu Asn Leu Val Leu Val Asp
65 70 75 80
Glu Glu Asp Arg Arg Tyr Phe Lys Gln Gln Glu Ile Thr Met Tyr Arg
85 90 95
Leu Gln Glu Ser Pro Pro Ala Ser
100

(2) INFORMATION FOR SEQ ID NO:2716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2716:

Met Glu Leu Glu Ile Arg Arg Arg Glu Ser Thr Gly Ser Gly Ser Asn
1 5 10 15
Thr Tyr Val Glu Thr Glu Thr Leu Ala Lys Phe Glu Leu Met Asp Gly
20 25 30
Ala Pro Val Arg Gly Glu Ser Ile Pro Val Arg Leu Phe Leu Thr Pro
35 40 45
Tyr Glu Leu Thr Pro Thr Tyr Arg Asn Ile Asn Asn Lys Phe Ser Val
50 55 60
Lys Tyr Tyr Leu Asn Leu Val Leu Val Asp Glu Glu Asp Arg Arg Tyr
65 70 75 80
Phe Lys Gln Gln Glu Ile Thr Met Tyr Arg Leu Gln Glu Ser Pro Pro
85 90 95
Ala Ser

(2) INFORMATION FOR SEQ ID NO:2717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2717:

Met Asp Gly Ala Pro Val Arg Gly Glu Ser Ile Pro Val Arg Leu Phe
1 5 10 15
Leu Thr Pro Tyr Glu Leu Thr Pro Thr Tyr Arg Asn Ile Asn Asn Lys
20 25 30
Phe Ser Val Lys Tyr Tyr Leu Asn Leu Val Leu Val Asp Glu Glu Asp
35 40 45
Arg Arg Tyr Phe Lys Gln Gln Glu Ile Thr Met Tyr Arg Leu Gln Glu
50 55 60
Ser Pro Pro Ala Ser
65

(2) INFORMATION FOR SEQ ID NO:2718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..466
(D) OTHER INFORMATION: / Ceres Seq. ID 1504370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2718:

ctactacgccc	tgccctctcca	tcattgtcgt	ggtgatccctc	ctgccctctcg	ccatcgccat	60
ggagggggccc	aaggtgtggg	cggggggctg	gcagacagca	gtcgccgaga	tcgggtcccaa	120
cttcgtctgg	tgggtggcgg	cgcagagcgt	gtttaccac	ctgtacaacc	agggttcccta	180
catgtccctg	gaagagatct	cgccgctcac	ctttcccatc	ggcaaaccca	tgaagcgcat	240
ctccgtcatc	gtcgcgtcca	tcattcatctt	ccagacgccc	gtccagcccca	tcaacgcgct	300
cgggggcgccc	atcgccatcc	tcggaaacctt	catctactcc	caggcccaagc	agtagccgccc	360
cttgsgcgcg	cgtctggctc	tcaggccctca	gttcagtcca	ccgccgaate	agctcgggcgc	420
tcgaagatat	aacagattat	ataacttttt	gaggatattct	acctag		

(2) INFORMATION FOR SEQ ID NO:2719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..143
(D) OTHER INFORMATION: / Ceres Seq. ID 1504371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2719:

Leu	Leu	Arg	Leu	Pro	Leu	His	His	Val	Ala	Gly	Asp	Pro	Pro	Ala	Leu
1			5						10					15	
Arg	His	Arg	His	Gly	Gly	Ala	Gln	Gly	Val	Gly	Gly	Gly	Leu	Ala	Asp
			20					25					30		
Ser	Ser	Arg	Arg	Asp	Arg	Ser	Gln	Leu	Arg	Leu	Val	Gly	Gly	Gly	Ala
		35				40					45				
Glu	Arg	Val	Leu	Pro	Pro	Val	Gln	Pro	Gly	Val	Leu	His	Val	Pro	Gly
		50				55					60				
Arg	Asp	Leu	Ala	Ala	His	Leu	Leu	His	Arg	Gln	His	His	Glu	Ala	His
		65			70					75				80	
Leu	Arg	His	Arg	Arg	Val	His	His	His	Leu	Pro	Asp	Ala	Arg	Pro	Ala
			85					90						95	
His	Gln	Arg	Ala	Arg	Gly	Arg	His	Arg	His	Pro	Arg	Asn	Leu	His	Leu
		100					105						110		
Leu	Pro	Gly	Gln	Ala	Val	Ala	Ala	Leu	Xaa	Arg	Ala	Ser	Gly	Ser	Gln
		115					120					125			
Ala	Ser	Val	Gln	Phe	Thr	Ala	Glu	Ser	Ala	Arg	Arg	Ser	Lys	Ile	
		130					135					140			

(2) INFORMATION FOR SEQ ID NO:2720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..117
(D) OTHER INFORMATION: / Ceres Seq. ID 1504372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2720:

Tyr	Tyr	Ala	Cys	Leu	Ser	Ile	Met	Ser	Leu	Val	Ile	Leu	Leu	Pro	Phe
1			5						10					15	
Ala	Ile	Ala	Met	Glu	Gly	Pro	Lys	Val	Trp	Ala	Ala	Gly	Trp	Gln	Thr
			20				25						30		
Ala	Val	Ala	Glu	Ile	Gly	Pro	Asn	Phe	Val	Trp	Trp	Val	Ala	Ala	Gln
		35					40					45			

Ser Val Phe Tyr His Leu Tyr Asn Gln Val Ser Tyr Met Ser Leu Asp
50 55 60
Glu Ile Ser Pro Leu Thr Phe Ser Ile Gly Asn Thr Met Lys Arg Ile
65 70 75 80
Ser Val Ile Val Ala Ser Ile Ile Ile Phe Gln Thr Pro Val Gln Pro
85 90 95
Ile Asn Ala Leu Gly Ala Ala Ile Ala Ile Leu Gly Thr Phe Ile Tyr
100 105 110
Ser Gln Ala Lys Gln
115

(2) INFORMATION FOR SEQ ID NO:2721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2721:

Met Ser Leu Val Ile Leu Leu Pro Phe Ala Ile Ala Met Glu Gly Pro
1 5 10 15
Lys Val Trp Ala Ala Gly Trp Gln Thr Ala Val Ala Glu Ile Gly Pro
20 25 30
Asn Phe Val Trp Trp Val Ala Ala Gln Ser Val Phe Tyr His Leu Tyr
35 40 45
Asn Gln Val Ser Tyr Met Ser Leu Asp Glu Ile Ser Pro Leu Thr Phe
50 55 60
Ser Ile Gly Asn Thr Met Lys Arg Ile Ser Val Ile Val Ala Ser Ile
65 70 75 80
Ile Ile Phe Gln Thr Pro Val Gln Pro Ile Asn Ala Leu Gly Ala Ala
85 90 95
Ile Ala Ile Leu Gly Thr Phe Ile Tyr Ser Gln Ala Lys Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:2722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..452
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2722:

ttagtgtata tatgttatct ggggacaagg aaagtgtctgc tatgaatgtg gcttcagttg 60
tcggtatcca ggcagacaag gttcttgcgt aagttaaacc acatgagaaa aagaagtcca 120
tatctgaact ccagaagaag cacaaggtag tcgccatggt tggtagcggc attaatgatg 180
ccgcagcact agcttcagct gatgttggaa tcgcaatggg tggaggtgtt ggggcagcta 240
gtgatgtatc ttcagttgta cttatgggca acaggttato ccagcttato gatgctttag 300
agttgagtaa agagaccatg aagacgggtga agcaaatct ttggtgggct ttcctgtata 360
acattgtggg actaccatt gctgctggag cattgcttcc agctacgggg acgatactga 420
caccatcaat agctggagct ctgatgggtt nt

(2) INFORMATION FOR SEQ ID NO:2723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..149
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504375
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2723:
Ser Val Tyr Met Leu Ser Gly Asp Lys Glu Ser Ala Ala Met Asn Val
1 5 10 15
Ala Ser Val Val Gly Ile Gln Ala Asp Lys Val Leu Ala Glu Val Lys
 20 25 30
Pro His Glu Lys Lys Lys Phe Ile Ser Glu Leu Gln Lys Glu His Lys
 35 40 45
Val Val Ala Met Val Gly Asp Gly Ile Asn Asp Ala Ala Leu Ala
50 55 60
Ser Ala Asp Val Gly Ile Ala Met Gly Gly Val Gly Ala Ala Ser
65 70 75 80
Asp Val Ser Ser Val Val Leu Met Gly Asn Arg Leu Ser Gln Leu Ile
 85 90 95
Asp Ala Leu Glu Leu Ser Lys Glu Thr Met Lys Thr Val Lys Gln Asn
 100 105 110
Leu Trp Trp Ala Phe Leu Tyr Asn Ile Val Gly Leu Pro Ile Ala Ala
 115 120
Gly Ala Leu Leu Pro Ala Thr Gly Thr Ile Leu Thr Pro Ser Ile Ala
130 135 140
Gly Ala Leu Met Gly
145

(2) INFORMATION FOR SEQ ID NO:2724:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 146 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..146
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504376
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2724:
Met Leu Ser Gly Asp Lys Glu Ser Ala Ala Met Asn Val Ala Ser Val
1 5 10 15
Val Gly Ile Gln Ala Asp Lys Val Leu Ala Glu Val Lys Pro His Glu
 20 25 30
Lys Lys Lys Phe Ile Ser Glu Leu Gln Lys Glu His Lys Val Val Ala
 35 40 45
Met Val Gly Asp Gly Ile Asn Asp Ala Ala Ala Leu Ala Ser Ala Asp
50 55 60
Val Gly Ile Ala Met Gly Gly Gly Val Gly Ala Ala Ser Asp Val Ser
65 70 75 80
Ser Val Val Leu Met Gly Asn Arg Leu Ser Gln Leu Ile Asp Ala Leu
 85 90 95
Glu Leu Ser Lys Glu Thr Met Lys Thr Val Lys Gln Asn Leu Trp Trp
 100 105 110
Ala Phe Leu Tyr Asn Ile Val Gly Leu Pro Ile Ala Ala Gly Ala Leu
 115 120 125
Leu Pro Ala Thr Gly Thr Ile Leu Thr Pro Ser Ile Ala Gly Ala Leu
130 135 140
Met Gly
145

(2) INFORMATION FOR SEQ ID NO:2725:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..136
(D) OTHER INFORMATION: / Ceres Seq. ID 1504377
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2725:
Met Asn Val Ala Ser Val Val Gly Ile Gln Ala Asp Lys Val Leu Ala
1 5 10 15
Glu Val Lys Pro His Glu Lys Lys Lys Phe Ile Ser Glu Leu Gln Lys
20 25 30
Glu His Lys Val Val Ala Met Val Gly Asp Gly Ile Asn Asp Ala Ala
35 40 45
Ala Leu Ala Ser Ala Asp Val Gly Ile Ala Met Gly Gly Val Gly
50 55 60
Ala Ala Ser Asp Val Ser Ser Val Val Leu Met Gly Asn Arg Leu Ser
65 70 75 80
Gln Leu Ile Asp Ala Leu Glu Leu Ser Lys Glu Thr Met Lys Thr Val
85 90 95
Lys Gln Asn Leu Trp Trp Ala Phe Leu Tyr Asn Ile Val Gly Leu Pro
100 105 110
Ile Ala Ala Gly Ala Leu Leu Pro Ala Thr Gly Thr Ile Leu Thr Pro
115 120 125
Ser Ile Ala Gly Ala Leu Met Gly
130 135

(2) INFORMATION FOR SEQ ID NO:2726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..440
(D) OTHER INFORMATION: / Ceres Seq. ID 1504382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2726:

accacaccca ccccaagaaa ccgtaagaag cgcagagtgt gagagagaga ggagcatcaa 60
ggacgacgtg ggcaagatga tgcaggtgtt cgtgaagacg ctggcgggga agacgatcac 120
gctggagagtg gaggcgacgc acgacgcgcgt nagaacgtga aggccatgat ccagggcaag 180
gaaggcatcc cgcgcggagga gcagcgcctc gtcttcgagg gcaagcagct ggacgacgac 240
ggccgcaccc tggccgacta cggcgtccag aaggagtoga cgctgcacct ggagctgcgc 300
ctccgcggcg gcagcagggg cggctacccc atgggatccc gccacgctc cgcgagctcg 360
gcgagaagta caacgagaac aagatggtct gccgcaagtg ctatgcgcgg cttccgccta 420
gggcaaccaa ctgccgcaag

(2) INFORMATION FOR SEQ ID NO:2727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..52
(D) OTHER INFORMATION: / Ceres Seq. ID 1504383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2727:

Pro His Pro Pro His Glu Thr Val Arg Ser Ala Glu Cys Glu Arg Glu

1 5 10 15
Arg Ser Ile Lys Asp Asp Val Gly Lys Met Met Gln Val Phe Val Lys
20 25 30
Thr Leu Ala Gly Lys Thr Ile Thr Leu Glu Val Glu Gly Ser Asp Asp
35 40 45
Ala Xaa Arg Thr
50

(2) INFORMATION FOR SEQ ID NO:2728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2728:

Met Ile Gln Gly Lys Glu Gly Ile Pro Pro Glu Glu Gln Arg Leu Val
1 5 10 15
Phe Ala Gly Lys Gln Leu Asp Asp Asp Gly Arg Thr Leu Ala Axc Tyr
20 25 30
Gly Val Gln Lys Glu Ser Thr Leu His Leu Glu Leu Arg Leu Arg Gly
35 40 45
Gly Ser Arg Gly Gly Tyr Pro Met Gly Ser Arg Pro Ala Ser Ala Ser
50 55 60
Ser Arg Arg Ser Thr Thr Arg Thr Arg Trp Ser Ala Ala Ser Ala Met
65 70 75 80
Arg Gly Phe Arg Leu Gly Gln Pro Thr Ala Ala
85 90

(2) INFORMATION FOR SEQ ID NO:2729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..234
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2729:

acatcgggaa gcgcgcgcgac gccgcagagg agacgcacgc aggttagcac gcgaagaagc 60
gaccatgagg gccagtggga agaagaagcgc catnaggagg ctcaagagga akcgcagaaa 120
gatgaggcag agatccaagt aggcagatcgc agatggattg tggacctgcac tctcttcggt 180
atatgtacta cctccgttct tgaatatatt taaatatatt tcggtgtcgt cggt

(2) INFORMATION FOR SEQ ID NO:2730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2730:

Thr Ser Gly Thr Pro Pro Thr Pro Gln Arg Arg Arg Ile Glu Val Ser
1 5 10 15

Thr Arg Arg Ser Asp His Glu Gly Gln Val Glu Glu Glu Ala His Xaa
20 25 30
Glu Ala Gln Glu Glu Xaa Gln Lys Asp Glu Ala Glu Ile Gln Val Gly
35 40 45
Arg Ser Arg Trp Ile Val Asp Leu Thr Leu Phe Val Ile Cys Thr Thr
50 55 60
Ser Val Leu Glu Tyr Phe
65 70

(2) INFORMATION FOR SEQ ID NO:2731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2731:

His Arg Glu Arg Arg Arg Arg Arg Arg Gly Asp Ala Ser Arg Leu Ala
1 5 10 15
Arg Glu Glu Ala Thr Met Arg Ala Lys Trp Lys Lys Lys Arg Xaa Arg
20 25 30
Arg Leu Lys Arg Xaa Arg Arg Lys Met Arg Gln Arg Ser Lys
35 40 45

(2) INFORMATION FOR SEQ ID NO:2732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..474
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2732:

cccagttgat gtggttaagt cgagaatgat ggggtgactca gcctacaaaa gcactctcga 60
ttgtttttgtg aagactctaa agaattgatgg cccctttggca ttttacaaag gcttctctgcc 120
aaactttgca agactgggat ctgtggaatgt gattatgttc ttgacattgg agcaggttca 180
aaagctgttt gtgaggaagg cgacaagctg aagatagagt ttttgcagtc aggtggcgta 240
caattgacgc acaggtgttt tcttctatag acaaaaagggg agaaatgaca cctcccctct 300
cgagaattgg ggaacaagga cagatctgac acctcaattg cgagaataaa aaataacagc 360
cgacagttgc atgatccctg aacgaataaa ttcagaacta gaaacagatg tcagtaacaa 420
acatgtgggtg aatgtttggaa cttgactgct ctagtctcagt gggcatctgt tggt

(2) INFORMATION FOR SEQ ID NO:2733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2733:

Pro Val Asp Val Val Lys Ser Arg Met Met Gly Asp Ser Ala Tyr Lys
1 5 10 15
Ser Thr Leu Asp Cys Phe Val Lys Thr Leu Lys Asn Asp Gly Pro Leu

	20		25		30										
Ala	Phe	Tyr	Lys	Gly	Phe	Leu	Pro	Asn	Phe	Ala	Arg	Leu	Gly	Ser	Trp
	35						40						45		
Asn	Val	Ile	Met	Phe	Leu	Thr	Leu	Glu	Gln	Val	Gln	Lys	Leu	Phe	Val
	50					55							60		
Arg	Lys	Ala	Thr	Ser											

65

(2) INFORMATION FOR SEQ ID NO:2734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61

(D) OTHER INFORMATION: / Ceres Seq. ID 1504402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2734:

Met	Met	Gly	Asp	Ser	Ala	Tyr	Lys	Ser	Thr	Leu	Asp	Cys	Phe	Val	Lys
1			5						10				15		
Thr	Leu	Lys	Asn	Asp	Gly	Pro	Leu	Ala	Phe	Tyr	Lys	Gly	Phe	Leu	Pro
		20				25						30			
Asn	Phe	Ala	Arg	Leu	Gly	Ser	Trp	Asn	Val	Ile	Met	Phe	Leu	Thr	Leu
		35				40					45				
Glu	Gln	Val	Gln	Lys	Leu	Phe	Val	Arg	Lys	Ala	Thr	Ser			
	50				55						60				

(2) INFORMATION FOR SEQ ID NO:2735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1504403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2735:

Met	Gly	Asp	Ser	Ala	Tyr	Lys	Ser	Thr	Leu	Asp	Cys	Phe	Val	Lys	Thr
1			5						10				15		
Leu	Lys	Asn	Asp	Gly	Pro	Leu	Ala	Phe	Tyr	Lys	Gly	Phe	Leu	Pro	Asn
		20				25						30			
Phe	Ala	Arg	Leu	Gly	Ser	Trp	Asn	Val	Ile	Met	Phe	Leu	Thr	Leu	Glu
		35				40					45				
Gln	Val	Gln	Lys	Leu	Phe	Val	Arg	Lys	Ala	Thr	Ser				
	50				55						60				